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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:30:23 ; Search time 120.706 Seconds  
(without alignments)  
31.079 Million cell updates/sec

Title: US-09-214-371-11  
Perfect score: 24  
Sequence: 1 XFXXXWXXX 9

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 1860064 seqs, 416830855 residues

Total number of hits satisfying chosen parameters: 1860064

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

SUMMARIES

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3	17	70.8	8	18	US-10-818-036-28 Sequence 28, Appl
4	17	70.8	8	18	US-10-818-036-30 Sequence 30, Appl
5	17	70.8	9	14	US-10-072-419-3 Sequence 3, Appli
6	17	70.8	9	16	US-10-869-768-3 Sequence 8, Appli
7	17	70.8	9	16	US-10-869-768-8 Sequence 3, Appli
8	17	70.8	9	16	US-10-869-768-8 Sequence 8, Appli
9	17	70.8	9	18	US-10-818-036-14 Sequence 14, Appl
10	17	70.8	9	18	US-10-818-036-15 Sequence 15, Appl
11	17	70.8	9	18	US-10-818-036-23 Sequence 23, Appl

12	17	70.8	9	18	US-10-818-036-25 Sequence 25, Appl
13	17	70.8	9	18	US-10-818-036-26 Sequence 26, Appl
14	17	70.8	9	18	US-10-818-036-29 Sequence 29, Appl
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; GENERAL INFORMATION:						
; APPLICANT: Schacter, Bernice Z						
; APPLICANT: Schacter, Lee P.						
; APPLICANT: Zeldin, Michael H.						
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM						
; FILE REFERENCE: 303544.3000-100						
; CURRENT APPLICATION NUMBER: US/10/818,036						
; CURRENT FILING DATE: 2004-04-05						
; NUMBER OF SEQ ID NOS: 38						
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; GENERAL INFORMATION:						
; APPLICANT: Schacter, Bernice Z						
; APPLICANT: Schacter, Lee P.						
; APPLICANT: Zeldin, Michael H.						
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM						
; FILE REFERENCE: 303544.3000-100						
; CURRENT APPLICATION NUMBER: US/10/818,036						
; CURRENT FILING DATE: 2004-04-05						
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; GENERAL INFORMATION:						
; APPLICANT: Schacter, Bernice Z						
; APPLICANT: Schacter, Lee P.						
; APPLICANT: Zeldin, Michael H.						
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM						
; FILE REFERENCE: 303544.3000-100						
; CURRENT APPLICATION NUMBER: US/10/818,036						
; CURRENT FILING DATE: 2004-04-05						
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; APPLICANT: Schacter, Bernice Z						
; APPLICANT: Schacter, Lee P.						
; APPLICANT: Zeldin, Michael H.						
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; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
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; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Huma
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
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; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Vanessa cardui
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; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Huma
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/869,768
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; Publication No. US20040224898A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Huma
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/869,768
; CURRENT FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: US 10/072,419
; PRIOR FILING DATE: 2002-02-07
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QY 2 FXXXW 6
Db 4 FTSSW 8
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; Sequence 14, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
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; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice Z  
; APPLICANT: Schacter, Lee P.  
; APPLICANT: Zeldin, Michael H.  
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM  
; FILE REFERENCE: 303544.3000-100  
; CURRENT APPLICATION NUMBER: US/10/818,036  
; CURRENT FILING DATE: 2004-04-05  
; NUMBER OF SEQ ID NOS: 38  
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US-10-818-036-15

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; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice Z  
; APPLICANT: Schacter, Lee P.  
; APPLICANT: Zeldin, Michael H.  
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM  
; FILE REFERENCE: 303544.3000-100  
; CURRENT APPLICATION NUMBER: US/10/818,036  
; CURRENT FILING DATE: 2004-04-05  
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; APPLICANT: Schacter, Bernice Z  
; APPLICANT: Schacter, Lee P.  
; APPLICANT: Zeldin, Michael H.  
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM  
; FILE REFERENCE: 303544.3000-100  
; CURRENT APPLICATION NUMBER: US/10/818,036  
; CURRENT FILING DATE: 2004-04-05  
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; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice Z  
; APPLICANT: Schacter, Lee P.  
; APPLICANT: Zeldin, Michael H.  
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM  
; FILE REFERENCE: 303544.3000-100  
; CURRENT APPLICATION NUMBER: US/10/818,036  
; CURRENT FILING DATE: 2004-04-05  
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US-10-818-036-26

Query Match 70.8%; Score 17; DB 18; Length 9;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
Db 4 FTASW 8

RESULT 14  
US-10-818-036-29  
; Sequence 29, Application US/10818036  
; Publication No. US20050222040A1  
; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice Z  
; APPLICANT: Schacter, Lee P.  
; APPLICANT: Zeldin, Michael H.

```

; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: AMIDATION
; US-10-818-036-29

Query Match          70.8%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
Db      4 FTASW 8

RESULT 15
US-09-842-776A-28
; Sequence 28, Application US/09842776A
; Publication No. US20040023316A1
; GENERAL INFORMATION:
; APPLICANT: CONNEX GMBH
; TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS
; TITLE OF INVENTION: IN THE STOOL
; FILE REFERENCE: 41735
; CURRENT APPLICATION NUMBER: US/09/842,776A
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/EP99/08212
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Complementarity determining region (CDR1) of an
; OTHER INFORMATION: antibody heavy chain directed to a beta-urease
; OTHER INFORMATION: epitope (alternative sequence)
; US-09-842-776A-28

Query Match          70.8%; Score 17; DB 11; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
Db      4 FSTSW 8

RESULT 16
US-10-996-316-139
; Sequence 139, Application US/10996316
; Publication No. US20050129690A1
; GENERAL INFORMATION:
; APPLICANT: Alexion Pharmaceuticals, Inc.
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: McWhirter, John
; APPLICANT: Kretz-Rommel, Anke
```

```

; TITLE OF INVENTION: POLYPEPTIDES AND ANTIBODIES DERIVED FROM CHRONIC LYMPHOCYTIC
; TITLE OF INVENTION: LEUKEMIA CELLS AND USES THEREOF
; FILE REFERENCE: 60 CIP IV (1087-43 CIP IV)
; CURRENT APPLICATION NUMBER: US/10/996,316
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: US 10/894,672
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 10/736,188
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/379,151
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: PCT/US01/47931
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/254,113
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 139
; LENGTH: 10
; TYPE: PRT
; ORGANISM: murine
; US-10-996-316-139

Query Match          70.8%; Score 17; DB 18; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
Db      4 FSAAW 8

RESULT 17
US-10-072-419-37
; Sequence 37, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Vanessa cardui
; US-10-072-419-37

Query Match          70.8%; Score 17; DB 14; Length 11;
Best Local Similarity 40.0%; Pred. No. 6.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
Db      4 FTSSW 8

RESULT 18
US-10-869-768-37
; Sequence 37, Application US/10869768
; Publication No. US20040224898A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/869,768
; CURRENT FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: US 10/072,419
; PRIOR FILING DATE: 2002-02-07
```

```
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Vanessa cardui
US-10-869-768-37

Query Match      70.8%; Score 17; DB 16; Length 11;
Best Local Similarity 40.0%; Pred. No. 6.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXW 6
Db      4 FTSSW 8

RESULT 19
US-10-354-240-87
; Sequence 87, Application US/10354240
; Publication No. US20030185847A1
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Iwama, Akiko
; APPLICANT: Kino, Kohsuke
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease
; FILE REFERENCE: SPO 103D1
; CURRENT APPLICATION NUMBER: US/10/354,240
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: PCT/JP97/00740
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 09/142,524
; PRIOR FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria japonica
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(15)
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 4
US-10-354-240-87

Query Match      70.8%; Score 17; DB 14; Length 15;
Best Local Similarity 40.0%; Pred. No. 8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXW 6
Db      9 FTAW 13

RESULT 20
US-10-354-240-88
; Sequence 88, Application US/10354240
; Publication No. US20030185847A1
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Iwama, Akiko
; APPLICANT: Kino, Kohsuke
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease
; FILE REFERENCE: SPO-103D1
; CURRENT APPLICATION NUMBER: US/10/354,240
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: PCT/JP97/00740
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 09/142,524
```

```
; PRIOR FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria japonica
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(15)
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 5
US-10-354-240-88

Query Match      70.8%; Score 17; DB 14; Length 15;
Best Local Similarity 40.0%; Pred. No. 8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXW 6
Db      4 FTAW 8

RESULT 21
US-09-963-339-10
; Sequence 10, Application US/09963339
; Publication No. US20030049700A1
; GENERAL INFORMATION:
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: 22108 AND 47916, NOVEL HUMAN THIOREDOXIN
; TITLE OF INVENTION: FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-090001
; CURRENT APPLICATION NUMBER: US/09/963,339
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/235,049
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-963-339-10

Query Match      70.8%; Score 17; DB 10; Length 19;
Best Local Similarity 40.0%; Pred. No. 9.3e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXW 6
Db      4 FSATW 8

RESULT 22
US-10-145-586-59
; Sequence 59, Application US/10145586
; Publication No. US20030138890A1
; GENERAL INFORMATION:
; APPLICANT: Alexandra Glucksmann, Maria
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: M. Galvin, Katherine
; APPLICANT: Weich, Nadine
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Bandaru, Rajasekhar
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS.
; TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LEUCINE-RICH
; TITLE OF INVENTION: REPEAT FAMILY MEMBERS, AND HUMAN RINGFINGER FAMILY MEMBER
; FILE REFERENCE: 10448-188001
; CURRENT APPLICATION NUMBER: US/10/145,586
; CURRENT FILING DATE: 2002-05-14
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 59  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-145-586-59

Query Match 70.8%; Score 17; DB 14; Length 19;  
Best Local Similarity 40.0%; Pred. No. 9.3e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
| |  
Db 4 FSATW 8

RESULT 23

US-10-931-260-265  
; Sequence 265, Application US/10931260  
; Publication No. US20050152927A1

GENERAL INFORMATION:

APPLICANT: Griffith, Irwin J.;  
Pollock, Joanne;  
Bond, Julian F.;  
Garman, Richard D;  
Kuo, Mei-Chang;  
Powers, Stephen P.;  
Exley, Mark A.;  
Chen, Xian;  
Shaked, Ze'ev

TITLE OF INVENTION: Allergenic Proteins And Peptides From  
Japanese Cedar Pollen

NUMBER OF SEQUENCES: 283

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lahive & Cockfield, LLP  
STREET: 28 State St  
CITY: Boston  
STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/931,260

FILING DATE: 30-Aug-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/240,203

FILING DATE: 29-Jan-1999

APPLICATION NUMBER: 08/467,023

FILING DATE: 1995-JUN-06

APPLICATION NUMBER: 08/350,225

FILING DATE: 1994-DEC-06

APPLICATION NUMBER: 08/226,248

FILING DATE: 1994-APR-08

APPLICATION NUMBER: PCT/US93/00139

FILING DATE: 1993-JAN-15

APPLICATION NUMBER: 07/938,990

FILING DATE: 1992-SEP-01

APPLICATION NUMBER: 07/730,452

FILING DATE: 1991-JUL-15

APPLICATION NUMBER: 07/729,134

FILING DATE: 1991-JUL-12

APPLICATION NUMBER: 07/975,179

FILING DATE: 1992-NOV-12

APPLICATION NUMBER: PCT/US92/05661

FILING DATE: 1992-JUL-10

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras, Esq.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IMI-028CD2CCPA2

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 742-4214

; INFORMATION FOR SEQ ID NO: 265:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal

; SEQUENCE DESCRIPTION: SEQ ID NO: 265:

US-10-931-260-265

Query Match 70.8%; Score 17; DB 18; Length 20;  
Best Local Similarity 40.0%; Pred. No. 9.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6

| |

Db 12 FSTAW 16

RESULT 24

US-10-931-260-264

; Sequence 264, Application US/10931260

; Publication No. US20050152927A1

GENERAL INFORMATION:

APPLICANT: Griffith, Irwin J.;

Pollock, Joanne;

Bond, Julian F.;

Garman, Richard D;

Kuo, Mei-Chang;

Powers, Stephen P.;

Exley, Mark A.;

Chen, Xian;

Shaked, Ze'ev

TITLE OF INVENTION: Allergenic Proteins And Peptides From

Japanese Cedar Pollen

NUMBER OF SEQUENCES: 283

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lahive & Cockfield, LLP

STREET: 28 State St

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/931,260

FILING DATE: 30-Aug-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/240,203

FILING DATE: 29-Jan-1999

APPLICATION NUMBER: 08/467,023

FILING DATE: 1995-JUN-06

APPLICATION NUMBER: 08/350,225

FILING DATE: 1994-DEC-06

APPLICATION NUMBER: 08/226,248

FILING DATE: 1994-APR-08

APPLICATION NUMBER: PCT/US93/00139

FILING DATE: 1993-JAN-15

APPLICATION NUMBER: 07/938,990

FILING DATE: 1992-SEP-01

APPLICATION NUMBER: 07/730,452

FILING DATE: 1991-JUL-15

APPLICATION NUMBER: 07/729,134

FILING DATE: 1991-JUL-12

APPLICATION NUMBER: 07/975,179

; FILING DATE: 1992-NOV-12
; APPLICATION NUMBER: PCT/US92/05661
; FILING DATE: 1992-JUL-10
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras, Esq.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IM1-028CD2CCPA2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 264:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 264:
US-10-931-260-264

Query Match 70.8%; Score 17; DB 18; Length 24;
Best Local Similarity 40.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 12 FSTAW 16

RESULT 25
US-10-338-777-404
; Sequence 404, Application US/10338777
; Publication No. US20030188343A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: United States Department of Agriculture
; APPLICANT: Bowen, Benjamin A
; APPLICANT: Haudenschild, Christian D
; APPLICANT: Buckler, Edward S
; TITLE OF INVENTION: Identification of Genes Associated with Growth in Plants
; FILE REFERENCE: 37-000510US
; CURRENT APPLICATION NUMBER: US/10/338,777
; CURRENT FILING DATE: 2003-01-07
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 404
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: example conservative variation of residues 2-26 of SEQ ID NO:31
US-10-338-777-404

Query Match 70.8%; Score 17; DB 14; Length 25;
Best Local Similarity 40.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 20 FAASW 24

RESULT 26
US-09-864-761-46828
; Sequence 46828, Application US/09864761
; Patent No. US 2002-044761A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wansheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENE EXPRESSION ANALYSIS BY MICROARRAY

; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 46828
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007739.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.62
; OTHER INFORMATION: EXPRESSED IN HEILA, SIGNAL = 0.66
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.68
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.61
US-09-864-761-46828

Query Match 70.8%; Score 17; DB 9; Length 27;
Best Local Similarity 40.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 4 FSATW 8

RESULT 27
US-08-424-550B-428
; Sequence 428, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY



APPLICANT: ANTHONY SCOTT MUERHOFF  
APPLICANT: JAMES C. ERKER  
APPLICANT: SHERI L. BUIJK  
APPLICANT: ISA K. MUSHAWAR  
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
REAGENTS AND METHODS FOR THEIR USE  
NUMBER OF SEQUENCES: 716  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
STREET: 100 ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/424,550B  
FILING DATE:  
CLASSIFICATION: 435435  
ATTORNEY/AGENT INFORMATION:  
NAME: POREMSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5527.PC.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 428:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-424-550B-428

Query Match 70.8%; Score 17; DB 8; Length 29;  
Best Local Similarity 40.0%; Pred. No. 1.2e+04;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 12 FASAW 16

RESULT 29  
US-10-424-599-160512  
; Sequence 160512, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 160512  
; LENGTH: 32  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_115960C.1.pap  
US-10-424-599-160512

Query Match 70.8%; Score 17; DB 15; Length 32;  
Best Local Similarity 40.0%; Pred. No. 1.3e+04;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 18 FTASW 22

RESULT 29  
US-10-032-201B-157  
; Sequence 157, Application US/10032201B  
; Publication No. US20030167524A1  
; GENERAL INFORMATION:  
; APPLICANT: Van Rooijen, Gijb  
; APPLICANT: Deckers, Harm  
; APPLICANT: Heifetz, Peter Bernard  
; APPLICANT: Briggs, Steven  
; APPLICANT: Dalmia, Bipin Kumar  
; APPLICANT: Del Val, Greg  
; APPLICANT: Zaplachinski, Steve  
; APPLICANT: Moloney, Maurice  
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED  
; TITLE OF INVENTION: COMPOSITIONS  
; FILE REFERENCE: 38814 351B  
; CURRENT APPLICATION NUMBER: US/10/032,201B  
; CURRENT FILING DATE: 2001-12-19  
; NUMBER OF SEQ ID NOS: 313  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 157  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Sus scrofa  
US-10-032-201B-157

Query Match 70.8%; Score 17; DB 14; Length 33;  
Best Local Similarity 40.0%; Pred. No. 1.3e+04;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 26 FSATW 30

RESULT 30  
US-10-029-386-28347  
; Sequence 28347, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G.  
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 28347  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AL133499.1  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.45  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.55  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.46  
; OTHER INFORMATION: SWISSPROT HIT: Q03368, EVALUATION 8.60e+00  
US-10-029-386-28347

Query Match 70.8%; Score 17; DB 14; Length 33;  
Best Local Similarity 40.0%; Pred. No. 1.3e+04;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6



```
; NAME: Zeller, James P.
; REGISTRATION NUMBER: 28,491
; REFERENCE/DOCKET NUMBER: 29473/35678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-193-795-10

Query Match 70.8%; Score 17; DB 14; Length 37;
Best Local Similarity 40.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
Db 11 FSASW 15

RESULT 34
US-10-962-760-10
; Sequence 10, Application US/10962760
; Publication No. US2005014359A1
; GENERAL INFORMATION:
; APPLICANT: Flohe, Leopold
; Nogeceke, Everson
; Kalisz, Henryk
; Montemartini, Marisa
; TITLE OF INVENTION: TRYPAEDOXIN, EXPRESSION PLASMID, PROCESS OF
; PRODUCTION, METHOD OF USE, TEST KIT, AND
; PHARMACEUTICAL COMPOSITION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Brown
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/962,760
; FILING DATE: 12-Oct-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP97/06983
; FILING DATE: 12-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, James P.
; REGISTRATION NUMBER: 28,491
; REFERENCE/DOCKET NUMBER: 29473/35678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-962-760-10

Query Match 70.8%; Score 17; DB 18; Length 37;
Best Local Similarity 40.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
Db 11 FSASW 15

RESULT 35
US-10-818-036-1
; Sequence 1, Application US/10818036
; Publication No. US2005022040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Search sequence
US-10-818-036-1

Query Match 70.8%; Score 17; DB 18; Length 37;
Best Local Similarity 40.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
Db 32 FTASW 36

RESULT 36
US-09-892-877-347
; Sequence 347, Application US/09892877
; Publication No. US20030077809A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et. al.
; TITLE OF INVENTION: 97 Human secreted proteins
; FILE REFERENCE: PZ028P1
; CURRENT APPLICATION NUMBER: US/09/892,877
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/437,658
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 347
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-892-877-347

Query Match 70.8%; Score 17; DB 10; Length 38;
Best Local Similarity 40.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6
Db 19 FAAAW 23
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RESULT 37  
US-09-948-783 87  
; Sequence 287, Application US/09948783  
; Publication No. US20030100051A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et. al.  
; TITLE OF INVENTION: 97 Human secreted proteins  
; FILE REFERENCE: P2028P2  
; CURRENT FILING DATE: 2001-03-10  
; PRIOR APPLICATION NUMBER: US/09/948,783  
; PRIOR FILING DATE: 2000-09-11  
; PRIOR APPLICATION NUMBER: 60/231,846  
; PRIOR FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: 09/892,877  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: 09/437,658  
; PRIOR FILING DATE: 1999-05-06  
; PRIOR APPLICATION NUMBER: PCT/US99/09847  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: 60/085,093  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: 60/085,094  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: 60/085,105  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: 60/085,180  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: 60/085,927  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,906  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,924  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,922  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,921  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,923  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,925  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,928  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,920  
; PRIOR FILING DATE: 1998-05-18  
; NUMBER OF SEQ ID NOS: 465  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 287  
; LENGTH: 38  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-948-783-287  
  
Query Match 70.8%; Score 17; DB 10; Length 38;  
Best Local Similarity 40.0%; Pred. No. 1.4e+04;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 2 FXXXW 6  
Db 9 AAAW 33  
  
RESULT 38  
US-09-057-951-6  
; Sequence 6, Application US/09057951  
; Patent No. US20020025551A1  
; GENERAL INFORMATION:  
; APPLICANT: Holtzman, Douglas  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE T129-RELATED  
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/057,951  
; FILING DATE: 09-APR-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D., Anita L.  
; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 09404/046001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 40 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-057-951-6  
  
Query Match 70.8%; Score 17; DB 9; Length 40;  
Best Local Similarity 40.0%; Pred. No. 1.5e+04;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 2 FXXXW 6  
Db 6 FSAW 10  
  
RESULT 39  
US-09-864-761-46093  
; Sequence 46093, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aeomica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 46093
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AF233390.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.3
; US-09-864-761-46093

Query Match 70.8%; Score 17; DB 9; Length 40;
Best Local Similarity 40.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 23 FTSSW 27

RESULT 40
US-10-105-150-6
; Sequence 6, Application US/10105150
; Publication No. US20020119524A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas
; TITLE OF INVENTION: NOVEL MOLECULES OF THE T129-RELATED
; PROTEIN FAMILY AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/105,150
; FILING DATE: 25-Mar-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/057,951
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 09404/046001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906

; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-105-150-6

Query Match 70.8%; Score 17; DB 13; Length 40;
Best Local Similarity 40.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6
Db 6 FSAW 10

Search completed: October 18, 2005, 15:50:34
Job time : 120.706 secs

*This Page Blank (uspto)*



GenCore version 5.1.6  
Copyright: (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 18, 2005, 15:17:40 ; Search time 123.353 Seconds  
(without alignments)  
37.362 Million cell updates/sec

Title: US-09-214-371-11  
Perfect score: 24  
Sequence: 1 XFXXXWXXX 9

Scoring table: BLOSUM62  
Gapop 10.0 ; Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : UniProt\_03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	70.8	9	1 AKH HELZE	P67787 heliothis z
2	17	70.8	13	2 Q9XLI2	Q9xli2 bemisia tab
3	17	70.8	26	2 Q9S880	Q9s880 spinacia ol
4	17	70.8	29	2 Q7RQ81	Q7rq81 plasmodium
5	17	70.8	32	2 O05602	O05602 pseudomonas
6	17	70.8	35	2 Q72FN9	Q72fn9 desulfovibr
7	17	70.8	36	2 Q9PV61	Q9pv61 mola mola (
8	17	70.8	38	1 PSAL PROMA	Q87786 prochlorococ
9	17	70.8	38	2 Q7U4F1	Q7u4f1 synchrococc
10	17	70.8	38	2 Q7V513	Q7v513 prochlorococ
11	17	70.8	38	2 Q9PV63	Q9pv63 pseudopleur
12	17	70.8	40	2 Q9PT24	Q9pt24 oncorhynchu
13	17	70.8	40	2 Q9PT28	Q9pt28 salarias sp
14	17	70.8	40	2 Q9PT29	Q9pt29 epinephelus
15	17	70.8	40	2 Q9PU00	Q9pu00 dicentrarch
16	17	70.8	40	2 Q9PU01	Q9pu01 dendrochiru
17	17	70.8	40	2 Q9PU02	Q9pu02 zeus faber
18	17	70.8	40	2 Q9PU03	Q9pu03 sargocentro
19	17	70.8	40	2 Q9PU04	Q9pu04 fundulus he
20	17	70.8	40	2 Q9PU05	Q9pu05 hemiramphus
21	17	70.8	40	2 Q9PU06	Q9pu06 lampris sp.
22	17	70.8	40	2 Q9PV62	Q9pv62 ostracion s
23	17	70.8	40	2 Q9PV64	Q9pv64 channa sp.
24	17	70.8	40	2 Q9PV65	Q9pv65 colisa lali
25	17	70.8	40	2 Q9PV66	Q9pv66 stromateus
26	17	70.8	40	2 Q9PV68	Q9pv68 acanthurus
27	17	70.8	40	2 Q9PV69	Q9pv69 cryptocentr
28	17	70.8	40	2 Q9PV70	Q9pv70 dissostichu
29	17	70.8	40	2 Q9PV71	Q9pv71 mullus sp.
30	17	70.8	40	2 Q9PV72	Q9pv72 lates calca
31	17	70.8	40	2 Q9PV73	Q9pv73 mastacemba

ALIGNMENTS

RESULT 1  
AKH\_HELZE STANDARD; PRT; 9 AA.  
AC P67787; P08901;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 25-OCT-2004 (Rel. 45, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Adipokinetic hormone (Hez-AKH).  
OS Heliothis zea (Corn earworm) (Bollworm).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;  
OC Noctuidae; Heliothinae; Helicoverpa.  
OX NCBI\_TaxID=7113;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=86186794; PubMed=3964263;  
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Holman G.M.,  
RA Wagner R.M., Ridgway R.L., Hayes D.K.;  
RT "Isolation and primary structure of a peptide from the corpora  
cardiaca of Heliothis zea with adipokinetic activity.";  
RL Biochem. Biophys. Res. Commun. 135:622-628(1986).  
CC -1- FUNCTION: This hormone, released from cells in the corpora  
cardiaca after the beginning of flight, causes release of  
diglycerides from the fat body and then stimulates the flight  
muscles to use these diglycerides as an energy source.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.  
DR PIR; A24244; A24244.  
DR InterPro; IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
KW Amidation; Direct protein sequencing; Flight; Neuropeptide;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 Pyrrolidone carboxylic acid.  
FT MOD\_RES 9 9 Glycine amide.  
SQ SEQUENCE 9 AA; 1026 MW; 403665A5A1A9D1A7 CRC64;  
  
Query Match 70.8%; Score 17; DB 1; Length 9;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXW 6  
| |  
Db 4 FTSSW 8  
  
RESULT 2  
Q9XLI2 PRELIMINARY; PRT; 13 AA.  
AC Q9XLI2;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome oxidase I (Fragment).  
OS Bemisia tabaci (Sweetpotato whitefly).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aleyrodiformes;  
OC Aleyrodioidea; Aleyrodidae; Aleyrodinae; Bemisia.  
OX NCBI\_TaxID=7038;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=10583831;  
RA Frohlich D.R., Torres-Jerez I., Bedford I.D., Markham P.G.,  
RA Brown J.K.;  
RT "A phylogeographical analysis of the Bemisia tabaci species complex  
based on mitochondrial DNA markers.";  
RL Mol. Ecol. 8:1683-1691(1999).  
DR EMBL; AF110703; AAD28415.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 1 1  
SQ SEQUENCE 13 AA; 1639 MW; 8DD68729F5744365 CRC64;

Query Match 70.8%; Score 17; DB 2; Length 13;  
Best Local Similarity 40.0%; Pred. No. 2.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXW 6  
| |  
Db 3 FTSSW 7  
  
RESULT 3  
Q9S880 PRELIMINARY; PRT; 26 AA.  
AC Q9S880;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Thioredoxin H2 (Fragment).  
OS Spinacia oleracea (Spinach).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllales; Amaranthaceae; Spinacia.  
OX NCBI\_TaxID=3562;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=91378382; PubMed=1897989;  
RA Marcus F., Chamberlain S.H., Chu C., Masiarz F.R., Shin S., Yee B.C.,  
RA Buchanan B.B.;  
RT "Plant thioredoxin h: an animal-like thioredoxin occurring in multiple  
cell compartments.";  
RL Arch. Biochem. Biophys. 287:195-198(1991).  
DR GO; GO:0005489; F:electron transporter activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR InterPro; IPR006662; Thiored.  
DR InterPro; IPR006663; Thioredoxin\_dom2.  
DR Pfam; PF00085; Thioredoxin; 1.  
DR PRINTS; PR00421; THIOREDOXIN.  
DR PROSITE; PS00194; THIOREDOXIN; 1.  
KW Redox-active center.  
FT NON\_TER 1 1  
FT NON\_TER 26 26  
SQ SEQUENCE 26 AA; 2880 MW; A5317FC47DDB8863 CRC64;  
  
Query Match 70.8%; Score 17; DB 2; Length 26;  
Best Local Similarity 40.0%; Pred. No. 4.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXW 6  
| |  
Db 6 FTASW 10  
  
RESULT 4  
Q7RQ81 PRELIMINARY; PRT; 29 AA.  
AC Q7RQ81;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
GN Name=PY01221;  
OS Plasmodium yoelii yoelii.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=73239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=17XNL;  
RX PubMed=12368865; DOI=10.1038/nature01099;  
RA Carlton J.M., Anguoli S., Suh B.B., Kooij T.W., Perte M.,  
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,  
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,  
RA Shallom S.J., van Aken S.B., Riedmuller S.B., Feldblyum T.V.,  
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,

RA	Florens L., Yates F.R. III, Raine J.D., Sindén R.E., Harris M.A.,
RA	Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA	van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA	Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA	Carucci D.J.;
RT	"Genome sequence and comparative analysis of the model rodent malaria
RT	parasite Plasmodium yoelii yoelii.";
RL	Nature 419:512-519(2002).
CC	-!- CAUTION: The sequence shown here is derived from an
CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC	preliminary data.
DR	EMBL; AABL01000318; EAA20511.1; -.
KW	Hypothetical protein.
SQ	SEQUENCE 29 AA; 3408 MW; F36142D3148EE117 CRC64;
Query Match 70.8%; Score 17; DB 2; Length 29;	
Best Local Similarity 40.0%; Pred. No. 5e+03;	
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
QY	2 FXXW 6
Db	11 FSASW 15
RESULT 5	
O05602	
ID	O05602 PRELIMINARY; PRT; 32 AA.
AC	O05602;
DT	01-JUL-1997 (TrEMBLrel. 04, Created)
DT	01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	Transposon Tn5041 DNA (Fragment).
OS	Pseudomonas sp.
OC	Bacteria; Proteobacteria.
OX	NCBI_TaxID=306;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=KHP41;
RX	MEDLINE=97419493; PubMed=9274008;
RA	Khloodii G.Y., Yurieva O.V., Gorlenko Z.M., Mindlin S.Z., Bass I.A.,
RA	Lomovskaya O.L., Kopteva A.V., Nikiforov V.G.;
RT	"Tn5041 : a chimeric mercury resistance transposon closely related to
RT	the toluene degradative transposon Tn4651.";
RL	Microbiology 143:2549-2556(1997).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=KHP41;
RA	Khloodii G.Y., Mindlin S.Z., Gorlenko Z.M., Bass I.A., Kalyaeva E.S.,
RA	Nikiforov V.;
RT	"Host-dependent transposition of Tn5041.";
RL	Russ. J. Genet. 36:365-373(2000).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	STRAIN=KHP41;
RX	MEDLINE=22315381; PubMed=12427948;
RA	Khloodii G., Gorlenko Z., Mindlin S., Hobman J., Nikiforov V.;
RT	"Tn5041-like transposons: molecular diversity, evolutionary
RT	relationships and distribution of distinct variants in environmental
RT	bacteria.";
RL	Microbiology 148:3569-3582(2002).
DR	EMBL; X98999; CAA67458.1; -.
FT	NON_TER 1 1
FT	NON_TER 32 32
SQ	SEQUENCE 32 AA; 3298 MW; AF42B5EEF917077A CRC64;
Query Match 70.8%; Score 17; DB 2; Length 32;	
Best Local Similarity 40.0%; Pred. No. 5.4e+03;	
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
QY	2 FXXW 6
Db	11 FSWSW 15

RESULT 6	
Q72FN9	
ID	Q72FN9 PRELIMINARY; PRT; 35 AA.
AC	Q72FN9;
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Hypothetical protein.
GN	OrderedLocusNames=DVU0174;
OS	Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB
OS	8303).
OC	Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC	Desulfovibrionaceae; Desulfovibrio.
OX	NCBI_TaxID=882;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	PubMed=15077118; DOI=10.1038/nbt959;
RA	Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
RA	Kolony J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
RA	Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
RA	Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
RA	Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D.,
RA	Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
RA	Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
RT	"The genome sequence of the anaerobic, sulfate-reducing bacterium
RT	Desulfovibrio vulgaris Hildenborough.";
RL	Nat. Biotechnol. 22:554-559(2004).
DR	EMBL; AE017309; AAS94658.1; -.
DR	TIGR; DVU0174; -.
KW	Complete proteome.
SQ	SEQUENCE 35 AA; 3907 MW; CD423DA7D1422A7E CRC64;
Query Match 70.8%; Score 17; DB 2; Length 35;	
Best Local Similarity 40.0%; Pred. No. 5.7e+03;	
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
QY	2 FXXW 6
Db	15 FATAW 19
RESULT 7	
Q9PV61	
ID	Q9PV61 PRELIMINARY; PRT; 36 AA.
AC	Q9PV61;
DT	01-MAY-2000 (TrEMBLrel. 13, Created)
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Dystrophin (Fragment).
GN	Name=Dyst;
OS	Mola mola (ocean sunfish).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC	Molidae; Mola.
OX	NCBI_TaxID=94237;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA	Venkatesh B., Ning Y., Brenner S.;
RT	"Late changes in spliceosomal introns define clades in vertebrate
RT	evolution.";
RL	Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR	EMBL; AF137130; AAD54215.1; -.
DR	HSSP; P11532; 1DXX.
DR	InterPro; IPR001715; Calponin-like.
FT	NON_TER 1 1
FT	NON_TER 36 36
SQ	SEQUENCE 36 AA; 4181 MW; DE01642A8CAAF18 CRC64;
Query Match 70.8%; Score 17; DB 2; Length 36;	
Best Local Similarity 40.0%; Pred. No. 5.9e+03;	

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 32 FSSW 36

RESULT 8  
PSAI\_PROMA STANDARD; PRT; 38 AA.  
ID PSAI\_PROMA STANDARD; PRT; 38 AA.  
AC O87786;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Photosystem I reaction center subunit VIII.  
GN Name=psai; OrderedLocusNames=Pro1678;  
OS Prochlorococcus marinus.  
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;  
OC Prochlorococcus.  
OX NCBI\_TaxID=1219;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SARG / CCMP 1375 / SS120;  
RA van der Staay G.W.M., Moon-van der Staay S.Y., Garczarek L.,  
RA Partensky F.;  
RT "Characterization of the photosystem I subunits Psai and Psal from two  
RT strains of the marine oxyphototrophic.";  
RL Photosyn. Res. 57:183-191(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SARG / CCMP 1375 / SS120;  
RX MEDLINE=22810154; PubMed=12917486; DOI=10.1073/pnas.1733211100;  
RA Dufresne A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M.,  
RA Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,  
RA Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B.,  
RA Scanlan D.J., Tandeau de Marsac N., Weissbach J., Wincker P.,  
RA Wolf Y.I., Hess W.R.;  
RT "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,  
RT a nearly minimal oxyphototrophic genome.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).  
CC -|- FUNCTION: May help in the organization of the psal subunit.  
CC -|- SIMILARITY: Belongs to the psai family.  
CC -----  
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CC -----  
CC EMBL; Z98594; CAB1178.1; ALT INIT.  
DR EMBL; AE017166; AAQ00722.1; -.  
DR HAMAP; MF 00431; atypical; 1.  
DR InterPro; IPR001302; PSI\_8.  
DR Pfam; PF00796; PSI\_8; 1.  
KW Complete proteome; Photosynthesis; Photosystem I; Transmembrane.  
FT TRANSMEM 12 32 potential.  
SQ SEQUENCE 38 AA; 4081 MW; 19DECDABA650A2F2 CRC64;  
Query Match 70.8%; Score 17; DB 1; Length 38;  
Best Local Similarity 40.0%; Pred. No. 6.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 5 FAATW 9

RESULT 9  
Q7U4F1 PRELIMINARY; PRT; 38 AA.  
ID Q7U4F1  
AC Q7U4F1;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Photosystem I subunit VIII (Psai).  
GN Name=psai; OrderedLocusNames=SYNW2117;  
OS Synchococcus sp. (strain WH8102).  
OC Bacteria; Cyanobacteria; Chroococcales; Synchococcus.  
OX NCBI\_TaxID=84588;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;  
RA Palenik B., Brahamsha B., Larimer F.W., Land M.L., Hauser L.,  
RA Chain P., Lamerdin J.E., Regala W., Allen E.E., McCarren J.,  
RA Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.;  
RT "The genome of a motile marine Synchococcus.";  
RL Nature 424:1037-1042(2003).  
DR EMBL; BX569694; CAE08632.1; -.  
KW Complete proteome.  
SQ SEQUENCE 38 AA; 3975 MW; 75BEAB4500A52503 CRC64;  
Query Match 70.8%; Score 17; DB 2; Length 38;  
Best Local Similarity 40.0%; Pred. No. 6.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 5 FAATW 9

RESULT 10  
Q7V513 PRELIMINARY; PRT; 38 AA.  
AC Q7V513;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Photosystem I subunit VIII (Psai).  
GN Name=psai; OrderedLocusNames=PMT1767;  
OS Prochlorococcus marinus (strain MIT 9313).  
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;  
OC Prochlorococcus.  
OX NCBI\_TaxID=74547;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;  
RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,  
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,  
RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,  
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,  
RA Webb E.A., Zinser E.R., Chisholm S.W.;  
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic  
RT niche differentiation.";  
RL Nature 424:1042-1047(2003).  
DR EMBL; BX572100; CAE21942.1; -.  
KW Complete proteome.  
SQ SEQUENCE 38 AA; 4097 MW; 017DCC1CD4C3F4E2 CRC64;  
Query Match 70.8%; Score 17; DB 2; Length 38;  
Best Local Similarity 40.0%; Pred. No. 6.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 5 FAATW 9

RESULT 11  
Q9PV63 PRELIMINARY; PRT; 38 AA.  
ID Q9PV63  
AC Q9PV63;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Dystrophin (Fragment).  
GN Name=Dyst;  
OS Pseudopleuronectes americanus (Winter flounder) (Pleuronectes americanus).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes; Pleuronectoidei; Pleuronectidae; Pseudopleuronectes.  
OX NCBI\_TaxID=8265;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267; Venkatesh B., Ning Y., Brenner S.;  
RA "Late changes in spliceosomal introns define clades in vertebrate evolution.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF137128; AAD54213.1; -.  
DR HSSP; P11532; 1DXX.  
DR InterPro; IPR001715; Calponin-like.  
FT NON\_TER 1  
FT NON\_TER 38 38  
SQ SEQUENCE 38 AA; 4424 MW; 41C67E01642A8CB0 CRC64;  
  
Query Match 70.8%; Score 17; DB 2; Length 38;  
Best Local Similarity 40.0%; Pred. No. 6.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXXW 6  
Db 32 FSSSW 36  
  
RESULT 12  
Q9PT24 PRELIMINARY; PRT; 40 AA.  
AC Q9PT24;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Dystrophin (Fragment).  
GN Name=Dyst;  
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=8022;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267; Venkatesh B., Ning Y., Brenner S.;  
RA "Late changes in spliceosomal introns define clades in vertebrate evolution.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF137093; AAD54187.1; -.  
DR HSSP; P11532; 1DXX.  
DR InterPro; IPR001715; Calponin-like.  
DR Pfam; PF00307; CH; 1.  
FT NON\_TER 1  
FT NON\_TER 40 40  
SQ SEQUENCE 40 AA; 4551 MW; B4865AA19BDB4B17 CRC64;  
  
Query Match 70.8%; Score 17; DB 2; Length 40;  
Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXXW 6  
Db 32 FSSSW 36  
  
RESULT 13  
Q9PT28 PRELIMINARY; PRT; 40 AA.  
ID Q9PT28

AC Q9PT28;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Dystrophin (Fragment).  
GN Name=Dyst;  
OS Salarias sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Blennioidei; Blenniidae; Salarias.  
OX NCBI\_TaxID=94312;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267; Venkatesh B., Ning Y., Brenner S.;  
RA "Late changes in spliceosomal introns define clades in vertebrate evolution.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF137121; AAD54206.1; -.  
DR EMBL; AF137120; AAD54206.1; JOINED.  
DR HSSP; P11532; 1DXX.  
DR InterPro; IPR001715; Calponin-like.  
DR Pfam; PF00307; CH; 1.  
FT NON\_TER 1  
FT NON\_TER 40 40  
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;  
  
Query Match 70.8%; Score 17; DB 2; Length 40;  
Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXXW 6  
Db 32 FSSSW 36  
  
RESULT 14  
Q9PT29 PRELIMINARY; PRT; 40 AA.  
ID Q9PT29  
AC Q9PT29;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Dystrophin (Fragment).  
GN Name=Dyst;  
OS Epinephelus coioides (Orange-spotted grouper).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae; Serranidae; Epinephelinae; Epinephelus.  
OX NCBI\_TaxID=94232;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267; Venkatesh B., Ning Y., Brenner S.;  
RA "Late changes in spliceosomal introns define clades in vertebrate evolution.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF137117; AAD54203.1; -.  
DR EMBL; AF137116; AAD54203.1; JOINED.  
DR HSSP; P11532; 1DXX.  
DR InterPro; IPR001715; Calponin-like.  
DR Pfam; PF00307; CH; 1.  
FT NON\_TER 1  
FT NON\_TER 40 40  
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;  
  
Query Match 70.8%; Score 17; DB 2; Length 40;  
Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXXW 6  
Db 32 FSSSW 36

Db 32 FSSW 36

RESULT 15

Q9PU00

ID Q9PU00 PRELIMINARY; PRT; 40 AA.

AC Q9PU00;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Dystrophin (Fragment).

GN Name=Dyst;

OS Dicotylarchus labrax (European sea bass).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;

OC Moronidae; Dicentrarchus.

OX NCBI\_TaxID=13489;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;

RA Venkatesh B., Ning Y., Brenner S.;

RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";

RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).

DR EMBL; AF137115; AAD54202.1; -.

DR EMBL; AF137114; AAD54202.1; JOINED.

DR HSSP; P11532; 1DXX.

DR InterPro; IPR001715; Calponin-like.

DR Pfam; PF00307; CH; 1.

FT NON\_TER 1 1

FT NON\_TER 40 40

SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;

Best Local Similarity 40.0%; Pred. No. 6.4e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6

Db 32 FSSW 36

RESULT 16

Q9PU01

ID Q9PU01 PRELIMINARY; PRT; 40 AA.

AC Q9PU01;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Dystrophin (Fragment).

GN Name=Dyst;

OS Dendrochirus zebra (Zebra turkeyfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Perciformes; Scorpaeniformes;

OC Scorpaenidae; Scorpaenidae; Pteroinae; Dendrochirus.

OX NCBI\_TaxID=94308;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;

RA Venkatesh B., Ning Y., Brenner S.;

RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";

RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).

DR EMBL; AF137112; AAD54200.1; -.

DR EMBL; AF137111; AAD54200.1; JOINED.

DR HSSP; P11532; 1DXX.

DR InterPro; IPR001715; Calponin-like.

DR Pfam; PF00307; CH; 1.

FT NON\_TER 1 1

FT NON\_TER 40 40

SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;

Best Local Similarity 40.0%; Pred. No. 6.4e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6

Db 32 FSSW 36

RESULT 17

Q9PU02

ID Q9PU02 PRELIMINARY; PRT; 40 AA.

AC Q9PU02;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Dystrophin (Fragment).

GN Name=Dyst;

OS Zeus faber (John Dory).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Zeiformes; Zeidae; Zeus.

OX NCBI\_TaxID=64108;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;

RA Venkatesh B., Ning Y., Brenner S.;

RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";

RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).

DR EMBL; AF137108; AAD55460.1; -.

DR EMBL; AF137107; AAD55460.1; JOINED.

DR HSSP; P11532; 1DXX.

DR InterPro; IPR001715; Calponin-like.

DR Pfam; PF00307; CH; 1.

FT NON\_TER 1 1

FT NON\_TER 40 40

SQ SEQUENCE 40 AA; 4645 MW; BA7D49A676A3642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;

Best Local Similarity 40.0%; Pred. No. 6.4e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6

Db 32 FSSW 36

RESULT 18

Q9PU03

ID Q9PU03 PRELIMINARY; PRT; 40 AA.

AC Q9PU03;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Dystrophin (Fragment).

GN Name=Dyst;

OS Sargocentron sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Beryciformes; Holocentridae;

OC Sargocentron.

OX NCBI\_TaxID=94226;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;

RA Venkatesh B., Ning Y., Brenner S.;

RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";

RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).

DR EMBL; AF137106; AAD54196.1; -.

SQ SEQUENCE 40 AA; 4638 MW; B49D49A67E0167E5 CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;

Best Local Similarity 40.0%; Pred. No. 6.4e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6

Db 32 FSSW 36

RESULT 17

Q9PU02

ID Q9PU02 PRELIMINARY; PRT; 40 AA.

AC Q9PU02;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Dystrophin (Fragment).

GN Name=Dyst;

OS Zeus faber (John Dory).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Zeiformes; Zeidae; Zeus.

OX NCBI\_TaxID=64108;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;

RA Venkatesh B., Ning Y., Brenner S.;

RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";

RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).

DR EMBL; AF137108; AAD55460.1; -.

DR EMBL; AF137107; AAD55460.1; JOINED.

DR HSSP; P11532; 1DXX.

DR InterPro; IPR001715; Calponin-like.

DR Pfam; PF00307; CH; 1.

FT NON\_TER 1 1

FT NON\_TER 40 40

SQ SEQUENCE 40 AA; 4645 MW; BA7D49A676A3642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;

Best Local Similarity 40.0%; Pred. No. 6.4e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6

Db 32 FSSW 36

RESULT 18

Q9PU03

ID Q9PU03 PRELIMINARY; PRT; 40 AA.

AC Q9PU03;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Dystrophin (Fragment).

GN Name=Dyst;

OS Sargocentron sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Beryciformes; Holocentridae;

OC Sargocentron.

OX NCBI\_TaxID=94226;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;

RA Venkatesh B., Ning Y., Brenner S.;

RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";

RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).

DR EMBL; AF137106; AAD54196.1; -.



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DR EMBL; AF137105; AAD54196.1; JOINED.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4579 MW; B49C92D67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
Db 32 FSSW 36

RESULT 19
Q9PU04
ID Q9PU04 PRELIMINARY; PRT; 40 AA.
AC Q9PU04;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Fundulus heteroclitus (Killifish) (Mummichog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Fundulidae; Fundulus.
OX NCBI_TaxID=8078;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137103; AAD54194.1; -.
DR EMBL; AF137102; AAD54194.1; JOINED.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
Db 32 FSSW 36

RESULT 20
Q9PU05
ID Q9PU05 PRELIMINARY; PRT; 40 AA.
AC Q9PU05;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Hemiramphus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Hemiramphidae; Hemiramphus.
OX NCBI_TaxID=94223;
RN [1]
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RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137101; AAD54193.1; -.
DR EMBL; AF137100; AAD54193.1; JOINED.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
Db 32 FSSW 36

RESULT 21
Q9PU06
ID Q9PU06 PRELIMINARY; PRT; 40 AA.
AC Q9PU06;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Lampiris sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Lampridiformes; Lamprididae; Lampiris.
OX NCBI_TaxID=94303;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137096; AAD54189.1; -.
DR EMBL; AF137095; AAD54189.1; JOINED.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
Db 32 FSSW 36

RESULT 22
Q9PV62
ID Q9PV62 PRELIMINARY; PRT; 40 AA.
AC Q9PV62;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Ostracion sp. IMCB-2002.
```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Ostraciidae; Ostracion; unclassified Ostracion.  
OX NCBI\_TaxID=188530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate evolution."  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF137129; AAD54214.1; -.  
DR HSSP; P11532; 1DXX.  
DR InterPro; IPR001715; Calponin-like.  
DR Pfam; PF00307; CH; 1.  
FT NON\_TER 1 1  
FT NON\_TER 40 40  
SQ SEQUENCE 40 AA; 4582 MW; B49D4BCBEE01642A CRC64;  
  
Query Match 70.8%; Score 17; DB 2; Length 40;  
Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXW 6  
Db 32 FSSW 36  
  
RESULT 23  
Q9PV64 PRELIMINARY; PRT; 40 AA.  
AC Q9PV64;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Dystrophin (Fragment).  
GN Name=Dyst;  
OS Channa sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Channoidei;  
OC Channidae; Channa.  
OX NCBI\_TaxID=94222;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate evolution."  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF137127; AAD54212.1; -.  
DR HSSP; P11532; 1DXX.  
DR InterPro; IPR001715; Calponin-like.  
DR Pfam; PF00307; CH; 1.  
FT NON\_TER 1 1  
FT NON\_TER 40 40  
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;  
  
Query Match 70.8%; Score 17; DB 2; Length 40;  
Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXW 6  
Db 32 FSSW 36  
  
RESULT 24  
Q9PV65 PRELIMINARY; PRT; 40 AA.  
ID Q9PV65  
AC Q9PV65;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Dystrophin (Fragment).  
GN Name=Dyst;  
OS Colisa lalia (dwarf gourami).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;  
OC Anabantoidei; Belontiidae; Colisa.  
OX NCBI\_TaxID=50373;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate evolution."  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF137126; AAD54211.1; -.  
DR HSSP; P11532; 1DXX.  
DR InterPro; IPR001715; Calponin-like.  
DR Pfam; PF00307; CH; 1.  
FT NON\_TER 1 1  
FT NON\_TER 40 40  
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;  
  
Query Match 70.8%; Score 17; DB 2; Length 40;  
Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXW 6  
Db 32 FSSW 36  
  
RESULT 25  
Q9PV66 PRELIMINARY; PRT; 40 AA.  
ID Q9PV66  
AC Q9PV66;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Dystrophin (Fragment).  
GN Name=Dyst;  
OS Stromateus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;  
OC Stromateoidei; Stromateidae; Stromateus.  
OX NCBI\_TaxID=94245;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate evolution."  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF137125; AAD54210.1; -.  
DR HSSP; P11532; 1DXX.  
DR InterPro; IPR001715; Calponin-like.  
DR Pfam; PF00307; CH; 1.  
FT NON\_TER 1 1  
FT NON\_TER 40 40  
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;  
  
Query Match 70.8%; Score 17; DB 2; Length 40;  
Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXW 6  
Db 32 FSSW 36

## RESULT 26

Q9PV68 ID Q9PV68 PRELIMINARY; PRT; 40 AA.  
AC Q9PV68;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
DE Dystrophin (Fragment).  
GN Name=Dyst;  
OS Acanthurus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;  
OC Acanthuroidei; Acanthuridae; Acanthurus.  
OX NCBI\_TaxID=94220;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate evolution."  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF137123; AAD54208.1; -.  
DR HSSP; P11532; 1DXX.  
DR InterPro; IPR001715; Calponin-like.  
DR Pfam; PF00307; CH; 1.  
FT NON\_TER 1 1  
FT NON\_TER 40 40  
SQ SEQUENCE 40 AA; 4592 MW; B48FFE566BDB542A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;  
Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 32 FSSSW 36

## RESULT 27

Q9PV69 ID Q9PV69 PRELIMINARY; PRT; 40 AA.  
AC Q9PV69;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
DE Dystrophin (Fragment).  
GN Name=Dyst;  
OS Cryptocentrus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Gobioidi;  
OC Gobiidae; Cryptocentrus.  
OX NCBI\_TaxID=94314;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate evolution."  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF137122; AAD54207.1; -.  
DR HSSP; P11532; 1DXX.  
DR InterPro; IPR001715; Calponin-like.  
DR Pfam; PF00307; CH; 1.  
DR PROSITE; PS50021; CH; 1.  
FT NON\_TER 1 1  
FT NON\_TER 40 40  
SQ SEQUENCE 40 AA; 4611 MW; B49D49A67E01756E CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;  
Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 32 FSSSW 36

## RESULT 28

Q9PV70 ID Q9PV70 PRELIMINARY; PRT; 40 AA.  
AC Q9PV70;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE Dystrophin (Fragment).  
GN Name=Dyst;  
OS Dissostichus mawsoni (Antarctic cod).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;  
OC Notothenioidi; Nototheniidae; Dissostichus.  
OX NCBI\_TaxID=36200;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate evolution."  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF137119; AAD54205.1; -.  
DR HSSP; P11532; 1DXX.  
DR InterPro; IPR001715; Calponin-like.  
DR Pfam; PF00307; CH; 1.  
FT NON\_TER 1 1  
FT NON\_TER 40 40  
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;  
Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 32 FSSSW 36

## RESULT 29

Q9PV71 ID Q9PV71 PRELIMINARY; PRT; 40 AA.  
AC Q9PV71;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
DE Dystrophin (Fragment).  
GN Name=Dyst;  
OS Mullus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;  
OC Mullidae; Mullus.  
OX NCBI\_TaxID=94224;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate evolution."  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF137118; AAD54204.1; -.  
DR HSSP; P11532; 1DXX.  
DR InterPro; IPR001715; Calponin-like.  
DR Pfam; PF00307; CH; 1.  
FT NON\_TER 1 1  
FT NON\_TER 40 40

SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;  
Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
|  
32 FSSSW 36

Db

RESULT 30  
Q9PV72 PRELIMINARY; PRT; 40 AA.

AC Q9PV72;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Dystrophin (Fragment).  
GN Name=Dyst;  
OS Latex calcarifer (Barramundi).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;  
OC Centropomidae; Latex.  
OX NCBI\_TaxID=8187;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate evolution."  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF137113; AAD54201.1; -.  
DR HSSP; P11532; 1DXX.  
DR InterPro; IPR001715; Calponin-like.  
DR Pfam; PF00307; CH; 1.  
FT NON\_TER 1 1  
FT NON\_TER 40 40  
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;  
Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
|  
32 FSSSW 36

Db

RESULT 31  
Q9PV73 PRELIMINARY; PRT; 40 AA.

AC Q9PV73;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Dystrophin (Fragment).  
GN Name=Dyst;  
OS Mastacembelus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Synbranchiiformes;  
OC Mastacembelidae; Mastacembelus.  
OX NCBI\_TaxID=94235;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate evolution."  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF137110; AAD54199.1; -.

DR HSSP; P11532; 1DXX.  
DR InterPro; IPR001715; Calponin-like.  
DR Pfam; PF00307; CH; 1.  
FT NON\_TER 1 1  
FT NON\_TER 40 40  
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;  
Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
|  
32 FSSSW 36

Db

RESULT 32  
Q9PV74 PRELIMINARY; PRT; 40 AA.

AC Q9PV74;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Dystrophin (Fragment).  
GN Name=Dyst;  
OS Hippocampus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;  
OC Syngnathidae; Hippocampus.  
OX NCBI\_TaxID=72047;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate evolution."  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF137109; AAD54198.1; -.  
DR HSSP; P11532; 1DXX.  
DR InterPro; IPR001715; Calponin-like.  
DR Pfam; PF00307; CH; 1.  
DR PROSITE; PS50021; CH; 1.  
FT NON\_TER 1 1  
FT NON\_TER 40 40  
SQ SEQUENCE 40 AA; 4541 MW; B49D487D0E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;  
Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
|  
32 FSSSW 36

Db

RESULT 33  
Q9PV75 PRELIMINARY; PRT; 40 AA.

AC Q9PV75;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Dystrophin (Fragment).  
GN Name=Dyst;  
OS Poecilia latipinna.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;  
OC Cyprinodontiformes; Poeciliidae; Poecilia.  
OX NCBI\_TaxID=48699;  
RN [1]  
RP SEQUENCE FROM N.A.

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RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137104; AAD54195.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
Db 32 FSSSW 36

RESULT 34
Q9PV77 PRELIMINARY; PRT; 40 AA.
AC Q9PV77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Mugil cephalus (Flathead mullet) (Mugil japonicus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Mugilomorpha; Mugilidae;
OC Mugil.
OX NCBI_TaxID=48193;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137098; AAD54191.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
Db 32 FSSSW 36

RESULT 35
Q9PV78 PRELIMINARY; PRT; 40 AA.
AC Q9PV78;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Lophius sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
```

```
OC Acanthomorpha; Paracanthopterygii; Lophiiformes; Lophiidae; Lophius.
OX NCBI_TaxID=30791;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137097; AAD54190.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
Db 32 FSSSW 36

RESULT 36
Q9PV79 PRELIMINARY; PRT; 40 AA.
AC Q9PV79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Galaxias maculatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Galaxiidae; Galaxias.
OX NCBI_TaxID=61620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137094; AAD54188.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4613 MW; BA7C92D67E01642A CRC64;

Query Match 70.8%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
Db 32 FSSSW 36

RESULT 37
Q9PV80 PRELIMINARY; PRT; 40 AA.
AC Q9PV80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
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OS Plecoglossus altivelis.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Osmeridae; Plecoglossus.  
OX NCBI\_TaxID=61084;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF137092; AAD54186.1; -.  
DR HSSP; P11532; 1DXX.  
DR InterPro; IPR001715; Calponin-like.  
DR Pfam; PF00307; CH; 1.  
FT NON\_TER 1 1  
FT NON\_TER 40 40  
SQ SEQUENCE 40 AA; 4512 MW; B4931BF59BDB542A CRC64;  
  
Query Match 70.8%; Score 17; DB 2; Length 40;  
Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 2 FXXXW 6  
Db 32 FSSSW 36  
  
RESULT 38  
Q9PV81 PRELIMINARY; PRT; 40 AA.  
AC Q9PV81;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Dystrophin (Fragment).  
GN Name=Dyst;  
OS Esoc lucius (Northern pike).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Esociformes;  
OC Esocidae; Esoc.  
OX NCBI\_TaxID=8010;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF137091; AAD54185.1; -.  
DR HSSP; P11532; 1DXX.  
DR InterPro; IPR001715; Calponin-like.  
DR Pfam; PF00307; CH; 1.  
FT NON\_TER 1 1  
FT NON\_TER 40 40  
SQ SEQUENCE 40 AA; 4542 MW; 09165AA193794B14 CRC64;  
  
Query Match 70.8%; Score 17; DB 2; Length 40;  
Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 2 FXXXW 6  
Db 32 FSSSW 36  
  
RESULT 39  
Q9PV82 PRELIMINARY; PRT; 40 AA.  
AC Q9PV82;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Dystrophin (Fragment).  
GN Name=Dyst;  
OS Barbus tetrazona.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Barbus.  
OX NCBI\_TaxID=94221;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF137090; AAD54184.1; -.  
DR HSSP; P11532; 1DXX.  
DR InterPro; IPR001715; Calponin-like.  
DR Pfam; PF00307; CH; 1.  
FT NON\_TER 1 1  
FT NON\_TER 40 40  
SQ SEQUENCE 40 AA; 4573 MW; 459B37C19BC3E736 CRC64;  
  
Query Match 70.8%; Score 17; DB 2; Length 40;  
Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 2 FXXXW 6  
Db 32 FSSSW 36  
  
RESULT 40  
Q9PV84 PRELIMINARY; PRT; 40 AA.  
AC Q9PV84;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Dystrophin (Fragment).  
GN Name=Dyst;  
OS Anguilla sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;  
OC Anguilla.  
OX NCBI\_TaxID=62126;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF137088; AAD54182.1; -.  
DR HSSP; P11532; 1DXX.  
DR InterPro; IPR001715; Calponin-like.  
DR Pfam; PF00307; CH; 1.  
DR PROSITE; PS50021; CH; 1.  
FT NON\_TER 1 1  
FT NON\_TER 40 40  
SQ SEQUENCE 40 AA; 4574 MW; 557846B66BDB5437 CRC64;  
  
Query Match 70.8%; Score 17; DB 2; Length 40;  
Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 2 FXXXW 6  
Db 32 FSSSW 36  
  
Search completed: October 18, 2005, 15:30:10  
Job time : 124.353 secs





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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:18:31 ; Search time 25.9412 Seconds  
(without alignments)  
33.381 Million cell updates/sec

Title: US-09-214-371-11  
Perfect score: 24  
Sequence: 1 XFXXWXXX 9

Scoring table: BLOSUM62  
Gapop 10.0 ; Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	70.8	9	A24244	adipokinetic hormo
2	17	70.8	53	T00172	hypothetical prote
3	17	70.8	53	D89989	hypothetical prote
4	17	70.8	63	T29202	hypothetical prote
5	17	70.8	65	A32613	adipokinetic hormo
6	17	70.8	67	T12860	hypothetical prote
7	17	70.8	70	A86942	hypothetical prote
8	17	70.8	72	S15137	thioredoxin h2 - s
9	17	70.8	77	S18581	pufQ protein - Rho
10	17	70.8	77	T50756	pufQ protein [impo
11	17	70.8	84	E69268	hypothetical prote
12	17	70.8	88	B46264	thioredoxin 2 - sl
13	17	70.8	98	F47624	Ig heavy chain V-I
14	17	70.8	99	S37444	gene E2 protein -
15	17	70.8	99	S37447	gene E2 protein -
16	17	70.8	99	S37441	gene E2 protein -
17	17	70.8	99	S37448	gene E2 protein -
18	17	70.8	99	S37442	gene E2 protein -
19	17	70.8	102	G71043	hypothetical prote
20	17	70.8	102	B56956	GTP-binding protei
21	17	70.8	104	A28086	thioredoxin - rabb
22	17	70.8	105	A30006	thioredoxin - chic
23	17	70.8	105	JH0568	thioredoxin [valid
24	17	70.8	105	JS0667	thioredoxin - rhes
25	17	70.8	105	S04107	thioredoxin - mous
26	17	70.8	105	S04352	thioredoxin - rat
27	17	70.8	107	T33843	hypothetical prote
28	17	70.8	108	AH2101	thioredoxin [impor
29	17	70.8	112	PH0980	Ig heavy chain V r

30	17	70.8	112	2	AF2549	hypothetical prote
31	17	70.8	113	1	S57775	thioredoxin h, cyt
32	17	70.8	114	1	JQ2242	thioredoxin h - Ar
33	17	70.8	115	1	G3HUN	Ig heavy chain V-I
34	17	70.8	115	2	PL0238	Ig heavy chain V r
35	17	70.8	115	2	G72642	probable surface p
36	17	70.8	116	2	T10739	thioredoxin - comm
37	17	70.8	117	2	PL0237	Ig heavy chain V r
38	17	70.8	117	2	PL0234	Ig heavy chain V r
39	17	70.8	117	2	PL0235	Ig heavy chain V r
40	17	70.8	118	1	S34812	thioredoxin h2 - c
41	17	70.8	118	2	S58118	thioredoxin (clone
42	17	70.8	118	2	S58120	thioredoxin (clone
43	17	70.8	118	2	T10170	thioredoxin - cast
44	17	70.8	118	2	PL0231	Ig heavy chain V r
45	17	70.8	118	2	F82424	diacylglycerol kin
46	17	70.8	119	2	T08142	thioredoxin h homo
47	17	70.8	119	2	D86330	F6F9.21 protein -
48	17	70.8	119	2	T50867	thioredoxin-like p
49	17	70.8	119	2	A24672	Ig heavy chain pre
50	17	70.8	119	2	B72526	hypothetical prote
51	17	70.8	122	2	T04090	probable thioredox
52	17	70.8	123	2	S34009	Ig heavy chain V r
53	17	70.8	125	2	T50866	probable thioredox
54	17	70.8	125	2	S58119	thioredoxin (clone
55	17	70.8	126	1	S16590	thioredoxin h1 - c
56	17	70.8	131	2	T50862	thioredoxin-like p
57	17	70.8	131	2	T50863	thioredoxin-like p
58	17	70.8	131	2	T50864	thioredoxin-like p
59	17	70.8	131	2	T50865	thioredoxin-like p
60	17	70.8	133	2	S58123	thioredoxin (clone
61	17	70.8	136	2	AI0124	probable prepilin
62	17	70.8	138	2	S03526	Ig heavy chain pre
63	17	70.8	141	2	T17760	hypothetical prote
64	17	70.8	141	2	S50690	hypothetical prote
65	17	70.8	141	2	C95330	probable nucleotid
66	17	70.8	142	2	I47190	Ig heavy chain var
67	17	70.8	144	2	A36324	growth arrest-spec
68	17	70.8	146	2	AI1809	hypothetical prote
69	17	70.8	147	2	F87432	hypothetical prote
70	17	70.8	149	2	T23939	probable protein d
71	17	70.8	150	2	D69100	hypothetical prote
72	17	70.8	152	2	F72702	hypothetical prote
73	17	70.8	156	2	T48047	hypothetical prote
74	17	70.8	158	2	S74730	hypothetical prote
75	17	70.8	160	2	A53293	flm3-region hypoth
76	17	70.8	160	2	S76328	hypothetical prote
77	17	70.8	161	2	AC0966	probable PTS syste
78	17	70.8	174	2	S73301	hypothetical prote
79	17	70.8	174	2	T02276	hypothetical prote
80	17	70.8	174	2	T29491	hypothetical prote
81	17	70.8	180	2	G70028	conserved hypotet
82	17	70.8	180	2	T51724	phosphotransferase
83	17	70.8	182	2	T17625	hypothetical prote
84	17	70.8	182	2	S53822	fucoxanthin chloro
85	17	70.8	183	2	T38917	hypothetical prote
86	17	70.8	189	2	T51064	hypothetical prote
87	17	70.8	191	2	S76398	hypothetical prote
88	17	70.8	194	2	T00482	probable thioredox
89	17	70.8	201	2	AC3593	probable integral
90	17	70.8	204	2	B82410	conserved hypotet
91	17	70.8	205	2	S75300	conserved hypotet
92	17	70.8	206	2	E83515	hypothetical prote
93	17	70.8	207	2	AC0006	probable membrane
94	17	70.8	207	2	T46415	hypothetical prote
95	17	70.8	208	1	D71802	hypothetical prote
96	17	70.8	208	1	G64715	conserved hypotet
97	17	70.8	211	2	S53824	fucoxanthin chloro
98	17	70.8	212	2	B47698	hemagglutinin hag2
99	17	70.8	216	2	S53821	fucoxanthin chloro
100	17	70.8	217	2	C70629	probable mutF3 pro

ALIGNMENTS

RESULT 1  
A24244  
adipokinetic hormone - bollworm  
N/Alternate names: Hez-AKH  
C/Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)  
C/Date: 31-Mar-1988 #sequence\_revision 23-Mar-1995 #text\_change 09-Jul-2004  
C/Accession: A24244  
R/Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway  
Biochem. Biophys. Res. Commun. 135, 622-628, 1986  
A/Title: Isolation and primary structure of a peptide from the corpora cardiaca of Helio  
A/Reference number: A24244; MUID:86186794; PMID:3964263  
A/Accession: A24244  
A/Molecule type: protein  
A/Residues: 1-9 <JAF>  
A/Cross-references: UNIPROT:P08901  
C/Superfamily: adipokinetic hormone  
C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F/9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 70.8%; Score 17; DB 2; Length 9;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| | |  
Db 4 FTSSW 8

RESULT 2  
T00172  
hypothetical protein 38 - Staphylococcus aureus phage phi PVL  
C/Species: Staphylococcus aureus phage phi PVL  
C/Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C/Accession: T00172  
R/Kaneko, J.; Kimura, T.; Kawakami, Y.; Tomita, T.; Kamio, Y.  
Biochim. Biotechnol. Biochem. 61, 1960-1962, 1997  
A/Title: Pantone-Valentine leukocidin genes in a phage-like particle isolated from mitomy  
A/Reference number: Z14119; MUID:98067870; PMID:9404084  
A/Accession: T00172  
A/Status: translated from GB/EMBL/DDBJ  
A/Molecule type: DNA  
A/Residues: 1-53 <KAN>  
A/Cross-references: UNIPROT:O80077; EMBL:AB009866; NID:d1204727; PIDN:BAA31912.1; PID:d1

Query Match 70.8%; Score 17; DB 2; Length 53;  
Best Local Similarity 40.0%; Pred. No. 1.3e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| | |  
Db 28 FTTAW 32

RESULT 3  
D89989  
hypothetical protein SAS063 [imported] - Staphylococcus aureus (strain N315)  
C/Species: Staphylococcus aureus  
C/Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C/Accession: D89989  
R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc  
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;  
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
Lancet 357, 1225-1240, 2001  
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.  
A/Reference number: A89758; MUID:21311952; PMID:11418146  
A/Accession: D89989  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-53 <KUR>

A/Cross-references: UNIPROT:Q99SQ2; GB:BA000018; PID:g13701784; PIDN:BAB43077.1; GSPDB:GA  
A/Experimental source: strain N315  
C/Genetics:  
A/Gene: SAS063

Query Match 70.8%; Score 17; DB 2; Length 53;  
Best Local Similarity 40.0%; Pred. No. 1.3e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| | |  
Db 28 FTTAW 32

RESULT 4  
T29202  
hypothetical protein F28F9.3 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T29202  
R/Nelson, J.; Wohldmann, P.  
submitted to the EMBL Data Library, September 1996  
A/Description: The sequence of C. elegans cosmid F28F9.  
A/Reference number: Z20587  
A/Accession: T29202  
A/Status: preliminary; translated from GB/EMBL/DDBJ  
A/Molecule type: DNA  
A/Residues: 1-63 <NEL>  
A/Cross-references: UNIPROT:Q94194; EMBL:U70850; PIDN:AAB09124.1; GSPDB:GN00022; CESP:F28  
A/Experimental source: strain Bristol N2; clone F28F9  
C/Genetics:  
A/Gene: CESP:F28F9.3  
A/Map position: 4  
A/Introns: 38/1

Query Match 70.8%; Score 17; DB 2; Length 63;  
Best Local Similarity 40.0%; Pred. No. 1.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| | |  
Db 30 FATAW 34

RESULT 5  
A32613  
adipokinetic hormone precursor - tobacco hornworm  
C/Species: Manduca sexta (tobacco hornworm)  
C/Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 09-Jul-2004  
C/Accession: A32613  
R/Bradfield, J.Y.; Keeley, L.L.  
J. Biol. Chem. 264, 12791-12793, 1989  
A/Title: Adipokinetic hormone gene sequence from Manduca sexta.  
A/Reference number: A32613; MUID:89327232; PMID:2753887  
A/Accession: A32613  
A/Molecule type: DNA  
A/Residues: 1-65 <BRA>  
A/Cross-references: UNIPROT:P08901; GB:J04972; NID:g159478; PIDN:AAA29299.1; PID:g159479  
C/Genetics:

A/Introns: #status absent  
C/Superfamily: adipokinetic hormone  
C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
F/1-19/Domain: signal sequence #status predicted <SIG>  
F/20-28/Product: adipokinetic hormone #status predicted <MAT>  
F/20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted  
F/28/Modified site: amidated carboxyl end (Gly) (amide in mature form from following gly

Query Match 70.8%; Score 17; DB 1; Length 65;  
Best Local Similarity 40.0%; Pred. No. 1.5e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| | |

Db 23 FTSSW 27

RESULT 6

T12860

hypothetical protein yopZ - Bacillus subtilis phage SPBc2

C;Species: Bacillus subtilis phage SPBc2

C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004

C;Accession: T12860; H69918

R;Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Mauel, C.; Karamata, D.

submitted to the EMBL Data Library, August 1997

A;Description: The complete nucleotide sequence of the Bacillus subtilis SPbetac2 prophage

A;Reference number: Z17583

A;Accession: T12860

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-67 <LAZ>

A;Cross-references: UNIPROT:O64109; EMBL:AF020713; NID:g3025478; PIDN:AAC1

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: H69918

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-67 <KUN>

A;Cross-references: GB:Z99114; GB:Z99115; GB:AL009126; NID:g2634478; PIDN:CAB13989.1; PI

A;Experimental source: strain 168

C;Genetics:

A;Gene: yopZ

Query Match 70.8%; Score 17; DB 2; Length 67;

Best Local Similarity 40.0%; Pred. No. 1.5e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6

Db 49 FASSW 53

RESULT 7

A86942

hypothetical protein [imported] - Mycobacterium leprae

C;Species: Mycobacterium leprae

C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004

C;Accession: A86942

R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho

R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,

eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq

A;Title: Massive gene decay in the leprosy bacillus.

A;Reference number: A86909; MUID:21128732; PMID:11234002

A;Accession: A86942

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-70 <STO>

A;Cross-references: UNIPROT:O69587; GB:AL450380; NID:g13092599; PIDN:CAC29773.1; GSPDB:C

C;Genetics:

A;Gene: ML0265

Query Match 70.8%; Score 17; DB 2; Length 70;

Best Local Similarity 40.0%; Pred. No. 1.6e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6

Db 14 FTTSW 18

RESULT 8

S15137

thioredoxin h2 - spinach (fragments)

C;Species: Spinacia oleracea (spinach)

C;Date: 25-Feb-1994 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004

C;Accession: S15137

R;Marcus, F.; Chamberlain, S.H.; Chu, C.; Masiarz, F.R.; Shin, S.; Yee, B.C.; Buchanan,

Arch. Biochem. Biophys. 287, 195-198, 1991

A;Title: Plant thioredoxin h: an animal-like thioredoxin occurring in multiple cell comp

A;Reference number: S15137; MUID:91378382; PMID:1897989

A;Accession: S15137

A;Molecule type: protein

A;Residues: 1-72 <MAR>

A;Cross-references: UNIPROT:Q9S881

C;Superfamily: thioredoxin; thioredoxin homology

C;Keywords: redox-active disulfide

Query Match 70.8%; Score 17; DB 2; Length 72;

Best Local Similarity 40.0%; Pred. No. 1.6e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6

Db 6 FTASW 10

RESULT 9

S18581

pufQ protein - Rhodobacter sphaeroides

C;Species: Rhodobacter sphaeroides

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004

C;Accession: S18581; S32854

R;Hunter, C.N.; McGlynn, P.; Ashby, M.K.; Burgess, J.G.; Olsen, J.D.

Mol. Microbiol. 5, 2649-2661, 1991

A;Title: DNA sequencing and complementation/deletion analysis of the bchA-puf operon reg

A;Reference number: S18580; MUID:92140030; PMID:1779756

A;Accession: S18581

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-77 <HUN>

A;Cross-references: UNIPROT:P16069; EMBL:X68795; NID:g49170; PID:g49175

C;Genetics:

A;Gene: pufQ

C;Superfamily: pufQ protein

Query Match 70.8%; Score 17; DB 2; Length 77;

Best Local Similarity 40.0%; Pred. No. 1.7e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6

Db 60 FASAW 64

RESULT 10

T50756

pufQ protein [imported] - Rhodobacter sphaeroides

C;Species: Rhodobacter sphaeroides

C;Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 09-Jul-2004

C;Accession: T50756

R;Choudhary, M.; Kaplan, S.

Nucleic Acids Res. 28, 862-867, 2000

A;Title: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides 2

A;Reference number: Z25222; MUID:20115911; PMID:10648776

A;Accession: T50756  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-77 <CHO>  
A;Cross-references: UNIPROT:P16069; EMBL:AF195122; PIDN:AAF24300.1  
A;Experimental source: strain 2.4.1  
C;Genetics:  
A;Gene: pufQ  
C;Superfamily: pufQ protein

Query Match 70.8%; Score 17; DB 2; Length 77;  
Best Local Similarity 40.0%; Pred. No. 1.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
|  
Db 60 FASAW 64

RESULT 11  
E69268  
hypothetical protein AF0149 - Archaeoglobus fulgidus  
C;Species: Archaeoglobus fulgidus  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C;Accession: E69268  
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.  
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo  
A;Reference number: A69250; MUID:98049343; PMID:9389475  
A;Accession: E69268  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-84 <KLE>  
A;Cross-references: UNIPROT:O30088; GB:AE001096; GB:AE000782; NID:g2689419; PIDN:AAB9108

Query Match 70.8%; Score 17; DB 2; Length 84;  
Best Local Similarity 40.0%; Pred. No. 1.8e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
|  
Db 42 FAAAW 46

RESULT 12  
B46264  
thioredoxin 2 - slime mold (Dictyostelium discoideum) (fragment)  
C;Species: Dictyostelium discoideum  
C;Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 16-Aug-2004  
C;Accession: B46264  
R;Wetterauer, B.; Jacquot, J.P.; Veron, M.  
J. Biol. Chem. 267, 9895-9904, 1992  
A;Title: Thioredoxins from Dictyostelium discoideum are a developmentally regulated mult  
A;Reference number: A46264; MUID:92250653; PMID:1577820  
A;Accession: B46264  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-88 <WET>  
A;Cross-references: UNIPROT:P29446; GB:M91382; NID:g167930; PIDN:AAA33259.1; PID:g167931  
C;Superfamily: Thioredoxin; thioredoxin homology  
F;8-88/Domain: thioredoxin homology <THR>

Query Match 70.8%; Score 17; DB 2; Length 88;  
Best Local Similarity 40.0%; Pred. No. 1.8e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
|  
Db 26 FSAAW 30

RESULT 13

F47624  
Ig heavy chain V-I region - African clawed frog (fragment)  
C;Species: Xenopus laevis (African clawed frog)  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
C;Accession: F47624  
R;Haire, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.  
J. Exp. Med. 171, 1721-1737, 1990  
A;Title: Eleven distinct V-H gene families and additional patterns of sequence variation  
A;Reference number: A47624; MUID:90237760; PMID:2110243  
A;Accession: F47624  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-98 <HAI>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 70.8%; Score 17; DB 2; Length 98;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6

Db 29 FSSTW 33

RESULT 14

S37444  
gene E2 protein - human papillomavirus type 5 (fragment)  
C;Species: human papillomavirus type 5  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S37444  
R;Deau, A.C.  
submitted to the EMBL Data Library, August 1993  
A;Reference number: S37440  
A;Accession: S37444  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-99 <DEA>  
A;Cross-references: UNIPROT:Q81977; EMBL:X74648  
C;Superfamily: papillomavirus E2 protein

Query Match 70.8%; Score 17; DB 2; Length 99;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6

Db 46 FSTTW 50

RESULT 15

S37447  
gene E2 protein - human papillomavirus type 5 (fragment)  
C;Species: human papillomavirus type 5  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S37447  
R;Deau, A.C.  
submitted to the EMBL Data Library, August 1993  
A;Reference number: S37440  
A;Accession: S37447  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-99 <DEA>  
A;Cross-references: UNIPROT:Q81979; EMBL:X74651; NID:g404204; PIDN:CAA52715.1; PID:g40420  
C;Superfamily: papillomavirus E2 protein

Query Match 70.8%; Score 17; DB 2; Length 99;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 46 FSTTW 50

RESULT 16  
S37441  
gene E2 protein - human papillomavirus type 5 (fragment)  
C:Species: human papillomavirus type 5  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S37441  
R:Deau, A.C.  
submitted to the EMBL Data Library, August 1993  
A:Reference number: S37440  
A:Accession: S37441  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-99 <DEA>  
A:Cross-references: UNIPROT:Q81973; EMBL:X74645; NID:g404161; PIDN:CAA52709.1; PID:g4041  
C:Superfamily: papillomavirus E2 protein

Query Match 70.8%; Score 17; DB 2; Length 99;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

QY 2 FXXXW 6  
|  
Db 46 FSTTW 50

RESULT 17  
S37448  
gene E2 protein - human papillomavirus type 5 (fragment)  
C:Species: human papillomavirus type 5  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S37448  
R:Deau, A.C.  
submitted to the EMBL Data Library, August 1993  
A:Reference number: S37440  
A:Accession: S37448  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-99 <DEA>  
A:Cross-references: UNIPROT:Q81981; EMBL:X74652  
C:Superfamily: papillomavirus E2 protein

Query Match 70.8%; Score 17; DB 2; Length 99;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

QY 2 FXXXW 6  
|  
Db 46 FSTTW 50

RESULT 18  
S37442  
gene E2 protein - human papillomavirus type 5 (fragment)  
C:Species: human papillomavirus type 5  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S37442  
R:Deau, A.C.  
submitted to the EMBL Data Library, August 1993  
A:Reference number: S37440  
A:Accession: S37442  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-99 <DEA>  
A:Cross-references: UNIPROT:Q81975; EMBL:X74646  
C:Superfamily: papillomavirus E2 protein

Query Match 70.8%; Score 17; DB 2; Length 99;

Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 46 FSTTW 50

RESULT 19  
G71043  
hypothetical protein PH1639 - Pyrococcus horikoshii  
C:Species: Pyrococcus horikoshii  
C:Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 12-Jul-2004  
C:Accession: G71043  
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin  
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi  
DNA Res. 5, 55-76, 1998  
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a  
A:Reference number: A71000; MUID:98344137; PMID:9679194  
A:Accession: G71043  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-102 <KAW>  
A:Cross-references: UNIPROT:O59305; GB:AP000006; NID:g3236133; PIDN:BAA30751.1; PID:g325  
A:Experimental source: strain OT3  
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank  
C:Genetics:  
A:Gene: PH1639

Query Match 70.8%; Score 17; DB 2; Length 102;  
Best Local Similarity 40.0%; Pred. No. 2.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 34 FASSW 38

RESULT 20  
B56956  
GTP-binding protein-associated protein (clone c) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Oct-1995 #sequence\_revision 19-Oct-1995 #text\_change 09-Jul-2004  
C:Accession: B56956  
R:Janoueix-Lerosey, I.; Jollivet, F.; Camonis, J.; Marche, P.N.; Goud, B.  
J. Biol. Chem. 270, 14801-14808, 1995  
A:Title: Two-hybrid system screen with the small GTP-binding protein Rab6. Identification  
A:Reference number: A56956; MUID:95301579; PMID:7782346  
A:Accession: B56956  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-102 <JAN>  
A:Cross-references: UNIPROT:Q62145; GB:L40934; NID:g722666; PIDN:AAA78788.1; PID:g722667

Query Match 70.8%; Score 17; DB 2; Length 102;  
Best Local Similarity 40.0%; Pred. No. 2.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 61 FASAW 65

RESULT 21  
A28086  
thioredoxin - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 30-Jun-1989 #sequence\_revision 26-May-1994 #text\_change 16-Aug-2004  
C:Accession: A28086  
R:Johnson, R.S.; Mathews, W.R.; Biemann, K.; Hopper, S.  
J. Biol. Chem. 263, 9589-9597, 1988  
A:Title: Amino acid sequence of thioredoxin isolated from rabbit bone marrow determined  
A:Reference number: A28086; MUID:88257078; PMID:3164311

A;Accession: A28086  
A;Molecule type: protein  
A;Residues: 1-104 <JOH>  
A;Cross-references: UNIPROT:P08628  
C;Superfamily: Thioredoxin; thioredoxin homology  
C;Keywords: redox-active disulfide  
F;8-91/Domain: thioredoxin homology <THR>  
F;31-34/Disulfide bonds: redox-active #status predicted

Query Match 70.8%; Score 17; DB 1; Length 104;  
Best Local Similarity 40.0%; Pred. No. 2.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
|  
Db 26 FSATW 30

RESULT 22  
A30006  
thioredoxin - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 31-Mar-1989 #sequence\_revision 26-May-1994 #text\_change 16-Aug-2004  
C;Accession: A30006  
R;Jones, S.W.; Luk, K.C.  
J. Biol. Chem. 263, 9607-9611, 1988  
A;Title: Isolation of a chicken thioredoxin cDNA clone: thioredoxin mRNA is differential  
A;Reference number: A30006; MUID:88257080; PMID:2838473  
A;Accession: A30006  
A;Molecule type: mRNA  
A;Residues: 1-105 <JON>  
A;Cross-references: UNIPROT:P08629; GB:J03882; NID:g212765; PIDN:AAA49092.1; PID:g212766  
C;Superfamily: Thioredoxin; thioredoxin homology  
C;Keywords: redox-active disulfide  
F;9-92/Domain: thioredoxin homology <THR>  
F;32-35/Disulfide bonds: redox-active #status predicted

Query Match 70.8%; Score 17; DB 1; Length 105;  
Best Local Similarity 40.0%; Pred. No. 2.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
|  
Db 27 FSATW 31

RESULT 23  
JH0568  
thioredoxin [validated] - human  
N;Alternate names: ATL-derived factor (ADF); eosinophil cytotoxicity-enhancing factor; t  
C;Species: Homo sapiens (man)  
C;Date: 30-Jun-1992 #sequence\_revision 26-May-1994 #text\_change 16-Aug-2004  
C;Accession: JH0568; S04106; S44375; A31993; PT0079; A60749; A38922; S53453; A60870  
R;Tonissen, K.F.; Wells, J.R.E.  
Gene 102, 221-228, 1991  
A;Title: Isolation and characterization of human thioredoxin-encoding genes.  
A;Reference number: JH0568; MUID:91340156; PMID:1874447  
A;Accession: JH0568  
A;Molecule type: DNA  
A;Residues: 1-105 <TON>  
A;Cross-references: UNIPROT:P10599; EMBL:X54539; NID:g37455; PIDN:CAA38410.1; PID:g82572  
R;Tagaya, Y.; Maeda, Y.; Mitsui, A.; Kondo, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai,  
EMBO J. 8, 757-764, 1989  
A;Title: ATL-derived factor (ADF), an IL-2 receptor/Tac inducer homologous to thioredoxi  
A;Reference number: S04106; MUID:89251607; PMID:2785919  
A;Accession: S04106  
A;Molecule type: mRNA  
A;Residues: 1-105 <TAG1>  
A;Cross-references: GB:X77584; NID:g453963; PIDN:CAA54687.1; PID:g453964  
A;Note: this sequence has been revised in reference S44375  
R;Tagaya, Y.; Maeda, Y.; Mitsui, A.; Kando, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai,  
EMBO J. 13, 2244, 1994  
A;Reference number: S44375; MUID:94244626; PMID:8187776

A;Contents: erratum  
A;Accession: S44375  
A;Molecule type: mRNA  
A;Residues: 1-105 <TAG2>  
A;Cross-references: EMBL:X77584; NID:g453963; PIDN:CAA54687.1; PID:g453964  
R;Wollman, E.E.; d'Auriol, L.; Rimsky, L.; Shaw, A.; Jacquot, J.P.; Wingfield, P.; Graber  
J. Biol. Chem. 263, 15506-15512, 1988  
A;Title: Cloning and expression of a cDNA for human thioredoxin.  
A;Reference number: A31993; MUID:89008454; PMID:3170595  
A;Accession: A31993  
A;Molecule type: mRNA  
A;Residues: 1-38, 'N', 40-73, 'T', 75-105 <WOL>  
A;Cross-references: GB:J04026; NID:g339648; PIDN:AAA74596.1; PID:g339649  
R;Martin, H.; Dean, M.  
Biochem. Biophys. Res. Commun. 175, 123-128, 1991  
A;Title: Identification of a thioredoxin-related protein associated with plasma membranes  
A;Reference number: PT0079; MUID:91151337; PMID:1998498  
A;Accession: PT0079  
A;Molecule type: protein  
A;Residues: 2-13, 'X', 15 <MAR>  
R;Silberstein, D.S.; Ali, M.H.; Baker, S.L.; David, J.R.  
J. Immunol. 143, 979-983, 1989  
A;Title: Human eosinophil cytotoxicity-enhancing factor. Purification, physical character  
A;Reference number: A60749; MUID:89309777; PMID:2745979  
A;Accession: A60749  
A;Molecule type: protein  
A;Residues: 2-12, 'K', 14-15, 'XX', 18-19, 'X', 21-22 <SIL>  
A;Note: the abstract is inconsistent with figure 4 in having one undetermined residue aft  
R;Rimsky, L.; Wakasugi, H.; Ferrara, P.; Robin, P.; Capdevielle, J.; Tursz, T.; Fradelizi  
J. Immunol. 136, 3304-3310, 1986  
A;Title: Purification to homogeneity and NH-2-terminal amino acid sequence of a novel int  
A;Reference number: A38922; MUID:86169684; PMID:3485686  
A;Accession: A38922  
A;Molecule type: protein  
A;Residues: 2-16 <WAK>  
R;Dean, M.F.; Martin, H.; Sansom, P.A.  
Biochem. J. 304, 861-867, 1994  
A;Title: Characterization of a thioredoxin-related surface protein.  
A;Reference number: S53453; MUID:95118305; PMID:7818492  
A;Accession: S53453  
A;Molecule type: protein  
A;Residues: 1-21;38-57 <DEA>  
A;Note: described to be a surface-associated thioredoxin  
R;Wakasugi, H.; Rimsky, L.; Mahe, Y.; Kamel, A.M.; Fradelizi, D.; Tursz, T.; Bertoglio, S  
Proc. Natl. Acad. Sci. U.S.A. 84, 804-808, 1987  
A;Title: Epstein-Barr virus-containing B-cell line produces an interleukin 1 that it uses  
A;Reference number: A60870; MUID:87118252; PMID:3027706  
A;Contents: annotation  
R;Weichsel, A.; Gasdaska, J.R.; Powis, G.; Montfort, W.R.  
submitted to the Brookhaven Protein Data Bank, February 1996  
A;Reference number: A65533; PDB:1ERT  
A;Contents: annotation; X-ray crystallography, 1.7 angstroms, reduced form, residues 1-10  
R;Weichsel, A.; Gasdaska, J.R.; Powis, G.; Montfort, W.R.  
submitted to the Brookhaven Protein Data Bank, February 1996  
A;Reference number: A65534; PDB:1ERU  
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, oxidized form, residues 1-  
R;Forman-Kay, J.D.; Clore, G.M.; Gronenborn, A.M.  
submitted to the Brookhaven Protein Data Bank, December 1990  
A;Reference number: A50924; PDB:4TRX  
A;Contents: annotation; conformation by (1)H-NMR, residues 1-73, 'T', 75-105  
R;Forman-Kay, J.D.; Clore, G.M.; Wingfield, P.T.; Gronenborn, A.M.  
Biochemistry 30, 2685-2698, 1991  
A;Title: High-resolution three-dimensional structure of reduced recombinant human thior  
A;Reference number: A38953; MUID:91159399; PMID:2001356  
A;Contents: annotation; conformation by (1)H- and (15)N-NMR  
C;Comment: This small ubiquitous protein functions in many intracellular biological path  
C;Genetics:  
A;Gene: GDB:TXN  
A;Cross-references: GDB:120475; OMIM:187700  
A;Map position: 9q31-9q31  
A;Introns: 8/3; 43/3; 63/3; 85/3  
C;Superfamily: Thioredoxin; thioredoxin homology  
C;Keywords: redox-active disulfide



F;2-105/Product: thioredoxin #status experimental <MAT>  
F;9-92/Domain: thioredoxin homology <THR>  
F;32-35/Disulfide bonds: redox-active #status experimental

Query Match 70.8%; Score 17; DB 1; Length 105;  
Best Local Similarity 40.0%; Pred. No. 2.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 27 FSATW 31

## RESULT 24

JS0667

thioredoxin - rhesus macaque

C;Species: Macaca mulatta (rhesus macaque)

C;Date: 30-Jun-1992 #sequence\_revision 26-May-1994 #text\_change 16-Aug-2004

C;Accession: JS0667

R;An, G.; Wu, R.

Biochem. Biophys. Res. Commun. 183, 170-175, 1992

A;Title: Thioredoxin gene expression is transcriptionally up-regulated by retinol in mon

A;Reference number: JS0667; MUID:92181438; PMID:1543487

A;Accession: JS0667

A;Molecule type: mRNA

A;Residues: 1-105 &lt;ANG&gt;

A;Cross-references: UNIPROT:P29451; GB:M84643; NID:G342338; PIDN:AAA36921.1; PID:G342339

C;Superfamily: Thioredoxin; thioredoxin homology

C;Keywords: redox-active disulfide

F;9-92/Domain: thioredoxin homology &lt;THR&gt;

F;32-35/Disulfide bonds: redox-active #status predicted

Query Match

70.8%; Score 17; DB 1; Length 105;

Best Local Similarity 40.0%; Pred. No. 2.1e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6

|

Db 27 FSATW 31

## RESULT 25

S04107

thioredoxin - mouse

N;Alternate names: ATL-derived factor (ADF)

C;Species: Mus musculus (house mouse)

C;Date: 21-Nov-1993 #sequence\_revision 17-Oct-1997 #text\_change 16-Aug-2004

C;Accession: JC4068; S44376; S04107

R;Matsui, M.; Taniguchi, Y.; Hirota, K.; Taketo, M.; Yodoi, J.

Gene 152, 165-171, 1995

A;Title: Structure of the mouse thioredoxin-encoding gene and its processed pseudogene.

A;Reference number: JC4068; MUID:95137382; PMID:7835695

A;Accession: JC4068

A;Molecule type: DNA

A;Residues: 1-105 &lt;MAT&gt;

A;Cross-references: UNIPROT:P10639; DDBJ:D21855; NID:G517128

R;Tagaya, Y.; Maeda, Y.; Mitsui, A.; Kando, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai,

EMBO J. 13, 2244, 1994

A;Reference number: S44375; MUID:94244626; PMID:8187776

A;Contents: erratum

A;Accession: S44376

A;Molecule type: mRNA

A;Residues: 1-105 &lt;TAG1&gt;

A;Cross-references: EMBL:X77585; NID:G453971; PIDN:CAA54688.1; PID:G453972

R;Tagaya, Y.; Maeda, Y.; Mitsui, A.; Kondo, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai,

EMBO J. 8, 757-764, 1989

A;Title: ATL-derived factor (ADF), an IL-2 receptor/Tac inducer homologous to thioredoxi

A;Reference number: S04106; MUID:89251607; PMID:2785919

A;Accession: S04107

A;Molecule type: mRNA

A;Residues: 1-93, 'N', 94-96, 'ALT', 100-104, 'S' &lt;TAG2&gt;

A;Cross-references: GB:X77585

C;Comment: This small ubiquitous protein functions in many intracellular biological path

## C;Genetics:

A;Gene: MGI:Txn

A;Cross-references: MGI:36258

A;Map position: 4:24.6

A;Introns: 29/2; 44/1; 84/2

C;Superfamily: Thioredoxin; thioredoxin homology

C;Keywords: redox-active disulfide

F;9-92/Domain: thioredoxin homology &lt;THR&gt;

F;32-35/Disulfide bonds: redox-active #status predicted

Query Match

70.8%; Score 17; DB 1; Length 105;

Best Local Similarity 40.0%; Pred. No. 2.1e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6

|

Db 27 FSATW 31

## RESULT 26

S04352

thioredoxin - rat

N;Alternate names: thioredoxin-related surface protein SASP

C;Species: Rattus norvegicus (Norway rat)

C;Date: 31-Mar-1990 #sequence\_revision 26-May-1994 #text\_change 16-Aug-2004

C;Accession: S04352; S66372

R;Tonissen, K.F.; Robins, A.J.; Wells, J.R.E.

Nucleic Acids Res. 17, 3973, 1989

A;Title: Nucleotide sequence of a cDNA encoding rat thioredoxin.

A;Reference number: S04352; MUID:89282399; PMID:2734107

A;Accession: S04352

A;Molecule type: mRNA

A;Residues: 1-105 &lt;TON&gt;

A;Cross-references: UNIPROT:P11232; EMBL:X14878; NID:G57385; PIDN:CAA33019.1; PID:G57386

R;Dean, M.F.; Martin, H.; Sansom, P.A.

Biochem. J. 304, 861-867, 1994

A;Title: Characterization of a thioredoxin-related surface protein.

A;Reference number: S53453; MUID:95118305; PMID:7818492

A;Accession: S66372

A;Molecule type: protein

A;Residues: 2-21 &lt;DEA&gt;

A;Note: 12-Lys, 15-Gly, 16-Leu, 17-Gln, and 18-Leu were also found

A;Note: described to be a surface-associated thioredoxin

C;Superfamily: Thioredoxin; thioredoxin homology

C;Keywords: redox-active disulfide

F;2-105/Product: thioredoxin #status experimental &lt;MAT&gt;

F;9-92/Domain: thioredoxin homology &lt;THR&gt;

F;32-35/Disulfide bonds: redox-active #status predicted

Query Match

70.8%; Score 17; DB 1; Length 105;

Best Local Similarity 40.0%; Pred. No. 2.1e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6

|

Db 27 FSATW 31

## RESULT 27

T33843

hypothetical protein Y44E3A.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T33843

R;Woessner, J.; Graves, T.; Keppler, D.

submitted to the EMBL Data Library, November 1998

A;Description: The sequence of C. elegans cosmid Y44E3A.

A;Reference number: Z21422

A;Accession: T33843

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-107 &lt;WOE&gt;

A;Cross-references: UNIPROT:Q9TXY8; EMBL:AF106589; PIDN:AAC78230.1; GSPDB:GN00019; CESP:

A;Experimental source: strain Bristol N2; clone Y44B3A

C;Genetics:

A;Gene: CESP:Y44E3A.3

A;Map position: 1

A;Introns: 31/2

C;Superfamily: thioredoxin; thioredoxin homology

Query Match 70.8%; Score 17; DB 2; Length 107;  
Best Local Similarity 40.0%; Pred. No. 2.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
| |  
Db 27 FTASW 31

RESULT 28

AH2101

thioredoxin [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 16-Aug-2004

C;Accession: AH2101

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AH2101

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-108 <KUR>

A;Cross-references: UNIPROT:Q8YUH9; GB:BA000019; PIDN:BAB74066.1; PID:gl7131459; GSPDB:G

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: ali2367

C;Superfamily: Thioredoxin; thioredoxin homology

Query Match 70.8%; Score 17; DB 2; Length 108;  
Best Local Similarity 40.0%; Pred. No. 2.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
| |  
Db 28 FTATW 32

RESULT 29

PH0980

Ig heavy chain V region (clone 17s.13) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C;Accession: PH0980

R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c

A;Reference number: PH0971; MUID:92381444; PMID:1512540

A;Accession: PH0980

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-112 <TIL>

A;Experimental source: B cell, strain [NZB x NZW]F1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 70.8%; Score 17; DB 2; Length 112;  
Best Local Similarity 40.0%; Pred. No. 2.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
| |  
Db 29 FSSSW 33

RESULT 30

AF2549

hypothetical protein all7681 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120bel

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004

C;Accession: AF2549

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AF2549

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-112 <KUR>

A;Cross-references: UNIPROT:Q8ZS31; GB:AP003602; PIDN:BAB77324.1; PID:gl7134766; GSPDB:G

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: all7681

A;Genome: plasmid

Query Match 70.8%; Score 17; DB 2; Length 112;  
Best Local Similarity 40.0%; Pred. No. 2.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
| |  
Db 87 FASAW 91

RESULT 31

S57775

thioredoxin h, cytosolic [validated] - Chlamydomonas reinhardtii

C;Species: Chlamydomonas reinhardtii

C;Date: 27-Oct-1995 #sequence\_revision 21-Jan-1997 #text\_change 16-Aug-2004

C;Accession: S57775; S57799; S54868; S16090; S54870

R;Stein, M.; Jacquot, J.P.; Jeannette, E.; Decottignies, P.; Hodges, M.; Lancelin, J.M.;

Plant Mol. Biol. 28, 487-503, 1995

A;Title: Chlamydomonas reinhardtii thioredoxins: structure of the genes coding for the c

on and biochemical properties.

A;Reference number: S57774; MUID:95359406; PMID:7632918

A;Accession: S57775

A;Molecule type: DNA

A;Residues: 1-113 <STE>

A;Cross-references: UNIPROT:P80028; EMBL:X80887; NID:g840742; PIDN:CAA56850.1; PID:g84074

A;Accession: S57799

A;Molecule type: protein

A;Residues: 2-15 <STW>

R;Stein, M.; Hodges, M.; Jeanette, E.; Lancelin, J.M.; Jacquot, J.P.

submitted to the EMBL Data Library, April 1994

A;Description: Chlamydomonas reinhardtii thioredoxins I : cDNA and amino acid deduced se

A;Reference number: S54844

A;Accession: S54868

A;Molecule type: mRNA

A;Residues: 1-113 <STF>

A;Cross-references: EMBL:X78822; NID:g840740; PIDN:CAA55399.1; PID:g840741

R;Decottignies, P.; Schmitter, J.M.; Dutka, S.; Jacquot, J.P.; Miginiac-Maslow, M.

Eur. J. Biochem. 198, 505-512, 1991

A;Title: Characterization and primary structure of a second thioredoxin from the green a

A;Reference number: S16090; MUID:91249849; PMID:2040309

A;Accession: S16090

A;Molecule type: protein

A;Residues: 2-112 <MIG>

R;Mittard, V.; Blackledge, M.J.; Stein, M.; Jacquot, J.P.; Marion, D.; Lancelin, J.M.

submitted to the Brookhaven Protein Data Bank, May 1996

A;Reference number: A66748; PDB:ITOF

A;Contents: annotation; conformation by (1)H, (13)C, (15)N-NMR, residues 2-113

R;Mittard, V.; Morelle, N.; Brutscher, B.; Simorre, J.P.; Marion, D.; Stein, M.; Jacquot

Eur. J. Biochem. 229, 473-485, 1995

A;Title: (1)H, (13)C, (15)N-NMR resonance assignments of oxidized thioredoxin h from the

R spectroscopy and computer-assisted backbone assignment.  
A;Reference number: A58618; MUID:95262711; PMID:7744070  
A;Contents: annotation; conformation by (1)H, (13)C, (15)N-NMR  
C;Genetics:  
A;Introns: 27/3; 35/3; 69/3  
C;Superfamily: Thioresdoxin; thioresdoxin homology  
C;Keywords: redox-active disulfide  
F;2-113/Product: thioresdoxin h #status experimental <MAT>  
F;15-98/Domain: thioresdoxin homology <THR>  
F;37-40/Disulfide bonds: redox-active #status experimental

Query Match 70.8%; Score 17; DB 1; Length 113;  
Best Local Similarity 40.0%; Pred. No. 2.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 32 FTATW 36

RESULT 32

JQ2242  
thioresdoxin h - Arabidopsis thaliana  
N;Alternate names: protein F24M12.70  
C;Species: Arabidopsis thaliana (mouse-ear cross)  
C;Date: 19-May-1994 #sequence revision 26-May-1994 #text\_change 16-Aug-2004  
C;Accession: JQ2242; T45734; S29905  
R;Rivera-Madrid, R.; Marinho, P.; Brugidou, C.; Chartier, Y.; Meyer, Y.  
Plant Physiol. 102, 327-328, 1993  
A;Title: Nucleotide sequence of a cDNA clone encoding an Arabidopsis thaliana thioresdoxin  
A;Reference number: JQ2242; MUID:94151431; PMID:8108503  
A;Accession: JQ2242  
A;Molecule type: mRNA  
A;Residues: 1-114 <RIV>  
A;Cross-references: UNIPROT:P29448; EMBL:Z14084; NID:G16551; PIDN:CAA78462.1; PID:G16552  
R;Vitale, D.; Liguori, R.; Flores, M.; Argirou, A.; De Simone, V.; Mewes, H.W.; Lemcke,  
submitted to the Protein Sequence Database, December 1999  
A;Reference number: Z23012  
A;Accession: T45734  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-114 <VIT>  
A;Cross-references: EMBL:AL132980  
A;Experimental source: cultivar Columbia; BAC clone F24M12  
C;Genetics:

A;Gene: F24M12.70  
A;Map position: 3  
A;Introns: 30/3; 71/3  
C;Superfamily: Thioresdoxin; thioresdoxin homology  
C;Keywords: redox-active disulfide  
F;18-100/Domain: thioresdoxin homology <THR>  
F;40-43/Disulfide bonds: redox-active #status predicted

Query Match 70.8%; Score 17; DB 1; Length 114;  
Best Local Similarity 40.0%; Pred. No. 2.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 35 FTASW 39

RESULT 33

G3HUJN  
Ig heavy chain V-III region (Jon) - human (tentative sequence)  
C;Species: Homo sapiens (man)  
C;Date: 24-Apr-1984 #sequence revision 24-Apr-1984 #text\_change 09-Jul-2004  
C;Accession: A02063  
R;Capra, J.D.; Kehoe, J.M.  
Proc. Natl. Acad. Sci. U.S.A. 71, 845-848, 1974  
A;Title: Variable region sequences of five human immunoglobulin heavy chains of the V-HI  
A;Reference number: A93794; MUID:74142702; PMID:4522793  
A;Accession: A02063

A;Molecule type: protein  
A;Residues: 1-115 <CAP>  
A;Cross-references: UNIPROT:P01780  
C;Comment: This chain was isolated from an IgG3 myeloma protein.  
C;Genetics:

A;Gene: GDB:IGHV@  
A;Cross-references: GDB:128528; OMIM:147070  
A;Map position: 14q32.33-14q32.33  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>  
F;22-96/Disulfide bonds: #status predicted

Query Match 70.8%; Score 17; DB 1; Length 115;  
Best Local Similarity 40.0%; Pred. No. 2.3e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 29 FSTAW 33

RESULT 34

PL0238  
Ig heavy chain V region (anti-DNA, 6NVH and 6QVH) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996  
C;Accession: PL0238  
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.  
J. Exp. Med. 171, 265-297, 1990  
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic  
A;Reference number: PL0231; MUID:90111618; PMID:2104919  
A;Accession: PL0238  
A;Molecule type: mRNA  
A;Residues: 1-115 <SHL>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;1-30/Region: framework 1  
F;15-98/Domain: immunoglobulin homology <IMM>  
F;31-35/Region: complementarity-determining 1  
F;36-49/Region: framework 2  
F;50-66/Region: complementarity-determining 2  
F;67-98/Region: framework 3  
F;99-107/Region: complementarity-determining 3  
F;108-115/Region: framework 4

Query Match 70.8%; Score 17; DB 2; Length 115;  
Best Local Similarity 40.0%; Pred. No. 2.3e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 29 FSSSW 33

RESULT 35

G72642  
probable surface protein-1 APE0575 - Aeropyrum pernix (strain K1)  
C;Species: Aeropyrum pernix  
C;Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
C;Accession: G72642

R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah  
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K  
DNA Res. 6, 83-101, 1999  
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr  
A;Reference number: A72450; MUID:99310339; PMID:10382966  
A;Accession: G72642  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-115 <KAW>  
A;Cross-references: UNIPROT:Q9YEX3; DDBJ:AP000060; NID:G5104188; PIDN:BAA79543.1; PID:dl  
A;Experimental source: strain K1  
C;Genetics:

A;Gene: APE0575

Query Match 70.8%; Score 17; DB 2; Length 115;  
Best Local Similarity 40.0%; Pred. No. 2.3e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
| |  
Db 2 FSAW 6

RESULT 36

Tl0739

thioredoxin - common buckwheat

C;Species: Fagopyrum esculentum (common buckwheat)

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004

C;Accession: Tl0739

R;Fujino, K.

submitted to the EMBL Data Library, September 1996

A;Reference number: Z17109

A;Accession: Tl0739

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-116 <FUJ>

A;Cross-references: UNIPROT:Q96419; EMBL:D87984

A;Experimental source: cv. Kitayuki

C;Function:

A;Description: participates, by the reversible oxidation of an active center disulfide

C;Superfamily: thioredoxin; thioredoxin homology

C;Keywords: redox-active disulfide

F;17-99/Domain: thioredoxin homology <TXN>

Query Match 70.8%; Score 17; DB 2; Length 116;  
Best Local Similarity 40.0%; Pred. No. 2.3e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
| |  
Db 14 FTASW 38

RESULT 37

PL0237

Ig heavy chain V region (anti-DNA, 1A11VH) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996

C;Accession: PL0237

R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A

J. Exp. Med. 171, 265-297, 1990

A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic

A;Reference number: PL0231; MUID:90111618; PMID:2104919

A;Accession: PL0237

A;Molecule type: mRNA

A;Residues: 1-117 <SHL>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-30/Region: framework 1

F;15-98/Domain: immunoglobulin homology <IMM>

F;31-35/Region: complementarity-determining 1

F;36-49/Region: framework 2

F;50-66/Region: complementarity-determining 2

F;67-98/Region: framework 3

F;99-109/Region: complementarity-determining 3

F;110-117/Region: framework 4

Query Match 70.8%; Score 17; DB 2; Length 117;  
Best Local Similarity 40.0%; Pred. No. 2.3e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
| |  
Db 29 FSSSW 33

RESULT 38

PL0234

Ig heavy chain V region (anti-DNA, 3H9VH) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996

C;Accession: PL0234

R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A

J. Exp. Med. 171, 265-297, 1990

A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic

A;Reference number: PL0231; MUID:90111618; PMID:2104919

A;Accession: PL0234

A;Molecule type: mRNA

A;Residues: 1-117 <SHL>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-30/Region: framework 1

F;15-98/Domain: immunoglobulin homology <IMM>

F;31-35/Region: complementarity-determining 1

F;36-49/Region: framework 2

F;50-66/Region: complementarity-determining 2

F;67-98/Region: framework 3

F;99-109/Region: complementarity-determining 3

F;110-117/Region: framework 4

Query Match 70.8%; Score 17; DB 2; Length 117;  
Best Local Similarity 40.0%; Pred. No. 2.3e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
| |  
Db 29 FSSSW 33

RESULT 39

PL0235

Ig heavy chain V region (anti-DNA, 2F2VH and 4H8VH) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996

C;Accession: PL0235

R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A

J. Exp. Med. 171, 265-297, 1990

A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic

A;Reference number: PL0231; MUID:90111618; PMID:2104919

A;Accession: PL0235

A;Molecule type: mRNA

A;Residues: 1-117 <SHL>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-30/Region: framework 1

F;15-98/Domain: immunoglobulin homology <IMM>

F;31-35/Region: complementarity-determining 1

F;36-49/Region: framework 2

F;50-66/Region: complementarity-determining 2

F;67-98/Region: framework 3

F;99-109/Region: complementarity-determining 3

F;110-117/Region: framework 4

Query Match 70.8%; Score 17; DB 2; Length 117;  
Best Local Similarity 40.0%; Pred. No. 2.3e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
| |  
Db 29 FSSSW 33

RESULT 40

S34812

thioredoxin h2 - common tobacco

C;Species: Nicotiana tabacum (common tobacco)

C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 16-Aug-2004

C;Accession: S34812

R;Brugidou, C.; Marty, I.; Chartier, Y.; Meyer, Y.  
Mol. Gen. Genet. 238, 285-293, 1993  
A;Title: The Nicotiana tabacum genome encodes two cytoplasmic thioredoxin genes which are  
A;Reference number: S34812; MUID:93241165; PMID:8479434  
A;Accession: S34812  
A;Molecule type: DNA  
A;Residues: 1-118 <BRU>  
A;Cross-references: UNIPROT:Q07090; EMBL:Z11803; NID:g297518; PIDN:CAA77847.1; PID:g2975  
C;Genetics:  
A;Introns: 29/3; 70/3  
C;Superfamily: Thioredoxin; thioredoxin homology  
F;17-99/Domain: thioredoxin homology <THR>

Query Match 70.8%; Score 17; DB 1; Length 118;  
Best Local Similarity 40.0%; Pred. No. 2.3e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |  
Db 34 FTASW 38

Search completed: October 18, 2005, 15:31:04  
Job time : 26.9412 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:31:13 ; Search time 122.824 Seconds  
(without alignments)  
28.340 Million cell updates/sec

Title: US-09-214-371-11  
Perfect score: 24  
Sequence: 1 XFXXXWXXX.9

Scoring table: BLOSUM62  
Gapop 10.0 ; Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 716780

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : A Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	70.8	9	7	ADC07129 Honeybee
2	17	70.8	9	7	ADC07134 Painted l
3	17	70.8	10	3	AAB10010 H. pylori
4	17	70.8	10	4	AAB86090 H. pylori
5	17	70.8	10	4	AAB86058 H. pylori
6	17	70.8	11	7	ADC07163 Painted l
7	17	70.8	13	4	AAE05735 Complemen
8	17	70.8	13	6	ABG75574 CDR3 pept
9	17	70.8	14	4	AAM98088 Human pep
10	17	70.8	15	2	AAR97874 Japan ced
11	17	70.8	15	2	AAR97875 Japan ced
12	17	70.8	15	2	AAW57758 Residues
13	17	70.8	19	5	AAE23038 Human thi
14	17	70.8	20	2	AAW42165 T-cell ep
15	17	70.8	20	4	AAG62999 Complemen
16	16	66.7	5	8	ADR68284 Androgen
17	16	66.7	6	2	AAW76953 Fusion im
18	16	66.7	6	6	ABR46309 Staphyloc
19	16	66.7	6	6	ABR46270 Staphyloc
20	16	66.7	6	6	ABR46702 Staphyloc
21	16	66.7	6	6	ABR47093 Staphyloc
22	16	66.7	6	6	ABR45149 Staphyloc
23	16	66.7	6	6	ABR45486 Staphyloc
24	16	66.7	6	6	ABR45878 Staphyloc
25	16	66.7	6	6	ABR46661 Staphyloc

26	16	66.7	6	6	ABR47053	Abr47053	Staphyloc
27	16	66.7	6	6	ABR45190	Abr45190	Staphyloc
28	16	66.7	6	6	ABR45877	Abr45877	Staphyloc
29	16	66.7	6	6	ABR46310	Abr46310	Staphyloc
30	16	66.7	6	6	ABR47094	Abr47094	Staphyloc
31	16	66.7	6	6	ABR46701	Abr46701	Staphyloc
32	16	66.7	6	6	ABR47054	Abr47054	Staphyloc
33	16	66.7	6	6	ABR45525	Abr45525	Staphyloc
34	16	66.7	6	6	ABR45918	Abr45918	Staphyloc
35	16	66.7	6	6	ABR45189	Abr45189	Staphyloc
36	16	66.7	6	6	ABR45485	Abr45485	Staphyloc
37	16	66.7	6	6	ABR45150	Abr45150	Staphyloc
38	16	66.7	6	6	ABR45526	Abr45526	Staphyloc
39	16	66.7	6	6	ABR46269	Abr46269	Staphyloc
40	16	66.7	6	6	ABR46662	Abr46662	Staphyloc
41	16	66.7	6	6	ABR45917	Abr45917	Staphyloc
42	16	66.7	6	7	ADL17086	Adl17086	Phage-dis
43	16	66.7	7	5	ABP53945	Abp53945	VEGFR-3 b
44	16	66.7	7	7	ADB47984	Adb47984	Novel hum
45	16	66.7	7	8	ADJ55539	Adj55539	Novel hum
46	16	66.7	8	2	AAV18082	Aay18082	Histamine
47	16	66.7	8	6	ABR53957	Abr53957	Beta-secr
48	16	66.7	8	6	ABR54100	Abr54100	Beta-secr
49	16	66.7	8	6	ABR54133	Abr54133	Beta-secr
50	16	66.7	8	6	ABR54102	Abr54102	Beta-secr
51	16	66.7	8	6	ABR54137	Abr54137	Beta-secr
52	16	66.7	8	6	ABR54108	Abr54108	Beta-secr
53	16	66.7	8	6	ABR54106	Abr54106	Beta-secr
54	16	66.7	8	6	ABR54135	Abr54135	Beta-secr
55	16	66.7	8	6	ABR53955	Abr53955	Beta-secr
56	16	66.7	8	6	ABR54129	Abr54129	Beta-secr
57	16	66.7	8	6	ABR54139	Abr54139	Beta-secr
58	16	66.7	8	6	ABR54104	Abr54104	Beta-secr
59	16	66.7	8	6	ABR54131	Abr54131	Beta-secr
60	16	66.7	8	6	ABR53953	Abr53953	Beta-secr
61	16	66.7	8	6	ABR54127	Abr54127	Beta-secr
62	16	66.7	8	6	ABR54141	Abr54141	Beta-secr
63	16	66.7	8	7	ADC07151	Adc07151	Libanasid
64	16	66.7	8	7	ADC07141	Adc07141	Phymateus
65	16	66.7	8	7	ADC07150	Adc07150	Crickete A
66	16	66.7	8	7	ADC07130	Adc07130	Desert lo
67	16	66.7	8	7	ADC07137	Adc07137	Migratory
68	16	66.7	8	7	ADC07156	Adc07156	Onitis AK
69	16	66.7	8	8	ADR69591	Adr69591	Novel hyb
70	16	66.7	8	8	ADL27410	Adl27410	Amino aci
71	16	66.7	9	2	AAV48085	Aay48085	Immunogen
72	16	66.7	9	4	AAE01057	Aae01057	Human sec
73	16	66.7	9	5	ABP53956	Abp53956	VEGFR-3 b
74	16	66.7	9	5	ABP47522	Abp47522	N. mening
75	16	66.7	9	5	ABG97262	Abg97262	Human leu
76	16	66.7	9	5	AAE31347	Aae31347	Human tyr
77	16	66.7	9	8	ADH41183	Adh41183	Human rar
78	16	66.7	9	8	ADH41163	Adh41163	Human rar
79	16	66.7	9	8	ADK09130	Adk09130	Human pap
80	16	66.7	9	8	ADK09595	Adk09595	Human pap
81	16	66.7	9	8	ADN65877	Adn65877	HLA bindi
82	16	66.7	9	8	ADQ71598	Adq71598	Cancer re
83	16	66.7	9	8	ADQ72073	Adq72073	Cancer re
84	16	66.7	9	8	ADQ68606	Adq68606	Cancer re
85	16	66.7	9	8	ADQ72380	Adq72380	Cancer re
86	16	66.7	9	8	ADQ69652	Adq69652	Cancer re
87	16	66.7	9	8	ADQ72453	Adq72453	Cancer re
88	16	66.7	9	8	ADQ69664	Adq69664	Cancer re
89	16	66.7	9	8	ADQ71463	Adq71463	Cancer re
90	16	66.7	9	8	ADQ72148	Adq72148	Cancer re
91	16	66.7	9	8	ADQ72299	Adq72299	Cancer re
92	16	66.7	9	8	ADQ69952	Adq69952	Cancer re
93	16	66.7	9	8	ADQ70871	Adq70871	Cancer re
94	16	66.7	9	8	ADQ72479	Adq72479	Cancer re
95	16	66.7	9	8	ADQ70635	Adq70635	Cancer re
96	16	66.7	9	8	ADQ68180	Adq68180	Cancer re
97	16	66.7	9	8	ADQ70322	Adq70322	Cancer re
98	16	66.7	9	8	ADQ72207	Adq72207	Cancer re

99	16	66.7	9	8	ADP26276	Plasmodiu	Adp26276
100	16	66.7	10	1	AAP50792	Sequence	Aap50792
101	16	66.7	10	1	AAP82754	Example o	Aap82754
102	16	66.7	10	3	AAB26399	Human CAS	Aab26399
103	16	66.7	10	3	AAB26393	Human CAS	Aab26393
104	16	66.7	10	4	AAB87239	Breast-ca	Aab87239
105	16	66.7	10	4	ABB52440	Human API	Abb52440
106	16	66.7	10	4	AAB35295	Murine PS	Aab35295
107	16	66.7	10	5	ABG93457	AlcR amin	Abg93457
108	16	66.7	10	5	AAU72831	Anti-NKG2	Aau72831
109	16	66.7	10	5	ABG78903	Multiple	Abg78903
110	16	66.7	10	6	ABR01558	Human ant	Abro1558
111	16	66.7	10	6	ABR58766	Alzheimer	Abr58766
112	16	66.7	10	6	AAO31089	Human D5-	Aao31089
113	16	66.7	10	7	ADB79048	Human ant	Adb79048
114	16	66.7	10	7	ADC07160	Corn earw	Adc07160
115	16	66.7	10	7	ADC07162	Tenthredo	Adc07162
116	16	66.7	10	8	ADE85702	Human Eph	Ades702
117	16	66.7	10	8	ADH17813	AbM softw	Adhl7813
118	16	66.7	10	8	ADK09671	Human pap	Adk09671
119	16	66.7	10	8	ADK09188	Human pap	Adk09188
120	16	66.7	10	8	ADN31802	Human Alz	Adn31802
121	16	66.7	10	8	ADM78084	Human SJB	Adm78084
122	16	66.7	10	8	ADP47006	Murine he	Adp47006
123	16	66.7	10	8	ADP47009	Murine he	Adp47009
124	16	66.7	10	8	ADQ72837	Cancer re	Adq72837
125	16	66.7	10	8	ADQ73638	Cancer re	Adq73638
126	16	66.7	10	8	ADQ69470	Cancer re	Adq69470
127	16	66.7	10	8	ADQ72592	Cancer re	Adq72592
128	16	66.7	10	8	ADQ73094	Cancer re	Adq73094
129	16	66.7	10	8	ADQ69764	Cancer re	Adq69764
130	16	66.7	10	8	ADQ73285	Cancer re	Adq73285
131	16	66.7	10	8	ADQ73425	Cancer re	Adq73425
132	16	66.7	10	8	ADQ72862	Cancer re	Adq72862
133	16	66.7	10	8	ADQ73694	Cancer re	Adq73694
134	16	66.7	10	8	ADQ70508	Cancer re	Adq70508
135	16	66.7	10	8	ADQ68354	Cancer re	Adq68354
136	16	66.7	10	8	ADQ73492	Cancer re	Adq73492
137	16	66.7	10	8	ADQ73555	Cancer re	Adq73555
138	16	66.7	10	8	ADQ69105	Cancer re	Adq69105
139	16	66.7	10	8	ADQ68777	Cancer re	Adq68777
140	16	66.7	10	8	ADP47172	Human pho	Adp47172
141	16	66.7	10	8	ADP47157	Human pho	Adp47157
142	16	66.7	10	8	ADP47192	Human pho	Adp47192
143	16	66.7	10	8	ADP47139	Human pho	Adp47139
144	16	66.7	10	8	ADP47175	Human pho	Adp47175
145	16	66.7	10	8	ADR03387	Humanised	Adr03387
146	16	66.7	10	8	ADR03386	Humanised	Adr03386
147	16	66.7	10	8	ADR03383	Humanised	Adr03383
148	16	66.7	10	8	ADR19445	TRPI deri	Adr19445
149	16	66.7	10	8	ADR89805	Anti-CD70	Adr89805
150	16	66.7	11	5	ABP47662	N. mening	Abp47662
151	16	66.7	11	6	AAE31825	Androgen	Aae31825
152	16	66.7	11	6	AAE31805	Androgen	Aae31805
153	16	66.7	11	8	ADG15913	Synthetic	Adg15913
154	16	66.7	11	8	ADG15912	Synthetic	Adg15912
155	16	66.7	11	8	ADG15911	Synthetic	Adg15911
156	16	66.7	11	8	ADQ82020	Camelidae	Adq82020
157	16	66.7	12	2	AAW32654	Human pla	Aaw32654
158	16	66.7	12	2	AAW71784	Mimotope	Aaw71784
159	16	66.7	12	4	AAB60021	Internali	Aab60021
160	16	66.7	12	5	AAE29104	Human DBH	Aae29104
161	16	66.7	12	5	AAE29118	Human DBH	Aae29118
162	16	66.7	12	6	AAE30883	p300-bind	Aae30883
163	16	66.7	12	7	ADA88856	Internali	Ada88856
164	16	66.7	12	7	ADC28198	Synthetic	Adc28198
165	16	66.7	12	8	ADL23639	RAD51C pr	Adl23639
166	16	66.7	13	2	AAR70250	Pan DR-bi	Aar70250
167	16	66.7	13	2	AAW22121	Padre (pa	Aaw22121
168	16	66.7	13	2	AAW64575	Human Fac	Aaw64575
169	16	66.7	13	3	AAW52558	Universal	Aaw52558
170	16	66.7	13	3	AAB36289	Promiscuo	Aab36289
171	16	66.7	13	4	AAB99710	Pan-DR-bi	Aab99710

172	16	66.7	13	4	AAB73644		Aab73644
173	16	66.7	13	4	AAB20154		Aab20154
174	16	66.7	13	5	AAU80293		Aau80293
175	16	66.7	13	5	ABG31776		Abg31776
176	16	66.7	13	5	AAE26369		Aae26369
177	16	66.7	13	6	ABP72696	T cell ep	Abp72696
178	16	66.7	13	6	AAO30456	Pan DR ep	Aao30456
179	16	66.7	13	6	AAO30463	Pan DR ep	Aao30463
180	16	66.7	13	7	ABR82484	Universal	Abr82484
181	16	66.7	13	7	ADC81611	Universal	Adc81611
182	16	66.7	13	8	ADM06893	Pan DR bi	Adm06893
183	16	66.7	13	8	ADP73620	PADRE T c	Adp73620
184	16	66.7	13	8	ADP48563	Pan DR ep	Adp48563
185	16	66.7	13	8	ADP79777	HLA epito	Adp79777
186	16	66.7	14	2	AAR72636	Cladospo	Aar72636
187	16	66.7	14	2	AAW98495	Human pep	Aam98495
188	16	66.7	14	4	AAW98808	Human pep	Aam98808
189	16	66.7	14	5	AAW49498	Ophiostom	Aam49498
190	16	66.7	14	8	ADS54226	Anti-huma	Ads54226
191	16	66.7	15	2	AAW51379	Antigenic	Aar51379
192	16	66.7	15	2	AAW07992	gp120 pep	Aaw07992
193	16	66.7	15	2	AAW76978	Fusion im	Aaw76978
194	16	66.7	15	3	AAW29726	Ganglios	Aab29726
195	16	66.7	15	3	AAW83247	CYB5RP fa	Aay83247
196	16	66.7	15	3	AAW13300	Caenorhab	Aab13300
197	16	66.7	15	3	AAW29164	Peptide #	Aab29164
198	16	66.7	15	4	AAW57714	D.melanog	Aab57714
199	16	66.7	15	5	AAW47919	Human cla	Aam47919
200	16	66.7	15	5	AAO20307	Human ple	Aao20307
201	16	66.7	15	5	AAO20896	N-termina	Aao20896
202	16	66.7	15	5	AAW47805	Miniature	Aam47805
203	16	66.7	15	5	ABW77835	Peptide u	Abb77835
204	16	66.7	15	6	ABR44352	N-termina	Abt44352
205	16	66.7	15	6	ABP58627	Human end	Abp58627
206	16	66.7	15	7	ADF12276	Drosophil	Adf12276
207	16	66.7	15	8	ADQ74628	Cancer re	Adq74628
208	16	66.7	15	8	ADQ74366	Cancer re	Adq74366
209	16	66.7	15	8	ADQ73948	Cancer re	Adq73948
210	16	66.7	15	8	ADQ74000	Cancer re	Adq74000
211	16	66.7	15	8	ADQ74469	Cancer re	Adq74469
212	16	66.7	15	8	ADQ74001	Cancer re	Adq74001
213	16	66.7	15	8	ADQ74122	Cancer re	Adq74122
214	16	66.7	15	8	ADQ74177	Cancer re	Adq74177
215	16	66.7	15	8	ADQ74313	Cancer re	Adq74313
216	16	66.7	15	8	ADQ74213	Cancer re	Adq74213
217	16	66.7	15	8	ADR68288	Androgen	Adr68288
218	16	66.7	16	2	AAW73469	Human sec	Aaw73469
219	16	66.7	16	7	ADC22804	Human G p	Adc22804
220	16	66.7	16	7	AAE39001	Human RAT	Aae39001
221	16	66.7	16	7	ADH14277	Mutated e	Adh14277
222	16	66.7	17	2	AAW05080	Generic e	Aaw05080
223	16	66.7	17	2	AAW07949	gp120 pep	Aaw07949
224	16	66.7	17	2	AAW60595	Cladospo	Aaw60595
225	16	66.7	17	2	AAW22119	Human uri	Aay22119
226	16	66.7	17	3	AAW97262	Calycin c	Aay97262
227	16	66.7	17	5	ABG70457	CDR3 regi	Abg70457
228	16	66.7	17	5	AAU82493	Llama CDR	Aau82493
229	16	66.7	17	5	AAW71385	Yeast eno	Aab71385
230	16	66.7	17	6	ABO27485	Anti-Rh(D	Abo27485
231	16	66.7	17	6	ABO27486	Anti-Rh(D	Abo27486
232	16	66.7	17	7	ADC22805	Human G p	Adc22805
233	16	66.7	17	7	ADD71551	Human uri	Add71551
234	16	66.7	17	7	ADH14278	Mutated e	Adh14278
235	16	66.7	17	8	ABO57902	Human gen	Abo57902
236	16	66.7	17	8	ABO56359	Human gen	Abo56359
237	16	66.7	18	2	AAW18153	Cationic,	Aaw18153
238	16	66.7	18	3	AAW13301	Caenorhab	Aab13301
239	16	66.7	18	3	AAW13299	Caenorhab	Aab13299
240	16	66.7	18	5	AAU91098	Human sec	Aau91098
241	16	66.7	18	5	AAU91081	Human sec	Aau91081
242	16	66.7	18	5	ABG65209	Human alb	Abg65209
243	16	66.7	18	5	ABG65210	Human alb	Abg65210
244	16	66.7	18	8	ADL18453	Antimicro	Adl18453



245	16	66.7	18	8	ADL78477	Adl78477 Albumin f
246	16	66.7	18	8	ADL78476	Adl78476 Albumin f
247	16	66.7	19	3	AAB52193	Aab52193 Human ant
248	16	66.7	19	4	AAM21012	Aam21012 Peptide #
249	16	66.7	19	4	ABB43110	Abb43110 Peptide #
250	16	66.7	19	4	AAM36940	Aam36940 Peptide #
251	16	66.7	19	4	ABB26248	Abb26248 Protein #
252	16	66.7	19	4	AAM76834	Aam76834 Human bon
253	16	66.7	19	4	AAM64011	Aam64011 Human bra
254	16	66.7	19	4	ABG58507	Abg58507 Human liv
255	16	66.7	19	5	ABG45977	Abg45977 Human pep
256	16	66.7	19	8	ADR68329	Adr68329 Androgen
257	16	66.7	20	2	AAR63841	Aar63841 HIV-1 gp1
258	16	66.7	20	2	AAW08045	Aaw08045 HIV pepti
259	16	66.7	20	2	AAW08044	Aaw08044 HIV pepti
260	16	66.7	20	2	AAR88352	Aar88352 Adenomato
261	16	66.7	20	2	AAV02155	Aay02155 Peptide u
262	16	66.7	20	3	AAV07099	Aay70799 Murine an
263	16	66.7	20	3	AAB10376	Aab10376 HBV core
264	16	66.7	20	4	ABB50791	Abb50791 Human sec
265	16	66.7	20	5	AAE20323	Aae20323 Human B7-
266	16	66.7	20	5	ABP30920	Abp30920 OE8 antib
267	16	66.7	20	5	ABP30919	Abp30919 OE8 antib
268	16	66.7	20	6	ABO45048	Abo45048 Novel hum
269	16	66.7	20	7	ABO2528	Abo26528 Protein a
270	16	66.7	20	7	ADA08565	Ada08565 Human OE8
271	16	66.7	20	7	ADA08564	Ada08564 Human OE8
272	16	66.7	20	7	ADC99562	Adc99562 Cancer-re
273	16	66.7	20	7	ABW01365	Abw01365 Human HEA
274	16	66.7	20	7	ADF08907	Adf08907 Secreted
275	16	66.7	20	7	ADF08908	Adf08908 Secreted
276	16	66.7	20	7	ADF09113	Adf09113 Secreted
277	16	66.7	20	7	ADF09114	Adf09114 Secreted
278	16	66.7	20	7	ADG46195	Adg46195 OE8 antib
279	16	66.7	20	7	ADG46194	Adg46194 OE8 antib
280	16	66.7	20	8	ADR05597	Adr05597 Novel ssd
281	15	62.5	5	2	AAW17807	Aaw17807 Cyclic pe
282	15	62.5	5	2	AAW17812	Aaw17812 Cyclic pe
283	15	62.5	5	2	AAW17806	Aaw17806 Cyclic pe
284	15	62.5	5	2	AAV33038	Aay33038 Carbohydr
285	15	62.5	5	3	AAB07280	Aab07280 Motif bin
286	15	62.5	5	5	ABP67371	Abp67371 Human CD6
287	15	62.5	5	6	ABU87123	Abu87123 Carbohydr
288	15	62.5	5	8	ADR68292	Adr68292 Androgen
289	15	62.5	5	8	ADR68294	Adr68294 Androgen
290	15	62.5	6	1	AAP50709	Aap50709 Hexapepti
291	15	62.5	6	2	AAR54182	Aar54182 CHA255 11
292	15	62.5	6	2	AAR88913	Aar88913 p53/MDM2
293	15	62.5	6	2	AAR88915	Aar88915 p53/minim
294	15	62.5	6	2	AAW13606	Aaw13606 p53 prote
295	15	62.5	6	2	AAV04677	Aay04677 Peptide #
296	15	62.5	6	3	AAB17074	Aab17074 Mdm/hdm a
297	15	62.5	6	3	ABB73169	Abb73169 Mdm/hdm a
298	15	62.5	6	5	ABP67361	Abp67361 Human CD6
299	15	62.5	6	6	ABR46285	AbR46285 Staphyloc
300	15	62.5	6	6	ABR46643	AbR46643 Staphyloc
301	15	62.5	6	6	ABR45148	AbR45148 Staphyloc
302	15	62.5	6	6	ABR46479	AbR46479 Staphyloc
303	15	62.5	6	6	ABR47051	AbR47051 Staphyloc
304	15	62.5	6	6	ABR47069	AbR47069 Staphyloc
305	15	62.5	6	6	ABR45893	AbR45893 Staphyloc
306	15	62.5	6	6	ABR46491	AbR46491 Staphyloc
307	15	62.5	6	6	ABR46607	AbR46607 Staphyloc
308	15	62.5	6	6	ABR46700	AbR46700 Staphyloc
309	15	62.5	6	6	ABR45188	AbR45188 Staphyloc
310	15	62.5	6	6	ABR45173	AbR45173 Staphyloc
311	15	62.5	6	6	ABR45523	AbR45523 Staphyloc
312	15	62.5	6	6	ABR45875	AbR45875 Staphyloc
313	15	62.5	6	6	ABR45902	AbR45902 Staphyloc
314	15	62.5	6	6	ABR46286	AbR46286 Staphyloc
315	15	62.5	6	6	ABR46307	AbR46307 Staphyloc
316	15	62.5	6	6	ABR47086	AbR47086 Staphyloc
317	15	62.5	6	6	ABR45174	AbR45174 Staphyloc

318	15	62.5	6	6	ABR46423	AbR46423 Staphyloc
319	15	62.5	6	6	ABR46659	AbR46659 Staphyloc
320	15	62.5	6	6	ABR46719	AbR46719 Staphyloc
321	15	62.5	6	6	ABR46759	AbR46759 Staphyloc
322	15	62.5	6	6	ABR45182	AbR45182 Staphyloc
323	15	62.5	6	6	ABR45517	AbR45517 Staphyloc
324	15	62.5	6	6	ABR45518	AbR45518 Staphyloc
325	15	62.5	6	6	ABR46301	AbR46301 Staphyloc
326	15	62.5	6	6	ABR46379	AbR46379 Staphyloc
327	15	62.5	6	6	ABR46439	AbR46439 Staphyloc
328	15	62.5	6	6	ABR46475	AbR46475 Staphyloc
329	15	62.5	6	6	ABR46495	AbR46495 Staphyloc
330	15	62.5	6	6	ABR46531	AbR46531 Staphyloc
331	15	62.5	6	6	ABR46694	AbR46694 Staphyloc
332	15	62.5	6	6	ABR45501	AbR45501 Staphyloc
333	15	62.5	6	6	ABR45510	AbR45510 Staphyloc
334	15	62.5	6	6	ABR45901	AbR45901 Staphyloc
335	15	62.5	6	6	ABR45915	AbR45915 Staphyloc
336	15	62.5	6	6	ABR46268	AbR46268 Staphyloc
337	15	62.5	6	6	ABR45894	AbR45894 Staphyloc
338	15	62.5	6	6	ABR46308	AbR46308 Staphyloc
339	15	62.5	6	6	ABR46435	AbR46435 Staphyloc
340	15	62.5	6	6	ABR46535	AbR46535 Staphyloc
341	15	62.5	6	6	ABR46678	AbR46678 Staphyloc
342	15	62.5	6	6	ABR45166	AbR45166 Staphyloc
343	15	62.5	6	6	ABR45181	AbR45181 Staphyloc
344	15	62.5	6	6	ABR46293	AbR46293 Staphyloc
345	15	62.5	6	6	ABR46647	AbR46647 Staphyloc
346	15	62.5	6	6	ABR46693	AbR46693 Staphyloc
347	15	62.5	6	6	ABR46699	AbR46699 Staphyloc
348	15	62.5	6	6	ABR47077	AbR47077 Staphyloc
349	15	62.5	6	6	ABR47092	AbR47092 Staphyloc
350	15	62.5	6	6	ABR45147	AbR45147 Staphyloc
351	15	62.5	6	6	ABR45187	AbR45187 Staphyloc
352	15	62.5	6	6	ABR45484	AbR45484 Staphyloc
353	15	62.5	6	6	ABR45509	AbR45509 Staphyloc
354	15	62.5	6	6	ABR46267	AbR46267 Staphyloc
355	15	62.5	6	6	ABR45909	AbR45909 Staphyloc
356	15	62.5	6	6	ABR46383	AbR46383 Staphyloc
357	15	62.5	6	6	ABR46715	AbR46715 Staphyloc
358	15	62.5	6	6	ABR46755	AbR46755 Staphyloc
359	15	62.5	6	6	ABR47070	AbR47070 Staphyloc
360	15	62.5	6	6	ABR47085	AbR47085 Staphyloc
361	15	62.5	6	6	ABR45502	AbR45502 Staphyloc
362	15	62.5	6	6	ABR45876	AbR45876 Staphyloc
363	15	62.5	6	6	ABR46294	AbR46294 Staphyloc
364	15	62.5	6	6	ABR46419	AbR46419 Staphyloc
365	15	62.5	6	6	ABR46660	AbR46660 Staphyloc
366	15	62.5	6	6	ABR47052	AbR47052 Staphyloc
367	15	62.5	6	6	ABR47078	AbR47078 Staphyloc
368	15	62.5	6	6	ABR45165	AbR45165 Staphyloc
369	15	62.5	6	6	ABR45483	AbR45483 Staphyloc
370	15	62.5	6	6	ABR45524	AbR45524 Staphyloc
371	15	62.5	6	6	ABR45910	AbR45910 Staphyloc
372	15	62.5	6	6	ABR46685	AbR46685 Staphyloc
373	15	62.5	6	6	ABR46686	AbR46686 Staphyloc
374	15	62.5	6	6	ABR47091	AbR47091 Staphyloc
375	15	62.5	6	6	ABR45916	AbR45916 Staphyloc
376	15	62.5	6	6	ABR46302	AbR46302 Staphyloc
377	15	62.5	6	6	ABR46603	AbR46603 Staphyloc
378	15	62.5	6	6	ABR46677	AbR46677 Staphyloc
379	15	62.5	6	6	ABG73432	Abg73432 Human p53
380	15	62.5	6	6	ABG73433	Abg73433 Human p53
381	15	62.5	6	7	ABR82526	AbR82526 Human apy
382	15	62.5	6	7	ADJ73323	Adj73323 Mdm/hdm a
383	15	62.5	6	8	ADJ52957	Adj52957 CH1 delet
384	15	62.5	6	8	ADJ51918	Adj51918 CH1 delet
385	15	62.5	7	1	AAP93327	Aap93327 Sequence
386	15	62.5	7	2	AAR89921	Aar89921 Tryptic p
387	15	62.5	7	2	AAR89921	Aar89921 Antibody
388	15	62.5	7	2	AAR89925	Aar89925 p53 bindi
389	15	62.5	7	2	AAV34151	Aay34151 Angiopole
390	15	62.5	7	2	AAW94141	Aaw94141 FG loop s

391	15	62.5	7	3	AAy82380	Aay82380	Heptapept	464	15	62.5	8	6	ABR54070	Abr54070	Beta-secr
392	15	62.5	7	3	AAy57789	Aay57789	TRAM-inte	465	15	62.5	8	6	ABR54078	Abr54078	Beta-secr
393	15	62.5	7	3	AAB23205	Aab23205	Hsp47-bin	466	15	62.5	8	6	ABR54080	Abr54080	Beta-secr
394	15	62.5	7	3	AAB01512	Aab01512	Peptide w	467	15	62.5	8	6	ABR53951	Abr53951	Beta-secr
395	15	62.5	7	4	AAB73050	Aab73050	Luteinisi	468	15	62.5	8	6	ABR54049	Abr54049	Beta-secr
396	15	62.5	7	4	AAM47040	Aam47040	H11 bindi	469	15	62.5	8	6	ABR53996	Abr53996	Beta-secr
397	15	62.5	7	4	AAM46975	Aam46975	H11 bindi	470	15	62.5	8	6	ABR54000	Abr54000	Beta-secr
398	15	62.5	7	4	AAM46990	Aam46990	H11 bindi	471	15	62.5	8	6	ABR54047	Abr54047	Beta-secr
399	15	62.5	7	4	AAM46970	Aam46970	H11 bindi	472	15	62.5	8	6	ABR54025	Abr54025	Beta-secr
400	15	62.5	7	5	ABB94392	Abb94392	Ubiquitin	473	15	62.5	8	6	ABR53994	Abr53994	Beta-secr
401	15	62.5	7	5	ABP67352	Abp67352	Human CD6	474	15	62.5	8	6	ABR54023	Abr54023	Beta-secr
402	15	62.5	7	5	ABP67752	Abp67752	Human CD6	475	15	62.5	8	6	ABR54017	Abr54017	Beta-secr
403	15	62.5	7	5	ABG77724	Abg77724	Targettin	476	15	62.5	8	6	ADA44112	Ada44112	Human sec
404	15	62.5	7	7	ADL17146	Adl17146	Phage-dis	477	15	62.5	8	6	ABP71906	Abp71906	R. erythr
405	15	62.5	7	7	ADL17080	Adl17080	Phage-dis	478	15	62.5	8	7	ADC20439	Adc20439	Human sec
406	15	62.5	7	7	ADL17130	Adl17130	Phage-dis	479	15	62.5	8	7	ADC07142	Adc07142	Golden-wi
407	15	62.5	7	7	ADL17176	Adl17176	Phage-dis	480	15	62.5	8	7	ADC07143	Adc07143	Emperor d
408	15	62.5	7	7	ADL17077	Adl17077	Phage-dis	481	15	62.5	8	7	ADF10743	Adf10743	Human sec
409	15	62.5	7	7	ADL17227	Adl17227	Phage-dis	482	15	62.5	8	7	ADL17302	Adl17302	DENSIN-18
410	15	62.5	7	8	ADH08433	Adh08433	IGE produ	483	15	62.5	8	8	ADK01990	Adk01990	Hepatitis
411	15	62.5	7	8	ADI32411	Adi32411	FG loop p	484	15	62.5	8	8	ADK10578	Adk10578	Human pap
412	15	62.5	7	8	ADR68302	Adr68302	Androgen	485	15	62.5	8	8	ADQ28799	Adq28799	Human cel
413	15	62.5	8	2	AAR61038	Aar61038	Dynorphin	486	15	62.5	8	8	ADQ28800	Adq28800	Human cel
414	15	62.5	8	2	AAW94606	Aaw94606	Human ins	487	15	62.5	8	8	ADR69714	Adr69714	Novel hyb
415	15	62.5	8	2	AAy21268	Aay21268	Human sem	488	15	62.5	8	8	ADS00534	Ads00534	Human Apo
416	15	62.5	8	2	AAW37209	Aaw37209	Human onc	489	15	62.5	8	8	ADS00532	Ads00532	Human Apo
417	15	62.5	8	2	AAW37186	Aaw37186	Human onc	490	15	62.5	8	8	ADS00533	Ads00533	Human Apo
418	15	62.5	8	2	AAW37176	Aaw37176	Human onc	491	15	62.5	8	8	ADS00535	Ads00535	Human Apo
419	15	62.5	8	2	AAW37185	Aaw37185	Human onc	492	15	62.5	8	8	ADR99992	Adr99992	Human apo
420	15	62.5	8	2	AAW37206	Aaw37206	Human MDM	493	15	62.5	8	8	ADR99995	Adr99995	Human apo
421	15	62.5	8	2	AAW37177	Aaw37177	Human onc	494	15	62.5	8	8	ADR99994	Adr99994	Human apo
422	15	62.5	8	2	AAW37207	Aaw37207	Human MDM	495	15	62.5	8	8	ADR99993	Adr99993	Human apo
423	15	62.5	8	2	AAy25556	Aay25556	Human MHC	496	15	62.5	8	8	ADS54213	Ads54213	Human apo
424	15	62.5	8	3	AAy85386	Aay85386	IL-2 deri	497	15	62.5	8	8	ADS54215	Ads54215	Human apo
425	15	62.5	8	3	AAy85387	Aay85387	IL-2 deri	498	15	62.5	8	8	ADS54216	Ads54216	Human apo
426	15	62.5	8	3	AAy85388	Aay85388	IL-2 deri	499	15	62.5	8	8	ADS54214	Ads54214	Human apo
427	15	62.5	8	3	AAB09130	Aab09130	Hepatitis	500	15	62.5	9	2	AAR53342	Aar53342	Chimeric
428	15	62.5	8	4	AAB62220	Aab62220	Glycine m	501	15	62.5	9	2	AAW00686	Aaw00686	Peptide c
429	15	62.5	8	5	ABP67745	Abp67745	Human CD6	502	15	62.5	9	2	AAW45692	Aaw45692	HBV env 3
430	15	62.5	8	5	ABP67344	Abp67344	Human CD6	503	15	62.5	9	2	AAW39724	Aaw39724	Human car
431	15	62.5	8	6	ABP99660	Abp99660	Human sec	504	15	62.5	9	2	AAW43849	Aaw43849	Specific
432	15	62.5	8	6	ABP98083	Abp98083	Amino aci	505	15	62.5	9	2	AAW43845	Aaw43845	Specific
433	15	62.5	8	6	ABP98084	Abp98084	Amino aci	506	15	62.5	9	2	AAW81310	Aaw81310	Human iNO
434	15	62.5	8	6	ABP98081	Abp98081	Amino aci	507	15	62.5	9	2	AAW81250	Aaw81250	Human iNO
435	15	62.5	8	6	ABP98082	Abp98082	Amino aci	508	15	62.5	9	2	AAW72493	Aaw72493	Dengue vi
436	15	62.5	8	6	ABR01140	Abr01140	Human gen	509	15	62.5	9	2	AAW46351	Aaw46351	Amino aci
437	15	62.5	8	6	ADA98274	Ada98274	Human sec	510	15	62.5	9	2	AAW46349	Aaw46349	Amino aci
438	15	62.5	8	6	ABP68159	Abp68159	Bacillus	511	15	62.5	9	2	AAW46348	Aaw46348	Amino aci
439	15	62.5	8	6	ABP68163	Abp68163	Bacillus	512	15	62.5	9	2	AAW46350	Aaw46350	Amino aci
440	15	62.5	8	6	ABP68181	Abp68181	Bacillus	513	15	62.5	9	2	AAW37199	Aaw37199	Human onc
441	15	62.5	8	6	ABP68158	Abp68158	Bacillus	514	15	62.5	9	2	AAy46725	Aay46725	Immunogen
442	15	62.5	8	6	ABP68166	Abp68166	Bacillus	515	15	62.5	9	2	AAy25555	Aay25555	Human MHC
443	15	62.5	8	6	ABP68160	Abp68160	Bacillus	516	15	62.5	9	2	AAy27259	Aay27259	Human tum
444	15	62.5	8	6	ABR54027	Abr54027	Beta-secr	517	15	62.5	9	3	AAy84757	Aay84757	Antigenic
445	15	62.5	8	6	ABR54059	Abr54059	Beta-secr	518	15	62.5	9	3	AAy84765	Aay84765	Antigenic
446	15	62.5	8	6	ABR53990	Abr53990	Beta-secr	519	15	62.5	9	3	AAy84756	Aay84756	Antigenic
447	15	62.5	8	6	ABR54021	Abr54021	Beta-secr	520	15	62.5	9	3	AAy84758	Aay84758	Antigenic
448	15	62.5	8	6	ABR54074	Abr54074	Beta-secr	521	15	62.5	9	3	AAy84759	Aay84759	Antigenic
449	15	62.5	8	6	ABR53998	Abr53998	Beta-secr	522	15	62.5	9	3	AAy71328	Aay71328	Rat neur
450	15	62.5	8	6	ABR54015	Abr54015	Beta-secr	523	15	62.5	9	3	AAB23806	Aab23806	Phage dis
451	15	62.5	8	6	ABR53986	Abr53986	Beta-secr	524	15	62.5	9	3	AAB34807	Aab34807	Human sec
452	15	62.5	8	6	ABR54072	Abr54072	Beta-secr	525	15	62.5	9	3	AAB01629	Aab01629	Chimaeric
453	15	62.5	8	6	ABR54045	Abr54045	Beta-secr	526	15	62.5	9	4	AAB46945	Aab46945	Human SAR
454	15	62.5	8	6	ABR54068	Abr54068	Beta-secr	527	15	62.5	9	4	ABM00050	Abm00050	Savinas a
455	15	62.5	8	6	ABR53988	Abr53988	Beta-secr	528	15	62.5	9	4	ABM00058	Abm00058	Savinas a
456	15	62.5	8	6	ABR54053	Abr54053	Beta-secr	529	15	62.5	9	4	ABM00059	Abm00059	Savinas a
457	15	62.5	8	6	ABR54055	Abr54055	Beta-secr	530	15	62.5	9	4	AAb75691	Aab75691	HLA class
458	15	62.5	8	6	ABR54057	Abr54057	Beta-secr	531	15	62.5	9	4	AAG63257	Aag63257	Complemen
459	15	62.5	8	6	ABR54076	Abr54076	Beta-secr	532	15	62.5	9	4	AAM24637	Aam24637	Human MHC
460	15	62.5	8	6	ABR54082	Abr54082	Beta-secr	533	15	62.5	9	5	ABG79074	Abg79074	Human CEA
461	15	62.5	8	6	ABR54051	Abr54051	Beta-secr	534	15	62.5	9	5	ABG35129	Abg35129	Pancreati
462	15	62.5	8	6	ABR53992	Abr53992	Beta-secr	535	15	62.5	9	5	ABP47446	Abp47446	N. mening
463	15	62.5	8	6	ABR54019	Abr54019	Beta-secr	536	15	62.5	9	5	ABG97340	Abg97340	Human leu

537	15	62.5	9	5	ABG97341	Abg97341	Human	leu	610	15	62.5	9	6	ABJ61113	Abj61113	184P1E2-r
538	15	62.5	9	5	AAO18872	Aao18872	Human	CEA	611	15	62.5	9	6	ABJ61402	Abj61402	184P1E2-r
539	15	62.5	9	5	ABP67738	Abp67738	Human	CD6	612	15	62.5	9	6	ABJ58361	Abj58361	184P1E2-r
540	15	62.5	9	5	ABP67337	Abp67337	Human	CD6	613	15	62.5	9	6	ABJ60622	Abj60622	184P1E2-r
541	15	62.5	9	5	ABJ11741	Abj11741	Human	125	614	15	62.5	9	6	ABJ63441	Abj63441	184P1E2-r
542	15	62.5	9	5	ABJ12589	Abj12589	Human	125	615	15	62.5	9	6	ABJ63923	Abj63923	184P1E2-r
543	15	62.5	9	5	ABJ12352	Abj12352	Human	125	616	15	62.5	9	6	ABJ63965	Abj63965	184P1E2-r
544	15	62.5	9	5	ABJ11603	Abj11603	Human	125	617	15	62.5	9	6	ABJ57333	Abj57333	184P1E2-r
545	15	62.5	9	5	ABJ11833	Abj11833	Human	125	618	15	62.5	9	6	ABJ58971	Abj58971	184P1E2-r
546	15	62.5	9	5	ABJ12880	Abj12880	Human	125	619	15	62.5	9	6	ABJ60509	Abj60509	184P1E2-r
547	15	62.5	9	5	ABJ13175	Abj13175	Human	125	620	15	62.5	9	6	ABJ62494	Abj62494	184P1E2-r
548	15	62.5	9	5	ABJ12444	Abj12444	Human	125	621	15	62.5	9	6	ABJ64062	Abj64062	184P1E2-r
549	15	62.5	9	5	ABJ12211	Abj12211	Human	125	622	15	62.5	9	6	ABJ64839	Abj64839	184P1E2-r
550	15	62.5	9	5	ABJ09544	Abj09544	Hepatitis		623	15	62.5	9	6	ABJ65025	Abj65025	184P1E2-r
551	15	62.5	9	5	ABG60517	Abg60517	Selective		624	15	62.5	9	6	ABJ57376	Abj57376	184P1E2-r
552	15	62.5	9	5	AAE31317	Aae31317	Human	p53	625	15	62.5	9	6	ABJ63110	Abj63110	184P1E2-r
553	15	62.5	9	5	AAE31316	Aae31316	Human	p53	626	15	62.5	9	6	ABJ63111	Abj63111	184P1E2-r
554	15	62.5	9	5	AAE31395	Aae31395	Human	p53	627	15	62.5	9	6	ABJ62218	Abj62218	184P1E2-r
555	15	62.5	9	5	AAU09701	Aau09701	Anti-mela		628	15	62.5	9	6	ABO27023	AbO27023	Yellow fe
556	15	62.5	9	5	AAU96014	Aau96014	Carcino e		629	15	62.5	9	6	ABO27024	AbO27024	West nile
557	15	62.5	9	6	ABJ20021	Abj20021	MHC bindi		630	15	62.5	9	6	ABO27025	AbO27025	Murray va
558	15	62.5	9	6	ABR56915	Abr56915	Pancreat		631	15	62.5	9	6	ABO27026	AbO27026	Kunjin vi
559	15	62.5	9	6	ABR24615	Abr24615	Human	can	632	15	62.5	9	7	ADA07879	Ada07879	Viral pro
560	15	62.5	9	6	ABR24590	Abr24590	Human	can	633	15	62.5	9	7	ADA07878	Ada07878	Viral pro
561	15	62.5	9	6	ABR25041	Abr25041	Human	can	634	15	62.5	9	7	ADA07881	Ada07881	Viral pro
562	15	62.5	9	6	ABR25394	Abr25394	Human	can	635	15	62.5	9	7	ADA07880	Ada07880	Viral pro
563	15	62.5	9	6	ABR24408	Abr24408	Human	can	636	15	62.5	9	7	ADD26353	Add26353	Staphyloc
564	15	62.5	9	6	ABR24647	Abr24647	Human	can	637	15	62.5	9	7	ADD94560	Add94560	Human SIM
565	15	62.5	9	6	ABR230240	Abr230240	Human	can	638	15	62.5	9	7	ADD94768	Add94768	Human SIM
566	15	62.5	9	6	ABR25665	Abr25665	Human	can	639	15	62.5	9	7	ADD94574	Add94574	Human SIM
567	15	62.5	9	6	ABR25205	Abr25205	Human	can	640	15	62.5	9	7	ADG38574	Adg38574	Human car
568	15	62.5	9	6	ABR24809	Abr24809	Human	can	641	15	62.5	9	7	ADG38572	Adg38572	Human car
569	15	62.5	9	6	ABR25596	Abr25596	Human	can	642	15	62.5	9	7	AAO24240	Aao24240	MHC bindi
570	15	62.5	9	6	ABR23040	Abr23040	Human	can	643	15	62.5	9	7	AAO24239	Aao24239	MHC bindi
571	15	62.5	9	6	ABR21629	Abr21629	Human	can	644	15	62.5	9	7	ADI03011	Adi03011	Human mon
572	15	62.5	9	6	ABJ58972	Abj58972	184P1E2-r		645	15	62.5	9	7	ADL17217	Adl17217	Phage-dis
573	15	62.5	9	6	ABJ59510	Abj59510	184P1E2-r		646	15	62.5	9	7	ADL17251	Adl17251	Phage-dis
574	15	62.5	9	6	ABJ63247	Abj63247	184P1E2-r		647	15	62.5	9	7	ADL17455	Adl17455	Human SNT
575	15	62.5	9	6	ABJ65204	Abj65204	184P1E2-r		648	15	62.5	9	7	ADL17228	Adl17228	Phage-dis
576	15	62.5	9	6	ABJ61887	Abj61887	184P1E2-r		649	15	62.5	9	7	ADK65171	Adk65171	Human VEG
577	15	62.5	9	6	ABJ63999	Abj63999	184P1E2-r		650	15	62.5	9	7	ADK65120	Adk65120	Human VEG
578	15	62.5	9	6	ABJ64840	Abj64840	184P1E2-r		651	15	62.5	9	8	ADG89640	Adg89640	Class I H
579	15	62.5	9	6	ABJ60510	Abj60510	184P1E2-r		652	15	62.5	9	8	ADK39506	Adk39506	Hepatitis
580	15	62.5	9	6	ABJ62064	Abj62064	184P1E2-r		653	15	62.5	9	8	ADK10586	Adk10586	Human pap
581	15	62.5	9	6	ABJ62495	Abj62495	184P1E2-r		654	15	62.5	9	8	ADK03265	Adk03265	Hepatitis
582	15	62.5	9	6	ABJ65468	Abj65468	184P1E2-r		655	15	62.5	9	8	ADK05899	Adk05899	Hepatitis
583	15	62.5	9	6	ABJ58585	Abj58585	184P1E2-r		656	15	62.5	9	8	ADK10587	Adk10587	Human pap
584	15	62.5	9	6	ABJ59876	Abj59876	184P1E2-r		657	15	62.5	9	8	ADK05107	Adk05107	Hepatitis
585	15	62.5	9	6	ABJ59965	Abj59965	184P1E2-r		658	15	62.5	9	8	ADK10585	Adk10585	Human pap
586	15	62.5	9	6	ABJ61159	Abj61159	184P1E2-r		659	15	62.5	9	8	ADK05911	Adk05911	Hepatitis
587	15	62.5	9	6	ABJ64098	Abj64098	184P1E2-r		660	15	62.5	9	8	ADK10584	Adk10584	Human pap
588	15	62.5	9	6	ABJ64452	Abj64452	184P1E2-r		661	15	62.5	9	8	ADM12337	Adm12337	MHC class
589	15	62.5	9	6	ABJ60738	Abj60738	184P1E2-r		662	15	62.5	9	8	ADL19695	Adl19695	125P5C8 p
590	15	62.5	9	6	ABJ65172	Abj65172	184P1E2-r		663	15	62.5	9	8	ADL19077	Adl19077	125P5C8 p
591	15	62.5	9	6	ABJ59130	Abj59130	184P1E2-r		664	15	62.5	9	8	ADL18847	Adl18847	125P5C8 p
592	15	62.5	9	6	ABJ59833	Abj59833	184P1E2-r		665	15	62.5	9	8	ADL19603	Adl19603	125P5C8 p
593	15	62.5	9	6	ABJ59945	Abj59945	184P1E2-r		666	15	62.5	9	8	ADL19840	Adl19840	125P5C8 p
594	15	62.5	9	6	ABJ60623	Abj60623	184P1E2-r		667	15	62.5	9	8	ADL18985	Adl18985	125P5C8 p
595	15	62.5	9	6	ABJ63529	Abj63529	184P1E2-r		668	15	62.5	9	8	ADL20131	Adl20131	125P5C8 p
596	15	62.5	9	6	ABJ65631	Abj65631	184P1E2-r		669	15	62.5	9	8	ADL20425	Adl20425	125P5C8 p
597	15	62.5	9	6	ABJ60467	Abj60467	184P1E2-r		670	15	62.5	9	8	ADL19462	Adl19462	125P5C8 p
598	15	62.5	9	6	ABJ61114	Abj61114	184P1E2-r		671	15	62.5	9	8	ADO38557	Ado38557	Carcinoem
599	15	62.5	9	6	ABJ63481	Abj63481	184P1E2-r		672	15	62.5	9	8	ADP25801	Adp25801	Plasmodiu
600	15	62.5	9	6	ABJ61514	Abj61514	184P1E2-r		673	15	62.5	9	8	ADQ28798	Adq28798	Human cel
601	15	62.5	9	6	ABJ61798	Abj61798	184P1E2-r		674	15	62.5	9	8	ADP79788	Adp79788	Human HLA
602	15	62.5	9	6	ABJ62063	Abj62063	184P1E2-r		675	15	62.5	9	8	ADP80098	Adp80098	Human HLA
603	15	62.5	9	6	ABJ62639	Abj62639	184P1E2-r		676	15	62.5	10	2	AAR89917	Aar89917	Human p53
604	15	62.5	9	6	ABJ58529	Abj58529	184P1E2-r		677	15	62.5	10	2	AAR89918	Aar89918	Mouse p53
605	15	62.5	9	6	ABJ63337	Abj63337	184P1E2-r		678	15	62.5	10	2	AAW32713	Aaw32713	Human pla
606	15	62.5	9	6	ABJ64453	Abj64453	184P1E2-r		679	15	62.5	10	2	AAW13605	Aaw13605	p53 prote
607	15	62.5	9	6	ABJ61556	Abj61556	184P1E2-r		680	15	62.5	10	2	AAW37961	Aaw37961	Peptide s
608	15	62.5	9	6	ABJ62994	Abj62994	184P1E2-r		681	15	62.5	10	2	AAW62010	Aaw62010	Heavy cha
609	15	62.5	9	6	ABJ61053	Abj61053	184P1E2-r		682	15	62.5	10	2	AAW37198	Aaw37198	Human onc

683	15	62.5	10	2	AAY25554	Aay25554 Human MHC	756	15	62.5	10	6	ABJ67907	Abj67907 184PIE2-r
684	15	62.5	10	2	AAY40648	Aay40648 S2 deriva	757	15	62.5	10	6	ABJ68931	Abj68931 184PIE2-r
685	15	62.5	10	3	AAY82337	Aay82337 Humanised	758	15	62.5	10	6	ABJ65862	Abj65862 184PIE2-r
686	15	62.5	10	3	AAB29987	Aab29987 Scaffold	759	15	62.5	10	6	ABJ66586	Abj66586 184PIE2-r
687	15	62.5	10	4	AAM24682	Aam24682 Human MHC	760	15	62.5	10	6	ABJ67496	Abj67496 184PIE2-r
688	15	62.5	10	4	AAB76236	Aab76236 Tumour as	761	15	62.5	10	6	ABJ66002	Abj66002 184PIE2-r
689	15	62.5	10	4	AAB76069	Aab76069 Tumour as	762	15	62.5	10	6	ABJ67609	Abj67609 184PIE2-r
690	15	62.5	10	4	AAG87403	Aag87403 Saccharom	763	15	62.5	10	6	ABJ69115	Abj69115 184PIE2-r
691	15	62.5	10	4	AAG87402	Aag87402 Saccharom	764	15	62.5	10	6	ABJ65863	Abj65863 184PIE2-r
692	15	62.5	10	4	ABB52377	Abb52377 Human API	765	15	62.5	10	6	ABJ58400	Abj58400 184PIE2-r
693	15	62.5	10	4	AAB35294	Aab35294 Murine PS	766	15	62.5	10	6	ABJ68318	Abj68318 184PIE2-r
694	15	62.5	10	5	ABB06172	Abb06172 Gonadotro	767	15	62.5	10	6	ABJ68081	Abj68081 184PIE2-r
695	15	62.5	10	5	ABG70414	Abg70414 CDRI/H1 r	768	15	62.5	10	6	ABJ68082	Abj68082 184PIE2-r
696	15	62.5	10	5	AAU98467	Aau98467 Novel hum	769	15	62.5	10	6	ABJ68164	Abj68164 184PIE2-r
697	15	62.5	10	5	ABP67331	Abp67331 Human CD6	770	15	62.5	10	7	ADC07158	Adc07158 Platypleu
698	15	62.5	10	5	ABP67732	Abp67732 Human CD6	771	15	62.5	10	7	ADD94159	Add94159 Mouse HUI
699	15	62.5	10	5	ABJ13821	Abj13821 Human 125	772	15	62.5	10	7	ADD94141	Add94141 Mouse HUI
700	15	62.5	10	5	ABJ11673	Abj11673 Human 125	773	15	62.5	10	7	ADD94158	Add94158 Mouse HUI
701	15	62.5	10	5	ABJ13682	Abj13682 Human 125	774	15	62.5	10	7	ADD94162	Add94162 Mouse HUI
702	15	62.5	10	5	ABJ14107	Abj14107 Human 125	775	15	62.5	10	7	ADD94161	Add94161 Mouse HUI
703	15	62.5	10	5	ABJ13459	Abj13459 Human 125	776	15	62.5	10	7	ADD94160	Add94160 Mouse HUI
704	15	62.5	10	5	ABJ13896	Abj13896 Human 125	777	15	62.5	10	7	ADD94632	Add94632 Human SIM
705	15	62.5	10	5	ABJ11759	Abj11759 Human 125	778	15	62.5	10	7	ADF10400	Adf10400 Serum alb
706	15	62.5	10	5	ABJ14159	Abj14159 Human 125	779	15	62.5	10	7	ADL17313	Adl17313 DENGIN-18
707	15	62.5	10	5	AAU82450	Aau82450 Llana CDR	780	15	62.5	10	7	ADL17226	Adl17226 Phage-dis
708	15	62.5	10	5	AAU82812	Aau82812 Human Cal	781	15	62.5	10	7	ADL17327	Adl17327 Human scr
709	15	62.5	10	5	AAU82829	Aau82829 Human Cal	782	15	62.5	10	7	ADL17218	Adl17218 Phage-dis
710	15	62.5	10	6	ABP70583	Abp70583 Hepatitis	783	15	62.5	10	7	ADL17215	Adl17215 Phage-dis
711	15	62.5	10	6	ABO10708	Abol0708 Murine J4	784	15	62.5	10	7	ADL17219	Adl17219 Phage-dis
712	15	62.5	10	6	ABR25335	Abr25335 Human can	785	15	62.5	10	7	ADM07751	Adm07751 Canine im
713	15	62.5	10	6	ABR25737	Abr25737 Human can	786	15	62.5	10	7	ADM07748	Adm07748 Canine im
714	15	62.5	10	6	ABR25754	Abr25754 Human can	787	15	62.5	10	7	ADM07744	Adm07744 Canine im
715	15	62.5	10	6	ABR23106	Abr23106 Human can	788	15	62.5	10	8	ADG38998	Adg38998 Humanised
716	15	62.5	10	6	ABR21698	Abr21698 Human can	789	15	62.5	10	8	ADG78885	Adg78885 Human p53
717	15	62.5	10	6	ABR22470	Abr22470 Human can	790	15	62.5	10	8	ADI82158	Adi82158 Plasma re
718	15	62.5	10	6	ABR24908	Abr24908 Human can	791	15	62.5	10	8	ADJ50603	Adj50603 Human ser
719	15	62.5	10	6	ABR23870	Abr23870 Human can	792	15	62.5	10	8	ADK10594	Adk10594 Human pap
720	15	62.5	10	6	ABR25307	Abr25307 Human can	793	15	62.5	10	8	ADK03263	Adk03263 Hepatitis
721	15	62.5	10	6	ABR24723	Abr24723 Human can	794	15	62.5	10	8	ADK03268	Adk03268 Hepatitis
722	15	62.5	10	6	ABR20303	Abr20303 Human can	795	15	62.5	10	8	ADK10595	Adk10595 Human pap
723	15	62.5	10	6	ABR25496	Abr25496 Human can	796	15	62.5	10	8	ADK10596	Adk10596 Human pap
724	15	62.5	10	6	ABR24681	Abr24681 Human can	797	15	62.5	10	8	ADK05932	Adk05932 Hepatitis
725	15	62.5	10	6	ABR24520	Abr24520 Human can	798	15	62.5	10	8	ADK10593	Adk10593 Human pap
726	15	62.5	10	6	ABR21070	Abr21070 Human can	799	15	62.5	10	8	ADK10592	Adk10592 Human pap
727	15	62.5	10	6	ABR59148	Abr59148 Alzheimer	800	15	62.5	10	8	ADK03267	Adk03267 Hepatitis
728	15	62.5	10	6	ABR44652	Abr44652 Murine J4	801	15	62.5	10	8	ADL21058	Adl21058 125P5C8 p
729	15	62.5	10	6	ABR47280	Abr47280 Staphyloc	802	15	62.5	10	8	ADL21133	Adl21133 125P5C8 p
730	15	62.5	10	6	ABJ57466	Abj57466 184PIE2-r	803	15	62.5	10	8	ADL21133	Adl21133 125P5C8 p
731	15	62.5	10	6	ABJ58687	Abj58687 184PIE2-r	804	15	62.5	10	8	ADL21344	Adl21344 125P5C8 p
732	15	62.5	10	6	ABJ66221	Abj66221 184PIE2-r	805	15	62.5	10	8	ADL21396	Adl21396 125P5C8 p
733	15	62.5	10	6	ABJ67498	Abj67498 184PIE2-r	806	15	62.5	10	8	ADL20709	Adl20709 125P5C8 p
734	15	62.5	10	6	ABJ68257	Abj68257 184PIE2-r	807	15	62.5	10	8	ADL18917	Adl18917 125P5C8 p
735	15	62.5	10	6	ABJ69492	Abj69492 184PIE2-r	808	15	62.5	10	8	ADL20919	Adl20919 125P5C8 p
736	15	62.5	10	6	ABJ66633	Abj66633 184PIE2-r	809	15	62.5	10	8	ADN32081	Adn32081 Human Alz
737	15	62.5	10	6	ABJ66805	Abj66805 184PIE2-r	810	15	62.5	10	8	ADN48959	Adn48959 Peptide #
738	15	62.5	10	6	ABJ69386	Abj69386 184PIE2-r	811	15	62.5	10	8	ADN64792	Adn64792 HLA bindi
739	15	62.5	10	6	ABJ68555	Abj68555 184PIE2-r	812	15	62.5	10	8	ADO49156	Ado49156 Human car
740	15	62.5	10	6	ABJ69580	Abj69580 184PIE2-r	813	15	62.5	10	8	ADO77933	Ado77933 Gonadotro
741	15	62.5	10	6	ABJ58245	Abj58245 184PIE2-r	814	15	62.5	10	8	ADP47005	Adp47005 Murine he
742	15	62.5	10	6	ABJ67497	Abj67497 184PIE2-r	815	15	62.5	10	8	ADP47213	Adp47213 Human pho
743	15	62.5	10	6	ABJ67655	Abj67655 184PIE2-r	816	15	62.5	10	8	ADQ92367	Adq92367 Human hul
744	15	62.5	10	6	ABJ68357	Abj68357 184PIE2-r	817	15	62.5	10	8	ADQ92369	Adq92369 Human hul
745	15	62.5	10	6	ABJ58624	Abj58624 184PIE2-r	818	15	62.5	10	8	ADQ92371	Adq92371 Human hul
746	15	62.5	10	6	ABJ57961	Abj57961 184PIE2-r	819	15	62.5	10	8	ADQ92373	Adq92373 Human hul
747	15	62.5	10	6	ABJ66841	Abj66841 184PIE2-r	820	15	62.5	10	8	ADQ80558	Adq80558 TNF-alpha
748	15	62.5	10	6	ABJ57757	Abj57757 184PIE2-r	821	15	62.5	10	8	ADQ80562	Adq80562 TNF-alpha
749	15	62.5	10	6	ABJ67608	Abj67608 184PIE2-r	822	15	62.5	10	8	ADQ80556	Adq80556 TNF-alpha
750	15	62.5	10	6	ABJ67679	Abj67679 184PIE2-r	823	15	62.5	10	8	ADQ80560	Adq80560 TNF-alpha
751	15	62.5	10	6	ABJ68831	Abj68831 184PIE2-r	824	15	62.5	10	8	ADQ90780	Adq90780 Mouse com
752	15	62.5	10	6	ABJ68832	Abj68832 184PIE2-r	825	15	62.5	10	8	ADR03382	Adr03382 Humanised
753	15	62.5	10	6	ABJ68968	Abj68968 184PIE2-r	826	15	62.5	10	8	ADR03384	Adr03384 Humanised
754	15	62.5	10	6	ABJ69385	Abj69385 184PIE2-r	827	15	62.5	10	8	ADR03385	Adr03385 Humanised
755	15	62.5	10	6	ABJ69385	Abj69385 184PIE2-r	828	15	62.5	10	8	ADQ90923	Adq90923 Pancreati

829	15	62.5	10	8	ADSI18661	Adsl18661	Peptide s
830	15	62.5	10	8	ADP79877	Adp79877	Human HLA
831	15	62.5	10	8	ADP80344	Adp80344	Human HLA
832	15	62.5	10	8	ADT02867	Adt02867	Human p53
833	15	62.5	10	8	ADR70840	Adr70840	Synthetic
834	15	62.5	11	1	AAP71510	Aap71510	Growth ho
835	15	62.5	11	1	AAP82068	Aap82068	Polypepti
836	15	62.5	11	2	AAW05784	Aaw05784	Presenili
837	15	62.5	11	2	AAW11231	Aaw11231	Peptide A
838	15	62.5	11	2	AAW12288	Aaw12288	Mycobacte
839	15	62.5	11	2	AAW62114	Aaw62114	Human MDM
840	15	62.5	11	2	AAW25553	Aay25553	Human MHC
841	15	62.5	11	4	AAU27152	Aau27152	Human Leu
842	15	62.5	11	4	AAU26842	Aau26842	Human Leu
843	15	62.5	11	5	ABP47586	Abp47586	N. mening
844	15	62.5	11	5	ABP67727	Abp67727	Human CD6
845	15	62.5	11	5	ABP67326	Abp67326	Human CD6
846	15	62.5	11	5	AAU93631	Aau93631	Granulocy
847	15	62.5	11	5	AAW52269	Aam52269	Miniature
848	15	62.5	11	5	ABG67493	Abg67493	Human ADP
849	15	62.5	11	6	ABR59507	AbR59507	S. aureus
850	15	62.5	11	6	ADA23607	Ada23607	Alzheimer
851	15	62.5	11	8	ADG15910	Adg15910	Synthetic
852	15	62.5	11	8	ADG15914	Adg15914	Synthetic
853	15	62.5	11	8	ADJ25786	Adj25786	MDM2 bind
854	15	62.5	11	8	ADJ25912	Adj25912	MDM2 bind
855	15	62.5	11	8	ADN64806	Adn64806	HLA bindi
856	15	62.5	11	8	ADR20392	Adr20392	Tryptic d
857	15	62.5	11	8	ADP80368	Adp80368	Human HLA
858	15	62.5	12	1	AAP93573	Aap93573	Extracell
859	15	62.5	12	1	AAR77621	Aar77621	Ascorbate
860	15	62.5	12	2	AAR83344	Aar83344	Kb-bindin
861	15	62.5	12	2	AAW29957	Aaw29957	Cysteine
862	15	62.5	12	2	AAW18715	Aaw18715	C-src exo
863	15	62.5	12	2	AAW81309	Aaw81309	Human iNO
864	15	62.5	12	2	AAW81249	Aaw81249	Human iNO
865	15	62.5	12	2	AAW37190	Aaw37190	Human onc
866	15	62.5	12	2	AAW37184	Aaw37184	Human onc
867	15	62.5	12	2	AAW37195	Aaw37195	Human onc
868	15	62.5	12	2	AAW37171	Aaw37171	Human onc
869	15	62.5	12	2	AAW37182	Aaw37182	Human p53
870	15	62.5	12	2	AAW37188	Aaw37188	Human onc
871	15	62.5	12	2	AAW37189	Aaw37189	Human onc
872	15	62.5	12	2	AAW37222	Aaw37222	MDM2 bind
873	15	62.5	12	2	AAW25552	Aay25552	Human MHC
874	15	62.5	12	3	AAW66808	Aay66808	T cell an
875	15	62.5	12	3	AAW17076	Aab17076	Mdm/hdm a
876	15	62.5	12	3	AAW17087	Aab17087	Mdm/hdm a
877	15	62.5	12	3	AAW17089	Aab17089	Mdm/hdm a
878	15	62.5	12	3	AAW17081	Aab17081	Mdm/hdm a
879	15	62.5	12	3	AAW17078	Aab17078	Mdm/hdm a
880	15	62.5	12	3	AAW17090	Aab17090	Mdm/hdm a
881	15	62.5	12	3	AAW17088	Aab17088	Mdm/hdm a
882	15	62.5	12	3	AAW17075	Aab17075	Mdm/hdm a
883	15	62.5	12	3	AAW17077	Aab17077	Mdm/hdm a
884	15	62.5	12	3	AAW17077	Aay93809	Reactive
885	15	62.5	12	3	AAW93867	Aay93867	Reactive
886	15	62.5	12	4	AAW86005	Aab86005	DCM-assoc
887	15	62.5	12	5	ABW06167	Abb06167	Gonadotro
888	15	62.5	12	5	ABG78401	Abg78401	Memapsin
889	15	62.5	12	5	ABB73170	Abb73170	Mdm/hdm a
890	15	62.5	12	5	ABB73172	Abb73172	Mdm/hdm a
891	15	62.5	12	5	ABB73185	Abb73185	Mdm/hdm a
892	15	62.5	12	5	ABB73184	Abb73184	Mdm/hdm a
893	15	62.5	12	5	ABB73176	Abb73176	Mdm/hdm a
894	15	62.5	12	5	ABB73183	Abb73183	Mdm/hdm a
895	15	62.5	12	5	ABB73173	Abb73173	Mdm/hdm a
896	15	62.5	12	5	ABB73171	Abb73171	Mdm/hdm a
897	15	62.5	12	5	ABB73182	Abb73182	Mdm/hdm a
898	15	62.5	12	5	ABP67723	Abp67723	Human CD6
899	15	62.5	12	5	ABP67322	Abp67322	Human CD6
900	15	62.5	12	5	ABG60547	Abg60547	Selective
901	15	62.5	12	5			

902	15	62.5	12	5	ABB81664	Abb81664	Yellow me
903	15	62.5	12	6	AAE30893	Aae30893	MDM2-bind
904	15	62.5	12	6	AAE30886	Aae30886	MDM2-bind
905	15	62.5	12	6	ABP71371	Abp71371	Anti-OPGL
906	15	62.5	12	6	ABR00856	AbR00856	Bioactive
907	15	62.5	12	7	ADC35960	Adc35960	Peptidic
908	15	62.5	12	7	ADC36035	Adc36035	Chemokine
909	15	62.5	12	7	ADE78490	Ade78490	Peptide 3
910	15	62.5	12	7	ADI03010	Adi03010	Human mon
911	15	62.5	12	7	ADL17289	Adl17289	DENSIN-18
912	15	62.5	12	7	ADJ73326	Adj73326	Mdm/hdm a
913	15	62.5	12	7	ADJ73330	Adj73330	Mdm/hdm a
914	15	62.5	12	7	ADJ73339	Adj73339	Mdm/hdm a
915	15	62.5	12	7	ADJ73324	Adj73324	Mdm/hdm a
916	15	62.5	12	7	ADJ73336	Adj73336	Mdm/hdm a
917	15	62.5	12	7	ADJ73327	Adj73327	Mdm/hdm a
918	15	62.5	12	7	ADJ73337	Adj73337	Mdm/hdm a
919	15	62.5	12	7	ADJ73338	Adj73338	Mdm/hdm a
920	15	62.5	12	7	ADJ73325	Adj73325	Mdm/hdm a
921	15	62.5	12	8	ADI34264	Adi34264	Wild type
922	15	62.5	12	8	ADJ52964	Adj52964	CH1 delet
923	15	62.5	12	8	ADJ52960	Adj52960	CH1 delet
924	15	62.5	12	8	ADJ52959	Adj52959	CH1 delet
925	15	62.5	12	8	ADJ52971	Adj52971	CH1 delet
926	15	62.5	12	8	ADJ52972	Adj52972	CH1 delet
927	15	62.5	12	8	ADJ52970	Adj52970	CH1 delet
928	15	62.5	12	8	ADJ52958	Adj52958	CH1 delet
929	15	62.5	12	8	ADJ52961	Adj52961	CH1 delet
930	15	62.5	12	8	ADJ52973	Adj52973	CH1 delet
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932	15	62.5	12	8	ADJ51922	Adj51922	CH1 delet
933	15	62.5	12	8	ADJ51920	Adj51920	CH1 delet
934	15	62.5	12	8	ADJ51932	Adj51932	CH1 delet
935	15	62.5	12	8	ADJ51931	Adj51931	CH1 delet
936	15	62.5	12	8	ADJ51919	Adj51919	CH1 delet
937	15	62.5	12	8	ADJ51934	Adj51934	CH1 delet
938	15	62.5	12	8	ADJ51925	Adj51925	CH1 delet
939	15	62.5	12	8	ADJ51933	Adj51933	CH1 delet
940	15	62.5	12	8	ADJ57768	Adj57768	Surface g
941	15	62.5	12	8	ADJ57296	Adj57296	Provasopr
942	15	62.5	12	8	ADN65746	Adn65746	HLA bindi
943	15	62.5	12	8	ADR42787	Adr42787	Modulator
944	15	62.5	13	2	AAR49316	Aar49316	Beta2m po
945	15	62.5	13	2	AAW59205	Aaw59205	Seq ID 10
946	15	62.5	13	2	AAW40094	Aaw40094	Seq ID 10
947	15	62.5	13	2	AAW67036	Aaw67036	Polioviru
948	15	62.5	13	2	AAW25551	Aay25551	Human MHC
949	15	62.5	13	3	AAW57799	Aay57799	TRAM-inte
950	15	62.5	13	4	AAB20427	Aab20427	Anti-FIX/
951	15	62.5	13	4	AAB20390	Aab20390	Anti-FIX/
952	15	62.5	13	4	AAB86009	Aab86009	DCM-assoc
953	15	62.5	13	4	AAB86007	Aab86007	DCM-assoc
954	15	62.5	13	4	AAB86006	Aab86006	DCM-assoc
955	15	62.5	13	5	ABP68836	Abp68836	Marine sn
956	15	62.5	13	5	ABP67720	Abp67720	Human CD6
957	15	62.5	13	5	ABP67319	Abp67319	Human CD6
958	15	62.5	13	5	ABP59059	Abp59059	Peptide #
959	15	62.5	13	5	ADG67226	Adg67226	Human 5G1
960	15	62.5	13	5	ADG66202	Adg66202	Human pro
961	15	62.5	13	5	ADG66200	Adg66200	Human pro
962	15	62.5	13	5	ADG67227	Adg67227	Human 5G1
963	15	62.5	13	5	ADG66203	Adg66203	Human pro
964	15	62.5	13	5	ADG67228	Adg67228	Human pro
965	15	62.5	13	5	ADG66201	Adg66201	Human 5G1
966	15	62.5	13	5	ADG67229	Adg67229	Human 5G1
967	15	62.5	13	6	ABP76124	Abp76124	Human GEN
968	15	62.5	13	6	ABP76126	Abp76126	Human GEN
969	15	62.5	13	6	ABP76127	Abp76127	Human GEN
970	15	62.5	13	6	ABP76125	Abp76125	Human GEN
971	15	62.5	13	7	AAO30274	Aao30274	Trichoder
972	15	62.5	13	7	ADE36957	Ade36957	Interfaci
973	15	62.5	13	7	ADF75892	Adf75892	Antimicro
974	15	62.5	13	7	ADF75888	Adf75888	Antimicro

975 15 62.5 13 7 ADF75890 Adf75890 Antimicro  
976 15 62.5 13 7 ADI57984 AdI57984 Anti-TNF-  
977 15 62.5 13 7 ADI57985 AdI57985 Anti-TNF-  
978 15 62.5 13 7 ADI57983 AdI57983 Anti-TNF-  
979 15 62.5 13 7 ADI57986 AdI57986 Anti-TNF-  
980 15 62.5 13 8 ADH94540 Lecithin  
981 15 62.5 13 8 ADO57860 ADO57860 Human for  
982 15 62.5 13 8 ADO24819 ADO24819 Polioviru  
983 15 62.5 13 8 ADR05553 ADR05553 Novel ssD  
984 15 62.5 14 2 AAW09477 Aaw09477 Thrombopo  
985 15 62.5 14 2 AAW36764 Aaw36764 Thrombopo  
986 15 62.5 14 2 AAW36628 Aaw36628 Thrombopo  
987 15 62.5 14 2 AAW53471 Aaw53471 P2 predom  
988 15 62.5 14 2 AAW37197 Aaw37197 Human onc  
989 15 62.5 14 2 AAY25550 Aay25550 Human MHC  
990 15 62.5 14 2 AAY42867 Aay42867 Vpr-bindi  
991 15 62.5 14 3 AAB17012 AabI7012 TPO-mimet  
992 15 62.5 14 3 AAB13866 AabI3866 L2/HNK1 c  
993 15 62.5 14 4 AAB20428 Aab20428 Anti-FIX/  
994 15 62.5 14 4 AAM98166 Aam98166 Human pep  
995 15 62.5 14 4 AAM98390 Aam98390 Human pep  
996 15 62.5 14 4 AAM00740 Aam00740 Human pro  
997 15 62.5 14 4 AAM00739 Aam00739 Human pro  
998 15 62.5 14 4 AAG25847 Aau25847 Human thr  
999 15 62.5 14 4 AAG98212 Aag98212 Human SNP  
1000 15 62.5 14 4 AAB86012 Aab86012 DCM-assoc

ALIGNMENTS

RESULT 1  
ADC07129  
ID ADC07129 standard; peptide; 9 AA.  
XX  
AC ADC07129;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Honeybee AKH peptide.  
XX  
KW lipid mobilisation; insect; adipokinetic hormone; AKH; anorectic;  
KW antidiabetic; hypotensive; cardiant; antiarthritic; cytosstatic;  
KW nephrotropic; hepatotropic; analgesic; cerebroprotective; uropathic;  
KW obesity; type II diabetes; cholelithiasis; hypertension;  
KW coronary heart disease; atherosclerosis; glycosenosis; arthritis; cancer;  
KW renal failure; liver; chronic pain; sleep apnea; stroke;  
KW urinary incontinence; honeybee.  
XX  
OS Synthetic.  
OS Apis mellifera.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /label= OTHER  
FT /note= "OTHER = Pyroglutamic acid"  
FT Misc-difference 9 /note= "Preferably C-terminal amide"  
FT /note= "Preferably C-terminal amide"  
XX  
PN WO2003066080-A1.  
XX  
PD 14-AUG-2003.  
XX  
PF 07-FEB-2003; 2003WO-US003800.  
XX  
PR 07-FEB-2002; 2002US-00072419.  
XX  
PA (BLMB-) BLM GROUP.  
XX  
PI Schacter BZ, Schacter LP;  
XX  
DR WPI; 2003-712542/67.  
XX

PT Pharmaceutical composition useful for promoting weight loss, comprises an  
PT insect adipokinetic hormone, having a pyroglutamate residue at its amino  
PT terminus.  
XX  
PS Claim 29; Page 20; 82pp; English.  
XX  
CC The invention relates to a novel method of promoting lipid mobilisation  
CC in a human which comprises administering an insect adipokinetic hormone  
CC (AKH). The hormone of the invention demonstrates anorectic, antidiabetic,  
CC hypotensive, cardiant, antiarthritic, cytosstatic, nephrotropic,  
CC hepatotropic, analgesic, cerebroprotective and uropathic activities. The  
CC method of the invention may be useful for treating obesity, type II  
CC diabetes, cholelithiasis, hypertension, coronary heart disease, renal  
CC atherosclerosis, types I to VI glycosenosis, arthritis, cancer, renal  
CC failure, liver disease, chronic pain, sleep apnea, stroke and urinary  
CC incontinence. The current sequence is that of the honeybee AKH peptide of  
CC the invention.  
XX  
SQ Sequence 9 AA;  
Query Match 70.8%; Score 17; DB 7; Length 9;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 FXXXW 6  
Db 4 FTSSW 8  
RESULT 2  
ADC07134  
ID ADC07134 standard; peptide; 9 AA.  
XX  
AC ADC07134;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Painted lady AKH peptide.  
XX  
KW lipid mobilisation; insect; adipokinetic hormone; AKH; anorectic;  
KW antidiabetic; hypotensive; cardiant; antiarthritic; cytosstatic;  
KW nephrotropic; hepatotropic; analgesic; cerebroprotective; uropathic;  
KW obesity; type II diabetes; cholelithiasis; hypertension;  
KW coronary heart disease; atherosclerosis; glycosenosis; arthritis; cancer;  
KW renal failure; liver; chronic pain; sleep apnea; stroke;  
KW urinary incontinence; painted lady.  
XX  
OS Synthetic.  
OS Vanessa cardui.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /label= OTHER  
FT /note= "OTHER = Pyroglutamic acid"  
FT Misc-difference 9 /note= "Preferably C-terminal amide"  
FT /note= "Preferably C-terminal amide"  
XX  
PN WO2003066080-A1.  
XX  
PD 14-AUG-2003.  
XX  
PF 07-FEB-2003; 2003WO-US003800.  
XX  
PR 07-FEB-2002; 2002US-00072419.  
XX  
PA (BLMB-) BLM GROUP.  
XX  
PI Schacter BZ, Schacter LP;  
XX  
DR WPI; 2003-712542/67.  
XX  
PT Pharmaceutical composition useful for promoting weight loss, comprises an  
PT insect adipokinetic hormone, having a pyroglutamate residue at its amino



PT terminus.  
PS Claim 29; Page 20; 82pp; English.  
XX  
CC The invention relates to a novel method of promoting lipid mobilisation  
CC in a human which comprises administering an insect adipokinetic hormone  
CC (AKH). The hormone of the invention demonstrates anorectic, antidiabetic,  
CC hypotensive, cardiant, antiarthritic, cytostatic, nephrotropic,  
CC hepatotropic, analgesic, cerebroprotective and uropathic activities. The  
CC method of the invention may be useful for treating obesity, type II  
CC diabetes, cholelithiasis, hypertension, coronary heart disease,  
CC atherosclerosis, types I to VI glycogenosis, arthritis, cancer, renal  
CC failure, liver disease, chronic pain, sleep apnea, stroke and urinary  
CC incontinence. The current sequence is that of the painted lady AKH  
CC peptide of the invention.  
XX  
SQ Sequence 9 AA;  
Query Match 70.8%; Score 17; DB 7; Length 9;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 FXXXW 6  
Db 4 FTSSW 8  
RESULT 3  
AAB10010  
ID AAB10010 standard; protein; 10 AA.  
XX  
AC AAB10010;  
XX  
DT 01-NOV-2000 (first entry)  
XX  
DE H. pylori beta-urease-binding antibody heavy chain CDR1 protein #2.  
XX  
KW Acid-resistant microorganism; detection; faecal; intestine; infection;  
KW monoclonal antibody; heavy chain; complementarity determining region;  
KW CDR; beta-urease.  
XX  
OS Unidentified.  
XX  
PN WO200026671-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 29-OCT-1999; 99WO-EP008212.  
XX  
PR 29-OCT-1998; 98EP-00120517.  
PR 06-NOV-1998; 98EP-00120687.  
XX  
PA (CONN-) CONNEX GMBH.  
XX  
PI Reiter C, Cullmann G, Friedrichs U, Heppner P, Lakner M;  
PI Ringeis A;  
XX  
DR WPI; 2000-365747/31.  
DR N-PSDB; AAA40166.  
XX  
PT Detecting infection by acid-fast microbes for diagnosis of Helicobacter  
PT pylori, comprises reacting a fecal sample with two binding reagents for  
PT antigens that survive intestinal passage.  
XX  
PS Claim 26; Page 22; 84pp; German.  
XX  
CC This invention describes a novel method for the detection of a mammalian  
CC infection by an acid-resistant microorganism (A) by treating a faecal  
CC sample with at least two different monoclonal antibodies (MAb) (or their  
CC fragments or derivatives) or aptamers (collectively (I)) and detecting  
CC formation of a complex (C) between (I) and the corresponding antigen of  
CC (A). The first and second (I) bind to epitopes of different antigens  
CC (Ag). These epitopes are present, after passage through the intestines,

CC in at least some mammals, and have either: (i) their native structure; or  
CC (ii) a structure against which an antibody is produced by an animal  
CC infected or immunized with (A), or its extract, lysate, derived protein  
CC or fragment, or with a synthetic peptide. Practically all mammals display  
CC at least one of the specified epitopes. The method is used to detect  
CC infection by acid-fast bacteria, particularly of the genera Helicobacter,  
CC Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus, M.  
CC tuberculosis, C. jejuni and C. pylori. (I) may also be used  
CC therapeutically. The method is direct and non-invasive, and provides an  
CC inexpensive and easily standardizable diagnosis, despite possible  
CC degradation of antigens during passage through the intestines. This  
CC sequence represents a fragment of a H. pylori beta-urease-binding  
CC antibody heavy chain complementarity determining region CDR1 which is  
CC used to illustrate the method of the invention  
XX  
SQ Sequence 10 AA;  
Query Match 70.8%; Score 17; DB 3; Length 10;  
Best Local Similarity 40.0%; Pred. No. 3.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 FXXXW 6  
Db 4 FSTSW 8  
RESULT 4  
AAB86090  
ID AAB86090 standard; peptide; 10 AA.  
XX  
AC AAB86090;  
XX  
DT 17-JUL-2001 (first entry)  
XX  
DE H. pylori beta-urease derived antibody light chain CDR1 #1.  
XX  
KW Catalase; beta-urease; antibody; antigen; detection; infection; epitope;  
KW acid-resistant microorganism; complementarity determining region; CDR;  
KW feces; heavy chain; light chain.  
XX  
OS Unidentified.  
XX  
PN WO200127612-A2.  
XX  
PD 19-APR-2001.  
XX  
PF 12-OCT-2000; 2000WO-EP010057.  
XX  
PR 12-OCT-1999; 99EP-00120351.  
PR 16-MAR-2000; 2000EP-00105592.  
PR 31-MAR-2000; 2000EP-00107028.  
PR 10-MAY-2000; 2000EP-00110110.  
XX  
PA (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.  
XX  
PI Reiter C, Cullmann G, Lakner M, Truee A, Dehnert S, Schwartz G;  
PI Ringeis A;  
XX  
DR WPI; 2001-282086/29.  
DR N-PSDB; AAF88117.  
XX  
PT Detecting infections by acid-resistant microorganisms, particularly for  
PT diagnosing Helicobacter pylori, comprises immunochromatographic detection  
PT of antigen in feces.  
XX  
PS Claim 27; Page 27; 90pp; German.  
XX  
CC This invention describes a novel method for detecting infection by an  
CC acid-resistant microorganism (A), in a mammal, using  
CC immunochromatography. The method is used to diagnose infection by an acid  
CC -resistant microorganism (A), in a mammal, such as Helicobacter,  
CC Campylobacter or Mycobacterium, particularly H. pylori (most preferred),  
CC H. hepatica, C. jejuni and M. tuberculosis. The method is rapid, simple,  
CC inexpensive and non-invasive, and may indicate the stage of infection. A

CC test strip used in the method may include a filter to eliminate particles  
CC present in the sample and only a single receptor provides a reasonably  
CC secure diagnosis, with specificity and selectivity improved by detecting  
CC several epitopes (of catalase) or different antigens (catalase and beta-  
CC urease). The method can be automated. This sequence represents a  
CC complementarity determining region (CDR) from an antibody raised against  
CC the H. pylori catalase or beta-urease antigen which is used to illustrate  
CC the method of the invention

SQ Sequence 10 AA;  
  
Query Match 70.8%; Score 17; DB 4; Length 10;  
Best Local Similarity 40.0%; Pred. No. 3.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6  
| |  
Db 4 FTSW 8

RESULT 5  
AAB86058  
ID AAB86058 standard; peptide; 10 AA.

AC AAB86058;  
XX  
DT 17-JUL-2001 (first entry)

DE H. pylori beta-urease derived antibody light chain CDR1 #1.

XX  
KW Heavy chain; light chain; catalase; beta-urease; detection; CDR; antigen;  
KW infection; acid-resistant microorganism; fecal; antibody; diagnosis;  
KW antibacterial; complementarity determining region.

OS Unidentified.

XX WO200127613-A2.

PN 19-APR-2001.

XX 12-OCT-2000; 2000WO-EP010058.

XX 12-OCT-1999; 99EP-00120351.

PR 16-MAR-2000; 2000EP-0010592.

PR 31-MAR-2000; 2000EP-00107028.

PR 10-MAY-2000; 2000EP-00110110.

XX (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.

XX Reiter C, Cullmann G, Heppner P, Ringeis A, Mueller H, Haindl E;

XX WPI; 2001-282087/29.

DR N-PSDB; AAF88060.

XX  
PS Claim 23; Page 17; 89pp; German.

XX This invention describes a novel method for detecting, in a mammal,  
CC infection by an acid-resistant microorganism (A) which comprises reacting  
CC a fecal sample with: (i) a receptor (R) such that a complex is formed  
CC with an antigen (Ag) of (A); or (ii) two different R so that a three-part  
CC complex is formed with Ag, and the formation of a complex detected. R are  
CC specific for an Ag which, after passage through the intestines, at least  
CC in some mammals, retains a native (or corresponding) structure against  
CC which the mammal produces antibodies (when immunized or infected with  
CC (A), or its extracts, lysates or derived proteins (or fragments) or  
CC synthetic peptides). The products of the invention have antibacterial  
CC activity. The method is used to diagnose infection by Helicobacter,  
CC Campylobacter or Mycobacterium, particularly H. pylori (most preferred),  
CC H. hepatica, C. jejuni and M. tuberculosis, and also to monitor the

CC progress of treatment. Receptors, particularly antibodies, directed  
CC against Ag can be used therapeutically for treatment of infections. The  
CC method requires only one R to provide a reasonably secure diagnosis  
CC (although use of two R improves sensitivity), so is relatively  
CC inexpensive and more easily standardized. Also it is direct, non-  
CC invasive, suitable for automation and may indicate the stage of an  
CC infection. This sequence represents a complementarity determining region  
CC (CDR) from an antibody generated against a Helicobacter pylori antigen  
CC (catalase or beta-urease) which is used to illustrate the method of the  
CC invention

XX  
SQ Sequence 10 AA;

Query Match 70.8%; Score 17; DB 4; Length 10;  
Best Local Similarity 40.0%; Pred. No. 3.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6  
| |  
Db 4 FTSW 8

RESULT 6  
ADC07163  
ID ADC07163 standard; peptide; 11 AA.

XX  
AC ADC07163;

XX 18-DEC-2003 (first entry)

DT Painted lady AKH peptide 2.

XX  
DE  
KW lipid mobilisation; insect; adipokinetic hormone; AKH; anorectic;  
KW antidiabetic; hypotensive; cardiant; antiarthritic; cytostatic;  
KW nephrotropic; hepatotropic; analgesic; cerebroprotective; uropathic;  
KW obesity; type II diabetes; cholelithiasis; hypertension;  
KW coronary heart disease; atherosclerosis; glycosenosis; arthritis; cancer;  
KW renal failure; liver; chronic pain; sleep apnea; stroke;  
KW urinary incontinence; painted lady.

OS Synthetic.  
OS Vanessa cardui.

XX Key Location/Qualifiers  
FH Modified-site 1

FT /label= OTHER  
FT /note= "OTHER = Pyroglutamic acid"

FT Misc-difference 11  
FT /note= "Preferably C-terminal amide"

XX WO2003066080-A1.

PN 14-AUG-2003.

XX 07-FEB-2003; 2003WO-US003800.

XX 07-FEB-2002; 2002US-00072419.

XX (BLMB-) BLM GROUP.

XX Schacter BZ, Schacter LP;

XX WPI; 2003-712542/67.

XX Pharmaceutical composition useful for promoting weight loss, comprises an  
PT insect adipokinetic hormone, having a pyroglutamate residue at its amino  
PT terminus.

XX Claim 29; Page 20; 82pp; English.

XX The invention relates to a novel method of promoting lipid mobilisation  
CC in a human which comprises administering an insect adipokinetic hormone  
CC (AKH). The hormone of the invention demonstrates anorectic, antidiabetic,



CC hypotensive, cardiac, antiarthritic, cytostatic, nephrotropic, CC  
CC hepatotropic, analgesic, cerebroprotective and uropathic activities. The CC  
CC method of the invention may be useful for treating obesity, type II CC  
CC diabetes, cholelithiasis, hypertension, coronary heart disease, CC  
CC atherosclerosis, types I to VI glycosenosis, arthritis, cancer, renal CC  
CC failure, liver disease, chronic pain, sleep apnea, stroke and urinary CC  
CC incontinence. The current sequence is that of the painted lady AKH CC  
XX peptide 2 of the invention.  
SQ Sequence 11 AA;  
  
Query Match 70.8%; Score 17; DB 7; Length 11;  
Best Local Similarity 40.0%; Pred. No. 3.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXXW 6  
| |  
Db 4 FTSSW 8  
  
RESULT 7  
AAE05735  
ID AAE05735 standard; peptide; 13 AA.  
XX  
AC AAE05735;  
XX  
DT 24-SEP-2001 (first entry)  
XX  
DE Complementarity-determining region 3 (CDR3) of MoPhabs #7.  
XX  
KW CDR3; complementarity-determining region 3; monoclonal phage antibody;  
KW MoPhabs; antigen.  
XX  
OS Synthetic.  
XX  
XX US6265150-B1.  
PN  
XX  
PD 24-JUL-2001.  
XX  
PF 26-MAY-1998; 98US-00085072.  
XX  
PR 07-JUN-1995; 95US-00483633.  
PR 18-SEP-1997; 97US-00932892.  
XX  
XX (BECT ) BECTON DICKINSON & CO.  
PA (CRUC-) CRUCELL HOLLAND BV.  
XX  
PI Terstappen LW, Logtenberg T;  
XX  
DR WPI; 2001-463929/50.  
XX  
XX Obtaining a phage particle, useful for obtaining human antibodies against  
PT known and novel surface antigens, by incubating a phage library with  
PT target cells to allow binding of the antibody fragment to the antigen.  
XX  
XX Example 6; Col 6; 6pp; English.  
PS  
XX  
CC The invention relates to a method of obtaining a phage particle which has  
CC an antibody fragment directed against an antigen associated with the  
CC surface of target cells in a heterogeneous cell population. The method  
CC involves incubating a library of phage particles with the target cells to  
CC allow binding of the antibody fragment expressed on the surface of the  
CC phage particles to the antigen associated with the target cells. The  
CC method is useful for obtaining human antibodies against known and novel  
CC surface antigens in their native configuration, expressed on  
CC phenotypically defined subpopulations of cells. The present sequence is  
CC complementarity-determining region 3 (CDR3) of monoclonal phage  
CC antibodies (MoPhabs) used in the exemplification of the invention  
XX  
SQ Sequence 13 AA;  
  
Query Match 70.8%; Score 17; DB 4; Length 13;  
Best Local Similarity 40.0%; Pred. No. 4.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 FXXXW 6  
| |  
Db 6 FASSW 10  
  
RESULT 8  
ABG75574  
ID ABG75574 standard; peptide; 13 AA.  
XX  
AC ABG75574;  
XX  
DT 22-APR-2003 (first entry)  
XX  
DE CDR3 peptide sequence, #7, used in phage antibody construction.  
XX  
KW Phage; antibody; antigen; target cell; phage particle;  
KW cell-type specific phage antibody library; phage antibody; Phab;  
KW monoclonal phage antibody; MoPhab; blood cell; foetal bone marrow cell;  
KW complementarity determining region 3; CDR3; human.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN US2002132228-A1.  
XX  
PD 19-SEP-2002.  
XX  
PF 24-MAY-2001; 2001US-00865048.  
XX  
PR 07-JUN-1995; 95US-00483633.  
PR 18-SEP-1997; 97US-00932892.  
PR 26-MAY-1998; 98US-00085072.  
XX  
PA (TERS/) TERSTAPPEN L W M M.  
PA (LOGT/) LOGTENBERG T.  
XX  
PI Terstappen LMMM, Logtenberg T;  
XX  
DR WPI; 2003-174076/17.  
XX  
XX Obtaining phage having antibody specific for cell surface antigen of  
PT target cells in heterogeneous cell population, by incubating phage  
PT antibody library with target cells, and separating phage particles bound  
PT target cells.  
XX  
PS Example 6; Page 4; 5pp; English.  
XX  
CC The invention discloses a method for obtaining a phage comprising an  
CC antibody, or its fragment, directed against antigens associated with a  
CC target cells surface in a heterogeneous cell population. The method  
CC comprises providing a library of antibodies, or their fragments,  
CC expressed on the surface of phage particles, incubating the phage  
CC antibody library with the target cells, separating the target cells and  
CC phage particles associated with them from the phage particles not  
CC associated with the target cells and then recovering the phage particles.  
CC Also disclosed is a cell-type specific phage antibody library and an  
CC antibody, or antibody fragment, obtained using the method. The method is  
CC useful for obtaining a selection of phage antibodies (Phabs) and  
CC monoclonal phage antibodies (MoPhabs). The method is also useful for  
CC detecting known and novel structures on various populations of blood and  
CC foetal bone marrow cells. The sequence presented is an example of the  
CC partly randomised human complementarity determining region 3 (CDR3) used  
CC in the construction of the antibodies  
XX  
SQ Sequence 13 AA;  
  
Query Match 70.8%; Score 17; DB 6; Length 13;  
Best Local Similarity 40.0%; Pred. No. 4.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 FXXXW 6

Db	6	FASW 10	
RESULT 9			
AAM98088			
ID	AAM98088	standard; peptide; 14 AA.	
XX			
AC	AAM98088;		
XX			
DT	24-JAN-2002	(first entry)	
XX			
DE	Human peptide #1363	encoded by a SNP oligonucleotide.	
XX			
KW	Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;		
KW	neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;		
KW	amyloid protein; angiopoietin; apoptosis related protein; cadherin;		
KW	cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;		
KW	complement related protein; cytochrome; kinesis; cytokine; interferon;		
KW	interleukin; G-protein coupled receptor; thioesterase; inflammation;		
KW	multifactorial disease; autoimmune disease; infection;		
KW	nervous system disease.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200147944-A2.		
XX			
PD	05-JUL-2001.		
XX			
PF	28-DEC-2000;	2000WO-US035498.	
XX			
PR	28-DEC-1999;	99US-0173419P.	
XX			
PR	27-DEC-2000;	2000US-00173419.	
XX			
PA	(CURA-) CURAGEN CORP.		
XX			
PI	Shimkets RA, Leach M;		
XX			
DR	WPI; 2001-465210/50.		
XX			
PT	Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,		
PT	oncogenes and histones, useful for diagnosing and treating, e.g. cancer,		
PT	autoimmune diseases and infections.		
XX			
PS	Disclosure; Page 3967;	4143pp; English.	
XX			
CC	The present invention relates to oligonucleotides (see AAL26793-AAL34659)		
CC	encoding polymorphic variants of proteins related to amylases, amyloid		
CC	proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin,		
CC	polymerase, oncogenes, histones, kinases, colony stimulating factors,		
CC	complement related proteins, cytochromes, kinesins, cytokines,		
CC	interferons, interleukins, G-protein coupled receptors and thioesterases.		
CC	The present sequence is a peptide encoded by one such oligonucleotide.		
CC	The oligonucleotides and the peptides encoded by them may be used in the		
CC	prevention, diagnosis and treatment of diseases associated with		
CC	inappropriate expression of the proteins listed above. Disorders that may		
CC	be prevented, diagnosed and/or treated include multifactorial diseases		
CC	with a genetic component, such as autoimmune diseases (e.g. rheumatoid		
CC	arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus		
CC	and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,		
CC	brain, breast, colon and kidney, leukaemia), diseases of the nervous		
CC	system and an infection of pathogenic organisms		
XX			
SQ	Sequence 14 AA;		
Query Match	70.8%;	Score 17; DB 4; Length 14;	
Best Local Similarity	40.0%;	Pred. No. 4.4e+03;	
Matches	2; Conservative	0; Mismatches 3; Indels	0; Gaps 0;
Qy	2 FXXXW 6		
Db	6 FASTW 10		
RESULT 10			
AAR97874			
ID	AAR97874	standard; peptide; 15 AA.	
XX			
AC	AAR97874;		
XX			
DT	16-AUG-1996	(first entry)	
XX			
DE	Japan cedar pollen mature allergen Cry j II	amino acids 16-30.	
XX			
KW	Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;		
KW	Sugi pollinosis; diagnosis; treatment.		
XX			
OS	Cryptomeria japonica.		
XX			
PN	JP08047392-A.		
XX			
PD	20-FEB-1996.		
XX			
PF	07-NOV-1994;	94JP-00297840.	
XX			
PR	05-NOV-1993;	93JP-00276773.	
XX			
PR	26-MAY-1994;	94JP-00134868.	
XX			
PA	(MEIP ) MEIJI MILK PROD CO LTD.		
XX			
DR	WPI; 1996-166249/17.		
XX			
PT	Japan cedar pollen allergen Cry j II	epitope - comprises at least part of	
PT	specified 460 aminoacid protein.		
XX			
PS	Claim 8; Fig 3; 17pp; Japanese.		
XX			
CC	AAR97871-R97960 are overlapping peptides used for the epitope mapping of		
CC	the Japan cedar pollen allergen Cry j II. Cry j II and allergenic		
CC	peptides of it are useful in the diagnosis, prevention and treatment of		
CC	Sugi pollinosis, the allergic reaction to Japan cedar pollen. Significant		
CC	regions of the allergen were identified using the overlapping peptides of		
CC	the full epitope derived from a Cry j II antigen-specific T cell line.		
CC	Amino acids 66-80 (AAR97884) and 186-200 (R978908) of the full mature 460		
CC	amino acid allergen are the most allergenic of the 90 peptides tested		
XX			
SQ	Sequence 15 AA;		
Query Match	70.8%;	Score 17; DB 2; Length 15;	
Best Local Similarity	40.0%;	Pred. No. 4.7e+03;	
Matches	2; Conservative	0; Mismatches 3; Indels	0; Gaps 0;
Qy	2 FXXXW 6		
Db	9 FSTAW 13		
RESULT 11			
AAR97875			
ID	AAR97875	standard; peptide; 15 AA.	
XX			
AC	AAR97875;		
XX			
DT	16-AUG-1996	(first entry)	
XX			
DE	Japan cedar pollen mature allergen Cry j II	amino acids 21-35.	
XX			
KW	Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;		
KW	Sugi pollinosis; diagnosis; treatment.		
XX			
OS	Cryptomeria japonica.		
XX			
PN	JP08047392-A.		
XX			
PD	20-FEB-1996.		
XX			

PF 07-NOV-1994; 94JP-00297840.  
XX  
PR 05-NOV-1993; 93JP-00276773.  
PR 26-MAY-1994; 94JP-00134868.  
XX  
PA (MEIP ) MEIJI MILK PROD CO LTD.  
XX  
DR WPI; 1996-166249/17.  
XX  
PT Japan cedar pollen allergen Cry j II epitope - comprises at least part of  
PT specified 460 aminoacid protein.  
XX  
PS Claim 8; Fig 3; 17pp; Japanese.  
XX  
CC AAR97871-R97960 are overlapping peptides used for the epitope mapping of  
CC the Japan cedar pollen allergen Cry j II. Cry j II and allergenic  
CC peptides of it are useful in the diagnosis, prevention and treatment of  
CC Sugi pollinosis, the allergic reaction to Japan cedar pollen. Significant  
CC regions of the allergen were identified using the overlapping peptides of  
CC the full epitope derived from a Cry j II antigen-specific T cell line.  
CC Amino acids 66-80 (AAR97884) and 186-200 (R978908) of the full mature 460  
CC amino acid allergen are the most allergenic of the 90 peptides tested  
XX  
SQ Sequence 15 AA;  
  
Query Match 70.8%; Score 17; DB 2; Length 15;  
Best Local Similarity 40.0%; Pred. No. 4.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXXW 6  
Db | |  
4 FSTAW 8  
  
RESULT 12  
AAW57758  
ID AAW57758 standard; peptide; 15 AA.  
XX  
AC AAW57758;  
XX  
DT 17-SEP-1998 (first entry)  
XX  
DE Residues 16-30 of Cry j 2.  
XX  
KW Cry j 2; Japanese cedar pollen antigen; allergy; immunotherapy;  
KW HLA class II molecule.  
XX  
OS Cryptomeria japonica.  
XX  
PN WO9820902-A1.  
XX  
PD 22-MAY-1998.  
XX  
PF 12-NOV-1997; 97WO-JP004129.  
PR 13-NOV-1996; 96JP-00302053.  
XX  
PA (MEIP ) MEIJI MILK PROD CO LTD.  
XX  
PI Sone T, Kume A, Dairiki K, Kino K;  
XX  
DR WPI; 1998-297617/26.  
XX  
PT Peptides derived from Japanese cedar pollen antigens are  
PT immunotherapeutic agents - useful for allergy treatment and typing HLA  
PT class II molecules in allergy sufferers.  
XX  
PS Claim 12; Page 29; 50pp; Japanese.  
XX  
CC This sequence represents residues 16-30 of the Cry j 2 protein, and is a  
CC peptide of the invention. The peptides are derived from Japanese cedar  
CC pollen antigens, and are used as immunotherapeutic agents in the  
CC treatment of allergy. The peptides can be used for identification and

CC typing of the particular HLA class II molecules in an allergy sufferer,  
CC and also for peptide immunotherapy of an allergy. Using these peptides  
CC the immunotherapy can be targeted more specifically to the requirements  
CC of the individual patient, allowing more effective treatment of an  
CC allergy, including those patients for whom treatment with a conventional  
CC immunotherapeutic agent is ineffective  
XX  
SQ Sequence 15 AA;  
  
Query Match 70.8%; Score 17; DB 2; Length 15;  
Best Local Similarity 40.0%; Pred. No. 4.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXXW 6  
Db | |  
9 FSTAW 13  
  
RESULT 13  
AAE23038  
ID AAE23038 standard; peptide; 19 AA.  
XX  
AC AAE23038;  
XX  
DT 21-AUG-2002 (first entry)  
XX  
DE Human thioredoxin, 47916 peptide.  
XX  
KW Human; thioredoxin; 22108; 47916; haematopoietic disorder; leukaemia;  
KW cancer; lung; breast; thyroid; head; neck; prostate; genitourinary tract;  
KW cardiovascular disease; angina pectoris; arteriosclerosis; heart failure;  
KW brain disorder; brain abscess; meningitis; Alzheimer's disease; sarcoma;  
KW cytostatic; carcinoma; cardiac; neuroprotective; antiinflammatory;  
KW gene therapy; nootropic.  
XX  
OS Homo sapiens.  
XX  
PN WO200226803-A2.  
XX  
PD 04-APR-2002.  
XX  
PF 25-SEP-2001; 2001WO-US029967.  
XX  
PR 25-SEP-2000; 2000US-0235049P.  
XX  
PA (MILL-) MILLENIUM PHARM INC.  
XX  
PI Bandaru R, Kapeller-Libermann R;  
XX  
DR WPI; 2002-416475/44.  
XX  
PT New human thioredoxin nucleic acid and polypeptide molecules, designated  
PT 22108 and 47916, useful for diagnosing, preventing or treating cancer  
PT (e.g. carcinoma), cardiovascular diseases (e.g. heart failure) or brain  
PT disorders.  
XX  
PS Disclosure; Page 11; 124pp; English.  
XX  
CC The invention relates to human thioredoxin nucleic acid and polypeptide  
CC molecules, designated 22108 and 47916. The compound that modulates the  
CC activity or expression of 22108 and 47916 nucleic acid is useful for  
CC treating or preventing a disorder characterised by aberrant activity of  
CC 22108 and 47916-expressing cell, specifically for reducing or inhibiting  
CC the aberrant activity of the 22108 and 47916-expressing cancer cell. The  
CC 22108 and 47916 nucleic acid and polypeptide are useful for diagnosing,  
CC preventing or treating cancer in a subject (e.g. carcinoma, sarcoma,  
CC metastatic or haematopoietic disorders (e.g. leukaemia), or cancers of the  
CC lung, breast, thyroid, head neck, prostate or genito-urinary tract),  
CC cardiovascular diseases (e.g. angina pectoris, arteriosclerosis or heart  
CC failure) or brain disorders (e.g. brain abscess, meningitis, Alzheimer's  
CC diseases). The thioredoxin DNA is also useful in gene therapy. The  
CC present sequence is human thioredoxin, 47916 peptide  
XX

```
SQ Sequence 19 AA;
Query Match 70.8%; Score 17; DB 5; Length 19;
Best Local Similarity 40.0%; Pred. No. 5.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
Db 4 FSATW 8

RESULT 14
AAW42165
ID AAW42165 standard; peptide; 20 AA.
XX
AC AAW42165;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 16-JUN-1998 (first entry)
XX
DE T-cell epitope peptide 45 from Japanese cypress pollen antigen Chao2.
XX
KW Japanese cypress pollen; antigen; T-cell epitope; Chao1; Chao2;
KW diagnosis; allergy; spring tree pollen disease; pollinosis.
XX
OS Chamaecyparis obtusa.
XX
PN WO9747648-A1.
XX
PD 18-DEC-1997.
XX
PF 12-JUN-1997; 97WO-JP002031.
XX
PR 14-JUN-1996; 96JP-00153527.
XX
PA (MEIP ) MEIJI MILK PROD CO LTD.
XX
PI Kino K, Dairiri K;
XX
DR WPI; 1998-052242/05.
XX
PT T-cell epitope peptide portion of Japanese cypress pollen antigens Chao1
PT and Chao2 - used for diagnosis and treatment of spring tree pollen
PT disease.
XX
PS Claim 2; Page 36; 71pp; Japanese.
XX
CC The present sequence represents a T-cell epitope peptide from Japanese
CC cypress pollen antigen Chao2. The present invention describes peptides
CC which correspond to the T-cell epitope sites on Japanese cypress pollen
CC antigens Chao1 and Chao2. The peptides can be used as a reagent for the
CC diagnosis of allergy to Japanese cypress pollen, and as an antigen in the
CC treatment and prevention of spring tree pollen disease in which the
CC pollinosis involves reactivity to Japanese cypress pollen. (Updated on 25
CC -MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS
CC field.)
XX
SQ Sequence 20 AA;
Query Match 70.8%; Score 17; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 5.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
Db 8 FATTW 12

RESULT 15
AAG62999
ID AAG62999 standard; peptide; 20 AA.
XX
```

```
AC AAG62999;
XX
DT 01-OCT-2001 (first entry)
XX
DE Complementarity determining region 3 (CDR3) of VH chain of clone G101.
XX
KW Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW transferrin receptor; neurological disease; Alzheimer's disease;
KW prion disease; AIDS-related dementia; epilepsy; brain injury.
XX
OS Homo sapiens.
XX
PN WO200144300-A2.
XX
PD 21-JUN-2001.
XX
PF 27-NOV-2000; 2000WO-GB004501.
XX
PR 13-DEC-1999; 99US-0170599P.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Webster C, Osbourn J, Ward G, Miller K;
XX
DR WPI; 2001-398131/42.
XX
PT Mixture or panel of antibodies for selecting specific binding members
PT that cross the blood brain barrier, for use in delivering different
PT molecules and treating neurological diseases.
XX
PS Claim 1; Page 76; 109pp; English.
XX
CC AAG62970-AAG63005 represent complementarity determining region 3 (CDR3)
CC of VL and VH chains of antibodies of the invention. The specification
CC describes a mixture or panel of 5 different specific binding members,
CC each comprising an antibody VH and/or VL variable domain and capable,
CC when displayed on the surface of filamentous bacteriophage particles or
CC in the case of a specific binding member comprising the D5 VH and/or VL
CC variable domain when bound to human serum amyloid protein, to pass
CC through a mammalian blood brain barrier (BBB). The panel is useful for
CC the selection of specific binding members with a desired property such as
CC ability to cross BBB, ability to bind endothelial cells or other brain
CC cell antigen, ability to bind areas of inflammation in the brain or BBB
CC breakdown or ability to bind intracellular adhesion molecules and to bind
CC transferrin receptor. The antibodies are useful in diagnosis, prophylaxis
CC and treatment of human or animal body, including neurological diseases,
CC such as Alzheimer's disease, prion disease, AIDS-related dementia,
CC epilepsy and traumatic brain injury and any diseases involving
CC inflammation occurring within the brain or central nervous system
XX
SQ Sequence 20 AA;
Query Match 70.8%; Score 17; DB 4; Length 20;
Best Local Similarity 40.0%; Pred. No. 5.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
Db 4 FSSSW 8

RESULT 16
ADR68284
ID ADR68284 standard; peptide; 5 AA.
XX
AC ADR68284;
XX
DT 02-DEC-2004 (first entry)
XX
DE Androgen receptor interacting peptide SEQ ID NO:2.
XX
KW androgen receptor binding peptide; androgen receptor interacting peptide;
```

KW androgen receptor; cytostatic; gene therapy; prostate cancer.  
XX Mammalia.  
OS Synthetic.  
OS  
PN WO2004076473-A2.  
XX  
PD 10-SEP-2004.  
XX  
PF 10-FEB-2004; 2004WO-US003774.  
XX  
PR 12-FEB-2003; 2003US-0446955P.  
XX  
PA (KARO-) KARO BIO AB.  
XX  
PI Buehrer BM, Barnett TR;  
XX  
DR WPI; 2004-653365/63.  
XX  
PT New polypeptides that bind to the androgen receptor, useful for  
PT diagnosing or treating diseases associated with abnormal levels of  
PT activation of androgen receptor, e.g. prostate cancer, or in biological  
PT research.  
XX  
PS Disclosure; SEQ ID NO 2; 46pp; English.  
XX  
CC The present invention describes a polypeptide that binds to the androgen  
CC receptor, or a polypeptide that comprises at least 50% amino acid  
CC sequence identity to the polypeptide. Also described: (1) methods of  
CC analysing the surface conformation of a protein using one or more of the  
CC polypeptide sequences mentioned above; (2) methods of identifying  
CC modulators of protein function using one or more of the polypeptide  
CC sequences mentioned above; (3) a pharmaceutical composition comprising a  
CC pharmaceutical carrier and one or more of the polypeptide sequences  
CC described above; (4) a peptide that binds to the androgen receptor, the  
CC binding being competitively inhibited by the polypeptide described above;  
CC (5) a chimeric protein comprising the above polypeptide and at least a  
CC portion of a filamentous phage protein, the portion of the filamentous  
CC phage protein being sufficient for integration of the chimeric protein  
CC into the coat of phage particles to display the polypeptide; (6) a  
CC filamentous phage displaying the above polypeptide; (7) a method of  
CC diagnosing a disease in a patient characterised by abnormal levels of  
CC activation of androgen receptor, comprising providing a sample of body  
CC fluid or tissue of the patient, administering a diagnostic amount of the  
CC pharmaceutical composition described above, and assaying the amount of  
CC activated androgen receptor in the body fluid or tissue of the patient;  
CC and (8) a method of treating a patient suffering from a disease  
CC characterised by abnormal levels of activation of androgen receptor,  
CC comprising administering to the patient a therapeutic amount of the  
CC pharmaceutical composition described above. The androgen receptor  
CC interacting polypeptide has cytostatic activity, and can be used in gene  
CC therapy. The composition and methods are useful for diagnosing or  
CC treating patients suffering from diseases characterised by abnormal  
CC levels of activation of androgen receptor, such as prostate cancer. They  
CC may also be used in biological research, as therapeutics or for in vitro  
CC or in vivo classification of compounds. The present sequence represents  
CC an androgen receptor interacting peptide, which is used in the  
CC exemplification of the present invention.  
XX  
SQ Sequence 5 AA;  
  
Query Match 66.7%; Score 16; DB 8; Length 5;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXXW 6  
Db 1 FAALW 5  
  
RESULT 17  
AAW76953  
ID AAW76953 standard; peptide; 6 AA.

XX AAW76953;  
AC  
XX  
DT 25-JAN-1999 (first entry)  
XX  
DE Fusion immunoglobulin heavy chain HIV gp120 B cell epitope #93.  
XX  
KW B cell; T cell; epitope; immunoglobulin; heavy chain; gp120; IgH;  
KW human immune deficiency virus; HIV; tolerance; treatment; therapy;  
KW prophylaxis; vaccine; chemotherapy; immune response; modifier; tumour;  
KW microbial infection; autoimmune disease; antibody; apoptosis;  
KW antiviral T cell immunity.  
XX  
OS Mus sp.  
OS Homo sapiens.  
XX  
PN WO9836087-A1.  
XX  
PD 20-AUG-1998.  
XX  
PF 13-FEB-1998; 98WO-US002766.  
XX  
PR 13-FEB-1997; 97US-0040581P.  
XX  
PA (AMNA-) AMERICAN NAT RED CROSS.  
XX  
PI Scott D, Zambidis E;  
XX  
DR WPI; 1998-506315/43.  
XX  
PT New fusion immunoglobulin heavy chain including gp120 epitopes and  
PT related complete antibodies - DNA, vectors and transformed cells, used to  
PT induce tolerance to the epitopes for treatment of human immune deficiency  
PT virus infection.  
XX  
PS Disclosure; Page 40; 154pp; English.  
XX  
CC This sequence is an epitope used in the construction of a novel fusion  
CC immunoglobulin heavy chain (IgH) protein with a mammalian, especially  
CC human, IgH chain fused in frame at its N-terminus to one or more human  
CC immune deficiency virus (HIV) gp120 epitopes. Fusion Ig proteins and/or  
CC transfectant cells are used to tolerate subjects to gp120 epitopes and to  
CC maintain this tolerance, particularly for treatment of HIV infection,  
CC optionally together with other therapeutic/prophylactic agents such as  
CC vaccines, chemotherapeutic agents and immune response modifiers. Such  
CC proteins can be used against other diseases where an immune response is  
CC deleterious, e.g. microbial infection, tumours or autoimmune disease.  
CC Induction of tolerance suppresses production of antibodies against gp120,  
CC so prevents or inhibits 'bystander' apoptosis of uninfected T cells that  
CC are bound to gp120 protein, maximising induction of protective antiviral  
CC T cell immunity  
XX  
SQ Sequence 6 AA;  
  
Query Match 66.7%; Score 16; DB 2; Length 6;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXXW 6  
Db 2 FNSTW 6  
  
RESULT 18  
ABR46309  
ID ABR46309 standard; peptide; 6 AA.  
XX  
AC ABR46309;  
XX  
DT 10-JUN-2003 (first entry)  
XX  
DE Staphylococcus aureus CHIPS-related peptide #1499.  
XX

KW	CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;	OS	Staphylococcus aureus.
KW	formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;	OS	Synthetic.
KW	inflammation; cardiovascular disease; central nervous system disease;	XX	
KW	gastrointestinal disease; skin disease; genitourinary disease;	PN	WO2003006048-A1.
KW	joint disease; respiratory disease; HIV infection; antiinflammatory;	XX	
KW	cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;	PD	23-JAN-2003.
KW	gynecological; immunosuppressive; anti-HIV.	XX	
XX		PF	11-JUL-2001; 2001WO-EP008004.
OS	Staphylococcus aureus.	XX	
OS	Synthetic.	XX	
XX		PR	11-JUL-2001; 2001WO-EP008004.
XX		XX	
PN	WO2003006048-A1.	PA	(JARI-) JARI PHARM BV.
XX		XX	
XX		PI	Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
PD	23-JAN-2003.	PI	Van Strijp JAG;
XX		XX	
PF	11-JUL-2001; 2001WO-EP008004.	DR	WPI; 2003-256333/25.
XX		XX	
PR	11-JUL-2001; 2001WO-EP008004.	XX	
XX		PT	Combination of peptides derived from chemotaxis inhibiting protein from
PA	(JARI-) JARI PHARM BV.	PT	Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
XX		PT	prophylaxis and treatment of inflammation, cardiovascular, skin and
XX		PT	kidney diseases.
PI	Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;	XX	
PI	Van Strijp JAG;	XX	
XX		PS	Disclosure; Page 16; 89pp; English.
DR	WPI; 2003-256333/25.	XX	
XX		CC	The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
XX		CC	-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
PT	Combination of peptides derived from chemotaxis inhibiting protein from	CC	Staphylococcus aureus. The peptide fragments are useful in the
PT	Staphylococcus aureus (CHIPS) having CHIPS activity, useful in	CC	prophylaxis or treatment of diseases or disorders involving the C5a-
PT	prophylaxis and treatment of inflammation, cardiovascular, skin and	CC	receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
PT	kidney diseases.	CC	monocytes and endothelial cells or involving acute or chronic
XX		CC	inflammation reactions. The diseases or disorders include cardiovascular
XX		CC	diseases, skin diseases, genitourinary diseases, joint diseases,
PS	Disclosure; Page 16; 89pp; English.	CC	respiratory diseases and HIV infection
XX		XX	
CC	The present invention relates to peptides (ABR44811-ABR47162 and ABR47164	SQ	Sequence 6 AA;
CC	-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from		
CC	Staphylococcus aureus. The peptide fragments are useful in the		
CC	prophylaxis or treatment of diseases or disorders involving the C5a-		
CC	receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,		
CC	monocytes and endothelial cells or involving acute or chronic		
CC	inflammation reactions. The diseases or disorders include cardiovascular		
CC	diseases, skin diseases, genitourinary diseases, joint diseases,		
CC	respiratory diseases and HIV infection		
XX			
SQ	Sequence 6 AA;		
		Query Match	66.7%; Score 16; DB 6; Length 6;
		Best Local Similarity	40.0%; Pred. No. 1.8e+06;
		Matches	2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	2 FXXW 6		
Db	1 FSFSW 5		
RESULT 19			
ABR46270			
ID	ABR46270 standard; peptide; 6 AA.		
XX			
AC	ABR46270;		
XX			
DT	10-JUN-2003 (first entry)		
XX			
DE	Staphylococcus aureus CHIPS-related peptide #1460.		
XX			
KW	CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;		
KW	formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;		
KW	inflammation; cardiovascular disease; central nervous system disease;		
KW	gastrointestinal disease; skin disease; genitourinary disease;		
KW	joint disease; respiratory disease; HIV infection; antiinflammatory;		
KW	cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;		
KW	gynecological; immunosuppressive; anti-HIV.		
XX			
OS	Staphylococcus aureus.		
OS	Synthetic.		
XX			
PN	WO2003006048-A1.		
XX			
XX			
PI	Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;		
PI	Van Strijp JAG;		
XX			
DR	WPI; 2003-256333/25.		
XX			
XX			
PT	Combination of peptides derived from chemotaxis inhibiting protein from		
PT	Staphylococcus aureus (CHIPS) having CHIPS activity, useful in		
PT	prophylaxis and treatment of inflammation, cardiovascular, skin and		
PT	kidney diseases.		
XX			
XX			
PS	Disclosure; Page 16; 89pp; English.		
XX			
CC	The present invention relates to peptides (ABR44811-ABR47162 and ABR47164		
CC	-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from		
CC	Staphylococcus aureus. The peptide fragments are useful in the		
CC	prophylaxis or treatment of diseases or disorders involving the C5a-		
CC	receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,		
CC	monocytes and endothelial cells or involving acute or chronic		
CC	inflammation reactions. The diseases or disorders include cardiovascular		
CC	diseases, skin diseases, genitourinary diseases, joint diseases,		
CC	respiratory diseases and HIV infection		
XX			
SQ	Sequence 6 AA;		
		Query Match	66.7%; Score 16; DB 6; Length 6;
		Best Local Similarity	40.0%; Pred. No. 1.8e+06;
		Matches	2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	2 FXXW 6		
Db	1 FSFSW 5		
RESULT 20			
ABR46702			
ID	ABR46702 standard; peptide; 6 AA.		
XX			
AC	ABR46702;		
XX			
DT	10-JUN-2003 (first entry)		
XX			
DE	Staphylococcus aureus CHIPS-related peptide #1892.		
XX			
KW	CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;		
KW	formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;		
KW	inflammation; cardiovascular disease; central nervous system disease;		
KW	gastrointestinal disease; skin disease; genitourinary disease;		
KW	joint disease; respiratory disease; HIV infection; antiinflammatory;		
KW	cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;		
KW	gynecological; immunosuppressive; anti-HIV.		
XX			
OS	Staphylococcus aureus.		
OS	Synthetic.		
XX			
PN	WO2003006048-A1.		
XX			
XX			
PD	23-JAN-2003.		
XX			
XX			
PF	11-JUL-2001; 2001WO-EP008004.		



XX 11-JUL-2001; 2001WO-EP008004.  
XX (JARI-) JARI PHARM BV.  
PA Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;  
PI Van Strijp JAG;  
XX WPI; 2003-256333/25.  
DR  
XX  
XX Combination of peptides derived from chemotaxis inhibiting protein from  
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in  
PT prophylaxis and treatment of inflammation, cardiovascular, skin and  
PT kidney diseases.  
XX  
XX Disclosure; Page 17; 89pp; English.  
PS  
XX  
XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164  
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from  
CC Staphylococcus aureus. The peptide fragments are useful in the  
CC prophylaxis or treatment of diseases or disorders involving the C5a-  
CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,  
CC monocytes and endothelial cells or involving acute or chronic  
CC inflammation reactions. The diseases or disorders include cardiovascular  
CC diseases, disease of the central nervous system, gastrointestinal  
CC diseases, skin diseases, genitourinary diseases, joint diseases,  
CC respiratory diseases and HIV infection  
XX  
SQ Sequence 6 AA;  
Query Match 66.7%; Score 16; DB 6; Length 6;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 FXXXW 6  
Db 1 FTFSW 5  
RESULT 21  
ABR47093  
ID ABR47093 standard; peptide; 6 AA.  
XX  
XX ABR47093;  
AC  
XX  
XX 10-JUN-2003 (first entry)  
DT  
XX Staphylococcus aureus CHIPS-related peptide #2283.  
DE  
XX  
KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;  
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;  
KW inflammation; cardiovascular disease; central nervous system disease;  
KW gastrointestinal disease; skin disease; genitourinary disease;  
KW joint disease; respiratory disease; HIV infection; antiinflammatory;  
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;  
KW gynecological; immunosuppressive; anti-HIV.  
XX  
OS Staphylococcus aureus.  
OS Synthetic.  
XX  
XX WO2003006048-A1.  
PN  
XX  
XX 23-JAN-2003.  
PD  
XX  
XX 11-JUL-2001; 2001WO-EP008004.  
PF  
XX  
XX 11-JUL-2001; 2001WO-EP008004.  
PR  
XX  
XX (JARI-) JARI PHARM BV.  
PA  
XX  
XX Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;  
PI Van Strijp JAG;  
XX  
XX WPI; 2003-256333/25.  
DR  
XX  
XX Combination of peptides derived from chemotaxis inhibiting protein from  
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in  
PT prophylaxis and treatment of inflammation, cardiovascular, skin and  
PT kidney diseases.  
XX  
XX Disclosure; Page 17; 89pp; English.  
PS  
XX  
XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164  
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from  
CC Staphylococcus aureus. The peptide fragments are useful in the  
CC prophylaxis or treatment of diseases or disorders involving the C5a-  
CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,  
CC monocytes and endothelial cells or involving acute or chronic  
CC inflammation reactions. The diseases or disorders include cardiovascular  
CC diseases, disease of the central nervous system, gastrointestinal  
CC diseases, skin diseases, genitourinary diseases, joint diseases,  
CC respiratory diseases and HIV infection  
XX  
SQ Sequence 6 AA;  
Query Match 66.7%; Score 16; DB 6; Length 6;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 FXXXW 6  
Db 1 FTFSW 5  
RESULT 21  
ABR47093  
ID ABR47093 standard; peptide; 6 AA.  
XX  
XX ABR47093;  
AC  
XX  
XX 10-JUN-2003 (first entry)  
DT  
XX Staphylococcus aureus CHIPS-related peptide #339.  
DE  
XX  
KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;  
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;  
KW inflammation; cardiovascular disease; central nervous system disease;  
KW gastrointestinal disease; skin disease; genitourinary disease;  
KW joint disease; respiratory disease; HIV infection; antiinflammatory;  
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;  
KW gynecological; immunosuppressive; anti-HIV.  
XX  
OS Staphylococcus aureus.  
OS Synthetic.  
XX  
XX WO2003006048-A1.  
PN  
XX  
XX 23-JAN-2003.  
PD  
XX  
XX 11-JUL-2001; 2001WO-EP008004.  
PF  
XX  
XX 11-JUL-2001; 2001WO-EP008004.  
PR  
XX  
XX (JARI-) JARI PHARM BV.  
PA  
XX  
XX Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;  
PI Van Strijp JAG;  
XX  
XX WPI; 2003-256333/25.  
DR  
XX  
XX Combination of peptides derived from chemotaxis inhibiting protein from  
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in  
PT prophylaxis and treatment of inflammation, cardiovascular, skin and  
PT kidney diseases.  
XX  
XX Disclosure; Page 11; 89pp; English.  
PS



XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164  
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from  
CC Staphylococcus aureus. The peptide fragments are useful in the  
CC prophylaxis or treatment of diseases or disorders involving the C5a-  
CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,  
CC monocytes and endothelial cells or involving acute or chronic  
CC inflammation reactions. The diseases or disorders include cardiovascular  
CC diseases, disease of the central nervous system, gastrointestinal  
CC diseases, skin diseases, genitourinary diseases, joint diseases,  
CC respiratory diseases and HIV infection  
XX  
SQ Sequence 6 AA;  
Query Match 66.7%; Score 16; DB 6; Length 6;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 FXXW 6  
Db 1 FSFAW 5  
RESULT 23  
ABR45486  
ID ABR45486 standard; peptide; 6 AA.  
XX  
AC ABR45486;  
XX  
DT 10-JUN-2003 (first entry)  
XX  
DE Staphylococcus aureus CHIPS-related peptide #676.  
XX  
KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;  
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;  
KW inflammation; cardiovascular disease; central nervous system disease;  
KW gastrointestinal disease; skin disease; genitourinary disease;  
KW joint disease; respiratory disease; HIV infection; antiinflammatory;  
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;  
KW gynecological; immunosuppressive; anti-HIV.  
XX  
OS Staphylococcus aureus.  
OS Synthetic.  
XX  
PN WO2003006048-A1.  
XX  
PD 23-JAN-2003.  
XX  
PF 11-JUL-2001; 2001WO-EP008004.  
XX  
PR 11-JUL-2001; 2001WO-EP008004.  
XX  
PA (JARI-) JARI PHARM BV.  
XX  
PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;  
PI Van Strijp JAG;  
XX  
DR WPI; 2003-256333/25.  
XX  
PT Combination of peptides derived from chemotaxis inhibiting protein from  
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in  
PT prophylaxis and treatment of inflammation, cardiovascular, skin and  
PT kidney diseases.  
XX  
PS Disclosure; Page 13; 89pp; English.  
XX  
CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164  
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from  
CC Staphylococcus aureus. The peptide fragments are useful in the  
CC prophylaxis or treatment of diseases or disorders involving the C5a-  
CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,  
CC monocytes and endothelial cells or involving acute or chronic  
CC inflammation reactions. The diseases or disorders include cardiovascular  
CC diseases, disease of the central nervous system, gastrointestinal  
CC diseases, skin diseases, genitourinary diseases, joint diseases,  
CC respiratory diseases and HIV infection  
XX

CC diseases, disease of the central nervous system, gastrointestinal  
CC diseases, skin diseases, genitourinary diseases, joint diseases,  
CC respiratory diseases and HIV infection  
XX  
SQ Sequence 6 AA;  
Query Match 66.7%; Score 16; DB 6; Length 6;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 FXXW 6  
Db 1 FTFW 5  
RESULT 24  
ABR45878  
ID ABR45878 standard; peptide; 6 AA.  
XX  
AC ABR45878;  
XX  
DT 10-JUN-2003 (first entry)  
XX  
DE Staphylococcus aureus CHIPS-related peptide #1068.  
XX  
KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;  
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;  
KW inflammation; cardiovascular disease; central nervous system disease;  
KW gastrointestinal disease; skin disease; genitourinary disease;  
KW joint disease; respiratory disease; HIV infection; antiinflammatory;  
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;  
KW gynecological; immunosuppressive; anti-HIV.  
XX  
OS Staphylococcus aureus.  
OS Synthetic.  
XX  
PN WO2003006048-A1.  
XX  
PD 23-JAN-2003.  
XX  
PF 11-JUL-2001; 2001WO-EP008004.  
XX  
PR 11-JUL-2001; 2001WO-EP008004.  
XX  
PA (JARI-) JARI PHARM BV.  
XX  
PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;  
PI Van Strijp JAG;  
XX  
DR WPI; 2003-256333/25.  
XX  
PT Combination of peptides derived from chemotaxis inhibiting protein from  
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in  
PT prophylaxis and treatment of inflammation, cardiovascular, skin and  
PT kidney diseases.  
XX  
PS Disclosure; Page 14; 89pp; English.  
XX  
CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164  
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from  
CC Staphylococcus aureus. The peptide fragments are useful in the  
CC prophylaxis or treatment of diseases or disorders involving the C5a-  
CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,  
CC monocytes and endothelial cells or involving acute or chronic  
CC inflammation reactions. The diseases or disorders include cardiovascular  
CC diseases, disease of the central nervous system, gastrointestinal  
CC diseases, skin diseases, genitourinary diseases, joint diseases,  
CC respiratory diseases and HIV infection  
XX  
SQ Sequence 6 AA;  
Query Match 66.7%; Score 16; DB 6; Length 6;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 FXXW 6  
Db 1 FTFW 5

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
Db 1 FTFW 5

RESULT 25  
ABR46661  
ID ABR46661 standard; peptide; 6 AA.  
XX  
AC ABR46661;  
XX  
DT 10-JUN-2003 (first entry)  
XX  
DE Staphylococcus aureus CHIPS-related peptide #1851.  
XX  
KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;  
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;  
KW inflammation; cardiovascular disease; central nervous system disease;  
KW gastrointestinal disease; skin disease; genitourinary disease;  
KW joint disease; respiratory disease; HIV infection; antiinflammatory;  
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;  
KW gynecological; immunosuppressive; anti-HIV.  
XX  
OS Staphylococcus aureus.  
OS Synthetic.  
XX  
PN WO2003006048-A1.  
XX  
PD 23-JAN-2003.  
XX  
PF 11-JUL-2001; 2001WO-EP008004.  
XX  
PR 11-JUL-2001; 2001WO-EP008004.  
XX  
PA (JARI-) JARI PHARM BV.  
XX  
PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;  
PI Van Strijp JAG;  
XX  
DR WPI; 2003-256333/25.  
XX  
CC Combination of peptides derived from chemotaxis inhibiting protein from  
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in  
PT prophylaxis and treatment of inflammation, cardiovascular, skin and  
PT kidney diseases.  
XX  
PS Disclosure; Page 17; 89pp; English.  
XX  
CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164  
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from  
CC Staphylococcus aureus. The peptide fragments are useful in the  
CC prophylaxis or treatment of diseases or disorders involving the C5a-  
CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,  
CC monocytes and endothelial cells or involving acute or chronic  
CC inflammation reactions. The diseases or disorders include cardiovascular  
CC diseases, disease of the central nervous system, gastrointestinal  
CC diseases, skin diseases, genitourinary diseases, joint diseases,  
CC respiratory diseases and HIV infection  
XX  
SQ Sequence 6 AA;

Query Match 66.7%; Score 16; DB 6; Length 6;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
Db 1 FTFW 5

RESULT 26  
ABR46661  
ID ABR46661 standard; peptide; 6 AA.  
XX  
AC ABR46661;  
XX  
DT 10-JUN-2003 (first entry)  
XX  
DE Staphylococcus aureus CHIPS-related peptide #1851.  
XX  
KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;  
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;  
KW inflammation; cardiovascular disease; central nervous system disease;  
KW gastrointestinal disease; skin disease; genitourinary disease;  
KW joint disease; respiratory disease; HIV infection; antiinflammatory;  
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;  
KW gynecological; immunosuppressive; anti-HIV.  
XX  
OS Staphylococcus aureus.  
OS Synthetic.  
XX  
PN WO2003006048-A1.  
XX  
PD 23-JAN-2003.  
XX  
PF 11-JUL-2001; 2001WO-EP008004.  
XX  
PR 11-JUL-2001; 2001WO-EP008004.  
XX  
PA (JARI-) JARI PHARM BV.  
XX  
PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;  
PI Van Strijp JAG;  
XX  
DR WPI; 2003-256333/25.  
XX  
CC Combination of peptides derived from chemotaxis inhibiting protein from  
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in  
PT prophylaxis and treatment of inflammation, cardiovascular, skin and  
PT kidney diseases.  
XX  
PS Disclosure; Page 17; 89pp; English.  
XX  
CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164  
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from  
CC Staphylococcus aureus. The peptide fragments are useful in the  
CC prophylaxis or treatment of diseases or disorders involving the C5a-  
CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,  
CC monocytes and endothelial cells or involving acute or chronic  
CC inflammation reactions. The diseases or disorders include cardiovascular  
CC diseases, disease of the central nervous system, gastrointestinal  
CC diseases, skin diseases, genitourinary diseases, joint diseases,  
CC respiratory diseases and HIV infection  
XX  
SQ Sequence 6 AA;

Query Match 66.7%; Score 16; DB 6; Length 6;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
Db 1 FTFW 5

RESULT 27  
ABR45190  
ID ABR45190 standard; peptide; 6 AA.  
XX  
AC ABR45190;  
XX  
DT 10-JUN-2003 (first entry)  
XX  
DE Staphylococcus aureus CHIPS-related peptide #380.

ABR47053  
ID ABR47053 standard; peptide; 6 AA.  
XX  
AC ABR47053;  
XX  
DT 10-JUN-2003 (first entry)  
XX  
DE Staphylococcus aureus CHIPS-related peptide #2243.  
XX  
KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;  
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;  
KW inflammation; cardiovascular disease; central nervous system disease;  
KW gastrointestinal disease; skin disease; genitourinary disease;  
KW joint disease; respiratory disease; HIV infection; antiinflammatory;  
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;  
KW gynecological; immunosuppressive; anti-HIV.  
XX  
OS Staphylococcus aureus.  
OS Synthetic.  
XX  
PN WO2003006048-A1.  
XX  
PD 23-JAN-2003.  
XX  
PF 11-JUL-2001; 2001WO-EP008004.  
XX  
PR 11-JUL-2001; 2001WO-EP008004.  
XX  
PA (JARI-) JARI PHARM BV.  
XX  
PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;  
PI Van Strijp JAG;  
XX  
DR WPI; 2003-256333/25.  
XX  
CC Combination of peptides derived from chemotaxis inhibiting protein from  
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in  
PT prophylaxis and treatment of inflammation, cardiovascular, skin and  
PT kidney diseases.  
XX  
PS Disclosure; Page 19; 89pp; English.  
XX  
CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164  
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from  
CC Staphylococcus aureus. The peptide fragments are useful in the  
CC prophylaxis or treatment of diseases or disorders involving the C5a-  
CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,  
CC monocytes and endothelial cells or involving acute or chronic  
CC inflammation reactions. The diseases or disorders include cardiovascular  
CC diseases, disease of the central nervous system, gastrointestinal  
CC diseases, skin diseases, genitourinary diseases, joint diseases,  
CC respiratory diseases and HIV infection  
XX  
SQ Sequence 6 AA;

Query Match 66.7%; Score 16; DB 6; Length 6;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
Db 1 FTFW 5

RESULT 27  
ABR45190  
ID ABR45190 standard; peptide; 6 AA.  
XX  
AC ABR45190;  
XX  
DT 10-JUN-2003 (first entry)  
XX  
DE Staphylococcus aureus CHIPS-related peptide #380.

XX KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;  
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;  
KW inflammation; cardiovascular disease; central nervous system disease;  
KW gastrointestinal disease; skin disease; genitourinary disease;  
KW joint disease; respiratory disease; HIV infection; antiinflammatory;  
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;  
KW gynecological; immunosuppressive; anti-HIV.  
XX OS Staphylococcus aureus.  
OS Synthetic.  
XX WO2003006048-A1.  
XX PD 23-JAN-2003.  
XX PF 11-JUL-2001; 2001WO-EP008004.  
XX PR 11-JUL-2001; 2001WO-EP008004.  
XX PA (JARI-) JARI PHARM BV.  
XX PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;  
XX PI Van Strijp JAG;  
XX XX WPI; 2003-256333/25.  
DR CC Combination of peptides derived from chemotaxis inhibiting protein from  
XX Staphylococcus aureus (CHIPS) having CHIPS activity, useful in  
PT prophylaxis and treatment of inflammation, cardiovascular, skin and  
PT kidney diseases.  
XX PS Disclosure; Page 12; 89pp; English.  
XX CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164  
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from  
CC Staphylococcus aureus. The peptide fragments are useful in the  
CC prophylaxis or treatment of diseases or disorders involving the C5a-  
CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,  
CC monocytes and endothelial cells or involving acute or chronic  
CC inflammation reactions. The diseases or disorders include cardiovascular  
CC diseases, disease of the central nervous system, gastrointestinal  
CC diseases, skin diseases, genitourinary diseases, joint diseases,  
CC respiratory diseases and HIV infection  
XX SQ Sequence 6 AA;  
Query Match 66.7%; Score 16; DB 6; Length 6;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 FXXW 6  
| |  
Db 1 FTFSW 5  
RESULT 28  
ABR45877  
ID ABR45877 standard; peptide; 6 AA.  
XX AC ABR45877;  
XX DT 10-JUN-2003 (first entry)  
XX DE Staphylococcus aureus CHIPS-related peptide #1067.  
XX KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;  
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;  
KW inflammation; cardiovascular disease; central nervous system disease;  
KW gastrointestinal disease; skin disease; genitourinary disease;  
KW joint disease; respiratory disease; HIV infection; antiinflammatory;  
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;  
KW gynecological; immunosuppressive; anti-HIV.

XX OS Staphylococcus aureus.  
OS Synthetic.  
XX WO2003006048-A1.  
XX PD 23-JAN-2003.  
XX PF 11-JUL-2001; 2001WO-EP008004.  
XX PR 11-JUL-2001; 2001WO-EP008004.  
XX PA (JARI-) JARI PHARM BV.  
XX PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;  
XX PI Van Strijp JAG;  
XX XX WPI; 2003-256333/25.  
DR CC Combination of peptides derived from chemotaxis inhibiting protein from  
XX Staphylococcus aureus (CHIPS) having CHIPS activity, useful in  
PT prophylaxis and treatment of inflammation, cardiovascular, skin and  
PT kidney diseases.  
XX PS Disclosure; Page 14; 89pp; English.  
XX CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164  
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from  
CC Staphylococcus aureus. The peptide fragments are useful in the  
CC prophylaxis or treatment of diseases or disorders involving the C5a-  
CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,  
CC monocytes and endothelial cells or involving acute or chronic  
CC inflammation reactions. The diseases or disorders include cardiovascular  
CC diseases, disease of the central nervous system, gastrointestinal  
CC diseases, skin diseases, genitourinary diseases, joint diseases,  
CC respiratory diseases and HIV infection  
XX SQ Sequence 6 AA;  
Query Match 66.7%; Score 16; DB 6; Length 6;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 FXXW 6  
| |  
Db 1 FSFAW 5  
RESULT 29  
ABR46310  
ID ABR46310 standard; peptide; 6 AA.  
XX AC ABR46310;  
XX DT 10-JUN-2003 (first entry)  
XX DE Staphylococcus aureus CHIPS-related peptide #1500.  
XX KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;  
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;  
KW inflammation; cardiovascular disease; central nervous system disease;  
KW gastrointestinal disease; skin disease; genitourinary disease;  
KW joint disease; respiratory disease; HIV infection; antiinflammatory;  
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;  
KW gynecological; immunosuppressive; anti-HIV.  
XX OS Staphylococcus aureus.  
OS Synthetic.  
XX WO2003006048-A1.  
XX PD 23-JAN-2003.  
XX

PF	11-JUL-2001; 2001WO-EP0080004.
XX	
PR	11-JUL-2001; 2001WO-EP0080004.
XX	
PA	(JARI-) JARI PHARM BV.
XX	
PI	Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
PI	Van Strijp JAG;
XX	
DR	WPI; 2003-256333/25.
XX	
CC	Combination of peptides derived from chemotaxis inhibiting protein from Staphylococcus aureus (CHIPS) having CHIPS activity, useful in prophylaxis and treatment of inflammation, cardiovascular, skin and kidney diseases.
PS	Disclosure; Page 16; 89pp; English.
XX	
CC	The present invention relates to peptides (ABR44811-ABR47162 and ABR47164 -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from Staphylococcus aureus. The peptide fragments are useful in the prophylaxis or treatment of diseases or disorders involving the C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial cells or involving acute or chronic inflammation reactions. The diseases or disorders include cardiovascular diseases, disease of the central nervous system, gastrointestinal diseases, skin diseases, genitourinary diseases, joint diseases, respiratory diseases and HIV infection
XX	
SQ	Sequence 6 AA;
	Query Match 66.7%; Score 16; DB 6; Length 6; Best Local Similarity 40.0%; Pred. No. 1.8e+06; Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	2 FXXXW 6     1 FTFSW 5
Dd	
RESULT 30	
ABR47094	
ID	ABR47094 standard; peptide; 6 AA.
XX	
AC	ABR47094;
XX	
DT	10-JUN-2003 (first entry)
XX	
DE	Staphylococcus aureus CHIPS-related peptide #2284.
XX	
KW	CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR; formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell; inflammation; cardiovascular disease; central nervous system disease; gastrointestinal disease; skin disease; genitourinary disease; joint disease; respiratory disease; HIV infection; antiinflammatory; cardiant; cerebroprotective; neuroprotective; nootropic; dermatological; gynecological; immunosuppressive; anti-HIV.
OS	Staphylococcus aureus.
OS	Synthetic.
XX	
PN	WO2003006048-A1.
PD	23-JAN-2003.
XX	
PF	11-JUL-2001; 2001WO-EP0080004.
XX	
PR	11-JUL-2001; 2001WO-EP0080004.
XX	
PA	(JARI-) JARI PHARM BV.
XX	
PI	Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
PI	Van Strijp JAG;
XX	

XX	
DR	WPI; 2003-256333/25.
XX	
PT	Combination of peptides derived from chemotaxis inhibiting protein from Staphylococcus aureus (CHIPS) having CHIPS activity, useful in prophylaxis and treatment of inflammation, cardiovascular, skin and kidney diseases.
PT	
PT	
PT	
XX	
PS	Disclosure; Page 19; 89pp; English.
XX	
CC	The present invention relates to peptides (ABR44811-ABR47162 and ABR47164 -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from Staphylococcus aureus. The peptide fragments are useful in the prophylaxis or treatment of diseases or disorders involving the C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial cells or involving acute or chronic inflammation reactions. The diseases or disorders include cardiovascular diseases, disease of the central nervous system, gastrointestinal diseases, skin diseases, genitourinary diseases, joint diseases, respiratory diseases and HIV infection
XX	
SQ	Sequence 6 AA;
	Query Match 66.7%; Score 16; DB 6; Length 6; Best Local Similarity 40.0%; Pred. No. 1.8e+06; Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	2 FXXXW 6     1 FTFSW 5
Dd	
RESULT 30	
ABR47094	
ID	ABR47094 standard; peptide; 6 AA.
XX	
AC	ABR47094;
XX	
DT	10-JUN-2003 (first entry)
XX	
DE	Staphylococcus aureus CHIPS-related peptide #2284.
XX	
KW	CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR; formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell; inflammation; cardiovascular disease; central nervous system disease; gastrointestinal disease; skin disease; genitourinary disease; joint disease; respiratory disease; HIV infection; antiinflammatory; cardiant; cerebroprotective; neuroprotective; nootropic; dermatological; gynecological; immunosuppressive; anti-HIV.
OS	Staphylococcus aureus.
OS	Synthetic.
XX	
PN	WO2003006048-A1.
PD	23-JAN-2003.
XX	
PF	11-JUL-2001; 2001WO-EP0080004.
XX	
PR	11-JUL-2001; 2001WO-EP0080004.
XX	
PA	(JARI-) JARI PHARM BV.
XX	
PI	Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
PI	Van Strijp JAG;
XX	

PS Disclosure; Page 17; 89pp; English.

XX

CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164

CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from

CC Staphylococcus aureus. The peptide fragments are useful in the

CC prophylaxis or treatment of diseases or disorders involving the C5a-

CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,

CC monocytes and endothelial cells or involving acute or chronic

CC inflammation reactions. The diseases or disorders include cardiovascular

CC diseases, disease of the central nervous system, gastrointestinal

CC diseases, skin diseases, genitourinary diseases, joint diseases,

CC respiratory diseases and HIV infection

XX

SQ Sequence 6 AA;

Query Match 66.7%; Score 16; DB 6; Length 6;

Best Local Similarity 40.0%; Pred. No. 1.8e+06;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6

Db 1 FSFSW 5

RESULT 32

ABR47054

ID ABR47054 standard; peptide; 6 AA.

XX

AC ABR47054;

XX

DT 10-JUN-2003 (first entry)

XX

DE Staphylococcus aureus CHIPS-related peptide #2244.

XX

KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;

KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;

KW inflammation; cardiovascular disease; central nervous system disease;

KW gastrointestinal disease; skin disease; genitourinary disease;

KW joint disease; respiratory disease; HIV infection; antiinflammatory;

KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;

KW gynecological; immunosuppressive; anti-HIV.

XX

OS Staphylococcus aureus.

OS Synthetic.

XX

PN WO2003006048-A1.

XX

PD 23-JAN-2003.

XX

PF 11-JUL-2001; 2001WO-EP008004.

XX

PR 11-JUL-2001; 2001WO-EP008004.

XX

PA (JARI-) JARI PHARM BV.

XX

PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;

PI Van Strijp JAG;

XX

DR WPI; 2003-256333/25.

XX

XX Combination of peptides derived from chemotaxis inhibiting protein from

PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in

PT prophylaxis and treatment of inflammation, cardiovascular, skin and

PT kidney diseases.

XX

PS Disclosure; Page 19; 89pp; English.

XX

CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164

CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from

CC Staphylococcus aureus. The peptide fragments are useful in the

CC prophylaxis or treatment of diseases or disorders involving the C5a-

CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,

CC monocytes and endothelial cells or involving acute or chronic

XX

CC

CC inflammation reactions. The diseases or disorders include cardiovascular

CC diseases, disease of the central nervous system, gastrointestinal

CC diseases, skin diseases, genitourinary diseases, joint diseases,

CC respiratory diseases and HIV infection

XX

SQ Sequence 6 AA;

Query Match 66.7%; Score 16; DB 6; Length 6;

Best Local Similarity 40.0%; Pred. No. 1.8e+06;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6

Db 1 FTFW 5

RESULT 33

ABR45525

ID ABR45525 standard; peptide; 6 AA.

XX

AC ABR45525;

XX

DT 10-JUN-2003 (first entry)

XX

DE Staphylococcus aureus CHIPS-related peptide #715.

XX

KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;

KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;

KW inflammation; cardiovascular disease; central nervous system disease;

KW gastrointestinal disease; skin disease; genitourinary disease;

KW joint disease; respiratory disease; HIV infection; antiinflammatory;

KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;

KW gynecological; immunosuppressive; anti-HIV.

XX

OS Staphylococcus aureus.

OS Synthetic.

XX

PN WO2003006048-A1.

XX

PD 23-JAN-2003.

XX

PF 11-JUL-2001; 2001WO-EP008004.

XX

PR 11-JUL-2001; 2001WO-EP008004.

XX

PA (JARI-) JARI PHARM BV.

XX

PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;

PI Van Strijp JAG;

XX

DR WPI; 2003-256333/25.

XX

XX Combination of peptides derived from chemotaxis inhibiting protein from

PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in

PT prophylaxis and treatment of inflammation, cardiovascular, skin and

PT kidney diseases.

XX

PS Disclosure; Page 13; 89pp; English.

XX

CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164

CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from

CC Staphylococcus aureus. The peptide fragments are useful in the

CC prophylaxis or treatment of diseases or disorders involving the C5a-

CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,

CC monocytes and endothelial cells or involving acute or chronic

CC inflammation reactions. The diseases or disorders include cardiovascular

CC diseases, disease of the central nervous system, gastrointestinal

CC diseases, skin diseases, genitourinary diseases, joint diseases,

CC respiratory diseases and HIV infection

XX

SQ Sequence 6 AA;

Query Match 66.7%; Score 16; DB 6; Length 6;

Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
|  
Db 1 FSFSW 5

RESULT 34

ABR45918

ID ABR45918 standard; peptide; 6 AA.

XX

AC ABR45918;

XX

DT 10-JUN-2003 (first entry)

XX

DE Staphylococcus aureus CHIPS-related peptide #1108.

XX

KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;

KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;

KW inflammation; cardiovascular disease; central nervous system disease;

KW gastrointestinal disease; skin disease; genitourinary disease;

KW joint disease; respiratory disease; HIV infection; antiinflammatory;

KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;

KW gynecological; immunosuppressive; anti-HIV.

XX

OS Staphylococcus aureus.

OS Synthetic.

XX

PN WO2003006048-A1.

XX

PD 23-JAN-2003.

XX

PF 11-JUL-2001; 2001WO-EP008004.

XX

PR 11-JUL-2001; 2001WO-EP008004.

XX

PA (JARI-) JARI PHARM BV.

XX

PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;

PI Van Strijp JAG;

XX

DR WPI; 2003-256333/25.

XX

PT Combination of peptides derived from chemotaxis inhibiting protein from

PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in

PT prophylaxis and treatment of inflammation, cardiovascular, skin and

PT kidney diseases.

XX

PS Disclosure; Page 14; 89pp; English.

XX

CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164

CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from

CC Staphylococcus aureus. The peptide fragments are useful in the

CC prophylaxis or treatment of diseases or disorders involving the C5a-

CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,

CC monocytes and endothelial cells or involving acute or chronic

CC inflammation reactions. The diseases or disorders include cardiovascular

CC diseases, disease of the central nervous system, gastrointestinal

CC diseases, skin diseases, genitourinary diseases, joint diseases,

CC respiratory diseases and HIV infection

XX

SQ Sequence 6 AA;

Query Match

Best Local Similarity 66.7%; Score 16; DB 6; Length 6;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6

|

Db 1 FTFSW 5

RESULT 36

ABR45485

ID ABR45485 standard; peptide; 6 AA.

XX

AC ABR45485;

XX

DT 10-JUN-2003 (first entry)

XX

RESULT 35  
ABR45189  
ID ABR45189 standard; peptide; 6 AA.  
XX  
AC ABR45189;  
XX  
DT 10-JUN-2003 (first entry)  
XX  
DE Staphylococcus aureus CHIPS-related peptide #379.

XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;

KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;

KW inflammation; cardiovascular disease; central nervous system disease;

KW gastrointestinal disease; skin disease; genitourinary disease;

KW joint disease; respiratory disease; HIV infection; antiinflammatory;

KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;

KW gynecological; immunosuppressive; anti-HIV.

XX Staphylococcus aureus.

OS Synthetic.

XX WO2003006048-A1.

PN 23-JAN-2003.

XX

PF 11-JUL-2001; 2001WO-EP008004.

XX

PR 11-JUL-2001; 2001WO-EP008004.

XX

PA (JARI-) JARI PHARM BV.

XX

PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;

PI Van Strijp JAG;

XX

DR WPI; 2003-256333/25.

XX

PT Combination of peptides derived from chemotaxis inhibiting protein from

PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in

PT prophylaxis and treatment of inflammation, cardiovascular, skin and

PT kidney diseases.

XX

PS Disclosure; Page 12; 89pp; English.

XX

CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164  
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from  
CC Staphylococcus aureus. The peptide fragments are useful in the  
CC prophylaxis or treatment of diseases or disorders involving the C5a-  
CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,  
CC monocytes and endothelial cells or involving acute or chronic  
CC inflammation reactions. The diseases or disorders include cardiovascular  
CC diseases, disease of the central nervous system, gastrointestinal  
CC diseases, skin diseases, genitourinary diseases, joint diseases,  
CC respiratory diseases and HIV infection

XX

SQ Sequence 6 AA;

Query Match

Best Local Similarity 66.7%; Score 16; DB 6; Length 6;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6

|

Db 1 FSFSW 5



DE	Staphylococcus aureus	CHIPS-related peptide #675.	
XX			
KW	CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;		
KW	formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;		
KW	inflammation; cardiovascular disease; central nervous system disease;		
KW	gastrointestinal disease; skin disease; genitourinary disease;		
KW	joint disease; respiratory disease; HIV infection; antiinflammatory;		
KW	cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;		
KW	gynecological; immunosuppressive; anti-HIV.		
XX			
OS	Staphylococcus aureus.		
OS	Synthetic.		
XX			
PN	WO2003006048-A1.		
XX			
PD	23-JAN-2003.		
XX			
PF	11-JUL-2001; 2001WO-EP008004.		
XX			
PR	11-JUL-2001; 2001WO-EP008004.		
XX			
PA	(JARI-) JARI PHARM BV.		
XX			
PI	Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;		
PI	Van Strijp JAG;		
XX			
DR	WPI; 2003-256333/25.		
XX			
XX	Combination of peptides derived from chemotaxis inhibiting protein from		
PT	Staphylococcus aureus (CHIPS) having CHIPS activity, useful in		
PT	prophylaxis and treatment of inflammation, cardiovascular, skin and		
PT	kidney diseases.		
XX			
PS	Disclosure; Page 13; 89pp; English.		
XX			
CC	The present invention relates to peptides (ABR44811-ABR47162 and ABR47164		
CC	-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from		
CC	Staphylococcus aureus. The peptide fragments are useful in the		
CC	prophylaxis or treatment of diseases or disorders involving the C5a-		
CC	receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,		
CC	monocytes and endothelial cells or involving acute or chronic		
CC	inflammation reactions. The diseases or disorders include cardiovascular		
CC	diseases, skin diseases, genitourinary diseases, joint diseases,		
CC	respiratory diseases and HIV infection		
XX			
SQ	Sequence 6 AA;		
	Query Match 66.7%; Score 16; DB 6; Length 6;		
	Best Local Similarity 40.0%; Pred. No. 1.8e+06;		
	Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
QY	2 FXXXW 6		
Db	1 FSFAW 5		
RESULT 37			
ABR45150			
ID	ABR45150 standard; peptide; 6 AA.		
XX			
AC	ABR45150;		
XX			
DT	10-JUN-2003 (first entry)		
XX			
DE	Staphylococcus aureus CHIPS-related peptide #340.		
XX			
KW	CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;		
KW	formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;		
KW	inflammation; cardiovascular disease; central nervous system disease;		
KW	gastrointestinal disease; skin disease; genitourinary disease;		
KW	joint disease; respiratory disease; HIV infection; antiinflammatory;		
KW	cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;		

KW	gynecological; immunosuppressive; anti-HIV.		
XX			
OS	Staphylococcus aureus.		
OS	Synthetic.		
XX			
PN	WO2003006048-A1.		
XX			
PD	23-JAN-2003.		
XX			
PF	11-JUL-2001; 2001WO-EP008004.		
XX			
PR	11-JUL-2001; 2001WO-EP008004.		
XX			
PA	(JARI-) JARI PHARM BV.		
XX			
PI	Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;		
PI	Van Strijp JAG;		
XX			
DR	WPI; 2003-256333/25.		
XX			
XX	Combination of peptides derived from chemotaxis inhibiting protein from		
PT	Staphylococcus aureus (CHIPS) having CHIPS activity, useful in		
PT	prophylaxis and treatment of inflammation, cardiovascular, skin and		
PT	kidney diseases.		
XX			
PS	Disclosure; Page 11; 89pp; English.		
XX			
CC	The present invention relates to peptides (ABR44811-ABR47162 and ABR47164		
CC	-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from		
CC	Staphylococcus aureus. The peptide fragments are useful in the		
CC	prophylaxis or treatment of diseases or disorders involving the C5a-		
CC	receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,		
CC	monocytes and endothelial cells or involving acute or chronic		
CC	inflammation reactions. The diseases or disorders include cardiovascular		
CC	diseases, skin diseases, genitourinary diseases, joint diseases,		
CC	respiratory diseases and HIV infection		
XX			
SQ	Sequence 6 AA;		
	Query Match 66.7%; Score 16; DB 6; Length 6;		
	Best Local Similarity 40.0%; Pred. No. 1.8e+06;		
	Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
QY	2 FXXXW 6		
Db	1 FTFW 5		
RESULT 38			
ABR45526			
ID	ABR45526 standard; peptide; 6 AA.		
XX			
AC	ABR45526;		
XX			
DT	10-JUN-2003 (first entry)		
XX			
DE	Staphylococcus aureus CHIPS-related peptide #716.		
XX			
KW	CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;		
KW	formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;		
KW	inflammation; cardiovascular disease; central nervous system disease;		
KW	gastrointestinal disease; skin disease; genitourinary disease;		
KW	joint disease; respiratory disease; HIV infection; antiinflammatory;		
KW	cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;		
KW	gynecological; immunosuppressive; anti-HIV.		
XX			
OS	Staphylococcus aureus.		
OS	Synthetic.		
XX			
PN	WO2003006048-A1.		
XX			
PD	23-JAN-2003.		

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XX PF 11-JUL-2001; 2001WO-EP008004.
XX DR
XX PR 11-JUL-2001; 2001WO-EP008004.
XX PA (JARI-) JARI PHARM BV.
XX PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
XX PI Van Strijp JAG;
XX DR WPI; 2003-256333/25.
XX CC Combination of peptides derived from chemotaxis inhibiting protein from
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
PT prophylaxis and treatment of inflammation, cardiovascular, skin and
PT kidney diseases.
XX PS Disclosure; Page 13; 89pp; English.
XX CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
CC Staphylococcus aureus. The peptide fragments are useful in the
CC prophylaxis or treatment of diseases or disorders involving the C5a-
CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
CC monocytes and endothelial cells or involving acute or chronic
CC inflammation reactions. The diseases or disorders include cardiovascular
CC diseases, disease of the central nervous system, gastrointestinal
CC diseases, skin diseases, genitourinary diseases, joint diseases,
CC respiratory diseases and HIV infection
XX SQ Sequence 6 AA;
Query Match 66.7%; Score 16; DB 6; Length 6;
Best Local Similarity 40.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 FXXXW 6
Db 1 FTFSW 5
Sequence 6 AA;

RESULT 39
ABR46269
ID ABR46269 standard; peptide; 6 AA.
XX AC ABR46269;
XX DT 10-JUN-2003 (first entry)
XX DE Staphylococcus aureus CHIPS-related peptide #1459.
XX KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
KW inflammation; cardiovascular disease; central nervous system disease;
KW gastrointestinal disease; skin disease; genitourinary disease;
KW joint disease; respiratory disease; HIV infection; antiinflammatory;
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
KW gynecological; immunosuppressive; anti-HIV.
XX OS Staphylococcus aureus.
OS Synthetic.
XX PN WO2003006048-A1.
XX PD 23-JAN-2003.
XX PF 11-JUL-2001; 2001WO-EP008004.
XX PR 11-JUL-2001; 2001WO-EP008004.
XX PA (JARI-) JARI PHARM BV.
XX PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
XX PI Van Strijp JAG;
XX DR WPI; 2003-256333/25.
XX CC Combination of peptides derived from chemotaxis inhibiting protein from
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
PT prophylaxis and treatment of inflammation, cardiovascular, skin and
PT kidney diseases.
XX PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
XX PI Van Strijp JAG;
XX DR WPI; 2003-256333/25.
XX CC Combination of peptides derived from chemotaxis inhibiting protein from
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
PT prophylaxis and treatment of inflammation, cardiovascular, skin and
PT kidney diseases.

```



XX Disclosure; Page 17; 89pp; English.  
PS  
XX  
CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164  
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from  
CC Staphylococcus aureus. The peptide fragments are useful in the  
CC prophylaxis or treatment of diseases or disorders involving the C5a-  
CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,  
CC monocytes and endothelial cells or involving acute or chronic  
CC inflammation reactions. The diseases or disorders include cardiovascular  
CC diseases, disease of the central nervous system, gastrointestinal  
CC diseases, skin diseases, genitourinary diseases, joint diseases,  
CC respiratory diseases and HIV infection  
XX  
SQ Sequence 6 AA;

Query Match 66.7%; Score 16; DB 6; Length 6;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6  
| |  
Db 1 FTFW 5

Search completed: October 18, 2005, 15:54:57  
Job time : 123.824 secs

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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:46:49 ; Search time 31.2353 Seconds  
(without alignments)  
21.509 Million cell updates/sec

Title: US-09-214-371-11  
Perfect score: 24  
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 196327

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	17	70.8	15	4	US-09-142-524D-87
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4	16	66.7	6	1	US-07-920-519-10
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6	16	66.7	6	1	US-08-314-586-10
7	16	66.7	7	4	US-09-774-639-284
8	16	66.7	9	4	US-09-702-114A-28
9	16	66.7	10	1	US-08-208-886C-87
10	16	66.7	10	1	US-08-704-744-89
11	16	66.7	10	1	US-08-469-557-68
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13	16	66.7	11	1	US-08-277-660A-16
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18	16	66.7	11	3	US-09-035-686-30
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81	15	62.5	8	4	US-08-469-260A-252	Sequence 252, App
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84	15	62.5	8	4	US-09-402-181B-154	Sequence 154, App
85	15	62.5	8	4	US-09-721-456-154	Sequence 154, App
86	15	62.5	8	4	US-08-424-550B-252	Sequence 252, App
87	15	62.5	8	4	US-09-400-122A-17	Sequence 17, Appli
88	15	62.5	8	4	US-09-400-122A-18	Sequence 18, Appli
89	15	62.5	8	4	US-09-908-322-83	Sequence 83, Appli
90	15	62.5	8	5	PCT-US95-04018-71	Sequence 71, Appli
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92	15	62.5	8	6	5514646-28	Patent No. 5514646
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94	15	62.5	9	1	US-08-350-884-8	Sequence 8, Appli
95	15	62.5	9	1	US-08-350-884-11	Sequence 11, Appli
96	15	62.5	9	1	US-08-350-884-14	Sequence 14, Appli
97	15	62.5	9	1	US-08-709-173-5	Sequence 5, Appli
98	15	62.5	9	1	US-08-709-173-8	Sequence 8, Appli
99	15	62.5	9	1	US-08-709-173-11	Sequence 11, Appli
100	15	62.5	9	1	US-08-709-173-14	Sequence 14, Appli

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102	15	62.5	9	1	US-08-638-911A-15	Sequence 15, Appl	175	15	62.5	11	3	US-09-035-686-43	Sequence 43, Appl
103	15	62.5	9	1	US-08-638-911A-18	Sequence 18, Appl	176	15	62.5	11	3	US-09-035-686-44	Sequence 44, Appl
104	15	62.5	9	1	US-08-638-911A-21	Sequence 21, Appl	177	15	62.5	11	3	US-09-035-686-45	Sequence 45, Appl
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107	15	62.5	9	2	US-08-709-177-11	Sequence 11, Appl	180	15	62.5	11	4	US-09-069-827A-46	Sequence 46, Appl
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109	15	62.5	9	3	US-08-396-385-7	Sequence 7, Appli	182	15	62.5	11	4	US-09-620-091-444	Sequence 444, App
110	15	62.5	9	3	US-09-249-272-3	Sequence 3, Appli	183	15	62.5	11	5	PCT-US96-09473-2	Sequence 2, Appli
111	15	62.5	9	3	US-09-287-221-7	Sequence 7, Appli	184	15	62.5	12	1	US-08-439-114-4	Sequence 4, Appli
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114	15	62.5	9	4	US-08-634-332A-71	Sequence 71, Appl	187	15	62.5	12	4	US-08-634-332A-70	Sequence 70, Appl
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117	15	62.5	9	4	US-09-771-415-16	Sequence 16, Appl	190	15	62.5	12	4	US-09-428-082B-133	Sequence 133, App
118	15	62.5	9	4	US-09-239-043D-2374	Sequence 2374, Ap	191	15	62.5	12	4	US-09-428-082B-134	Sequence 134, App
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121	15	62.5	10	1	US-08-277-660A-7	Sequence 7, Appli	194	15	62.5	12	4	US-09-428-082B-144	Sequence 144, App
122	15	62.5	10	1	US-08-277-660A-8	Sequence 8, Appli	195	15	62.5	12	4	US-09-428-082B-145	Sequence 145, App
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136	15	62.5	10	4	US-09-490-702B-72	Sequence 72, Appl	209	15	62.5	14	3	US-08-973-225-213	Sequence 213, App
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138	15	62.5	10	5	PCT-US95-04018-64	Sequence 64, Appl	211	15	62.5	14	3	US-09-516-704-33	Sequence 33, Appl
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146	15	62.5	11	1	US-08-277-660A-20	Sequence 20, Appl	219	15	62.5	14	4	US-09-695-437A-26	Sequence 26, Appl
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149	15	62.5	11	1	US-08-424-957-24	Sequence 24, Appl	222	15	62.5	15	1	US-08-277-660A-5	Sequence 5, Appli
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157	15	62.5	11	1	US-08-424-957-40	Sequence 40, Appl	230	15	62.5	15	3	US-09-165-042-16	Sequence 16, Appl
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164	15	62.5	11	3	US-09-035-686-23	Sequence 23, Appl	237	15	62.5	15	4	US-08-634-332A-65	Sequence 65, Appl
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167	15	62.5	11	3	US-09-035-686-26	Sequence 26, Appl	240	15	62.5	15	4	US-09-157-689-51	Sequence 51, Appl
168	15	62.5	11	3	US-09-035-686-28	Sequence 28, Appl	241	15	62.5	15	4	US-09-157-689-52	Sequence 52, Appl
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171	15	62.5	11	3	US-09-035-686-34	Sequence 34, Appl	244	15	62.5	15	4	US-09-428-082B-140	Sequence 140, App
172	15	62.5	11	3	US-09-035-686-36	Sequence 36, Appl	245	15	62.5	15	4	US-09-428-082B-141	Sequence 141, App
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393	14	58.3	7	2	US-08-475-879-71	Sequence 71, Appl	466	14	58.3	10	2	US-08-751-300-96	Sequence 96, Appl
394	14	58.3	7	3	US-09-258-754-402	Sequence 402, App	467	14	58.3	10	2	US-08-751-300-97	Sequence 97, Appl
395	14	58.3	7	3	US-09-181-083-26	Sequence 26, Appl	468	14	58.3	10	2	US-08-751-300-98	Sequence 98, Appl
396	14	58.3	7	3	US-09-181-083-70	Sequence 70, Appl	469	14	58.3	10	2	US-08-751-300-99	Sequence 99, Appl
397	14	58.3	7	3	US-09-181-083-79	Sequence 79, Appl	470	14	58.3	10	3	US-08-485-324-16	Sequence 16, Appl
398	14	58.3	7	3	US-09-042-107-402	Sequence 402, App	471	14	58.3	10	3	US-08-447-506-16	Sequence 16, Appl
399	14	58.3	7	3	US-09-099-053-7	Sequence 7, Appli	472	14	58.3	10	3	US-08-235-437-16	Sequence 16, Appl
400	14	58.3	7	3	US-09-433-043B-71	Sequence 71, Appl	473	14	58.3	10	3	US-08-447-515-16	Sequence 16, Appl
401	14	58.3	7	4	US-09-722-250D-402	Sequence 402, App	474	14	58.3	10	3	US-09-181-083-74	Sequence 74, Appl
402	14	58.3	7	4	US-09-750-754-26	Sequence 26, Appl	475	14	58.3	10	3	US-07-901-713A-4	Sequence 4, Appli
403	14	58.3	7	4	US-09-750-754-70	Sequence 70, Appl	476	14	58.3	10	3	US-09-268-347-2	Sequence 2, Appli
404	14	58.3	7	4	US-09-750-754-79	Sequence 79, Appl	477	14	58.3	10	3	US-09-261-182-2	Sequence 2, Appli
405	14	58.3	7	4	US-09-676-475A-402	Sequence 402, App	478	14	58.3	10	4	US-09-490-702B-40	Sequence 40, Appl
406	14	58.3	8	2	US-08-466-103A-9	Sequence 9, Appli	479	14	58.3	10	4	US-09-750-754-74	Sequence 74, Appl
407	14	58.3	8	2	US-08-669-284B-31	Sequence 31, Appl	480	14	58.3	10	4	US-09-428-082B-142	Sequence 142, App
408	14	58.3	8	3	US-09-063-893A-8	Sequence 8, Appli	481	14	58.3	10	4	US-09-239-043D-2392	Sequence 2392, Ap
409	14	58.3	8	3	US-08-444-818-323	Sequence 323, App	482	14	58.3	10	4	US-09-620-091-46	Sequence 46, Appl
410	14	58.3	8	3	US-08-444-818-346	Sequence 346, App	483	14	58.3	10	4	US-09-043-813-2	Sequence 2, Appli
411	14	58.3	8	3	US-08-444-818-347	Sequence 347, App	484	14	58.3	10	4	US-09-043-813-5	Sequence 5, Appli
412	14	58.3	8	3	US-08-444-818-348	Sequence 348, App	485	14	58.3	10	4	US-09-043-813-8	Sequence 8, Appli
413	14	58.3	8	3	US-08-444-818-384	Sequence 384, App	486	14	58.3	10	4	US-09-043-813-11	Sequence 11, Appl
414	14	58.3	8	3	US-08-444-818-385	Sequence 385, App	487	14	58.3	10	4	US-09-043-813-14	Sequence 14, Appl
415	14	58.3	8	3	US-08-444-818-386	Sequence 386, App	488	14	58.3	10	4	US-09-043-813-17	Sequence 17, Appl
416	14	58.3	8	3	US-09-314-242-4	Sequence 4, Appli	489	14	58.3	10	4	US-09-043-813-20	Sequence 20, Appl
417	14	58.3	8	4	US-09-402-641-3	Sequence 3, Appli	490	14	58.3	10	4	US-09-043-813-23	Sequence 23, Appl
418	14	58.3	8	4	US-09-601-729-168	Sequence 168, App	491	14	58.3	10	4	US-09-043-813-26	Sequence 26, Appl
419	14	58.3	8	4	US-09-620-091-484	Sequence 484, App	492	14	58.3	10	4	US-09-043-813-29	Sequence 29, Appl
420	14	58.3	9	1	US-08-318-970B-23	Sequence 23, Appl	493	14	58.3	10	4	US-09-043-813-32	Sequence 32, Appl
421	14	58.3	9	2	US-08-417-174-77	Sequence 77, Appl	494	14	58.3	10	4	US-09-043-813-35	Sequence 35, Appl
422	14	58.3	9	3	US-08-676-818-16	Sequence 16, Appl	495	14	58.3	10	4	US-09-043-813-38	Sequence 38, Appl
423	14	58.3	9	3	US-09-267-439-77	Sequence 77, Appl	496	14	58.3	10	4	US-09-043-813-41	Sequence 41, Appl
424	14	58.3	9	3	US-09-407-549-16	Sequence 16, Appl	497	14	58.3	10	4	US-09-043-813-44	Sequence 44, Appl
425	14	58.3	9	4	US-09-402-641-5	Sequence 5, Appli	498	14	58.3	10	4	US-09-043-813-57	Sequence 57, Appl
426	14	58.3	9	4	US-09-073-138-77	Sequence 77, Appl	499	14	58.3	10	4	US-09-043-813-59	Sequence 59, Appl
427	14	58.3	9	4	US-09-870-089B-3	Sequence 3, Appli	500	14	58.3	10	4	US-09-043-813-63	Sequence 63, Appl
428	14	58.3	9	4	US-09-870-089B-7	Sequence 7, Appli	501	14	58.3	10	4	US-09-043-813-65	Sequence 65, Appl
429	14	58.3	9	4	US-09-870-089B-9	Sequence 9, Appli	502	14	58.3	10	4	US-09-043-813-76	Sequence 76, Appl
430	14	58.3	10	1	US-08-321-625-74	Sequence 74, Appl	503	14	58.3	10	4	US-09-756-247-16	Sequence 16, Appl
431	14	58.3	10	1	US-08-242-678D-5	Sequence 5, Appli	504	14	58.3	10	4	US-09-756-247-36	Sequence 36, Appl
432	14	58.3	10	1	US-08-487-568-88	Sequence 88, Appl	505	14	58.3	11	1	US-08-318-970B-10	Sequence 10, Appl
433	14	58.3	10	2	US-08-370-909-16	Sequence 16, Appl	506	14	58.3	11	1	US-08-321-625-10	Sequence 10, Appl
434	14	58.3	10	2	US-08-370-909-17	Sequence 17, Appl	507	14	58.3	11	1	US-08-424-957-35	Sequence 35, Appl
435	14	58.3	10	2	US-08-556-597-120	Sequence 120, App	508	14	58.3	11	2	US-08-486-839-9	Sequence 9, Appli
436	14	58.3	10	2	US-08-902-623-37	Sequence 37, Appl	509	14	58.3	11	3	US-08-485-324-14	Sequence 14, Appl
437	14	58.3	10	2	US-08-902-623-40	Sequence 40, Appl	510	14	58.3	11	3	US-09-151-011-9	Sequence 9, Appli
438	14	58.3	10	2	US-08-902-623-72	Sequence 72, Appl	511	14	58.3	11	3	US-08-447-506-14	Sequence 14, Appl
439	14	58.3	10	2	US-08-747-137-122	Sequence 122, App	512	14	58.3	11	3	US-08-235-437-14	Sequence 14, Appl
440	14	58.3	10	2	US-08-751-300-2	Sequence 2, Appli	513	14	58.3	11	3	US-09-035-686-35	Sequence 35, Appl
441	14	58.3	10	2	US-08-751-300-5	Sequence 5, Appli	514	14	58.3	11	3	US-08-447-515-14	Sequence 14, Appl
442	14	58.3	10	2	US-08-751-300-8	Sequence 8, Appli	515	14	58.3	11	3	US-09-181-083-10	Sequence 10, Appl
443	14	58.3	10	2	US-08-751-300-11	Sequence 11, Appl	516	14	58.3	11	3	US-09-224-785-5	Sequence 5, Appli
444	14	58.3	10	2	US-08-751-300-14	Sequence 14, Appl	517	14	58.3	11	3	US-09-186-958-5	Sequence 5, Appli
445	14	58.3	10	2	US-08-751-300-17	Sequence 17, Appl	518	14	58.3	11	3	US-09-186-958-6	Sequence 6, Appli
446	14	58.3	10	2	US-08-751-300-20	Sequence 20, Appl	519	14	58.3	11	3	US-09-186-958-8	Sequence 8, Appli
447	14	58.3	10	2	US-08-751-300-23	Sequence 23, Appl	520	14	58.3	11	3	US-09-186-958-9	Sequence 9, Appli
448	14	58.3	10	2	US-08-751-300-26	Sequence 26, Appl	521	14	58.3	11	3	US-09-669-271A-5	Sequence 5, Appli
449	14	58.3	10	2	US-08-751-300-29	Sequence 29, Appl	522	14	58.3	11	3	US-09-669-271A-6	Sequence 6, Appli
450	14	58.3	10	2	US-08-751-300-32	Sequence 32, Appl	523	14	58.3	11	3	US-09-669-271A-8	Sequence 8, Appli
451	14	58.3	10	2	US-08-751-300-35	Sequence 35, Appl	524	14	58.3	11	3	US-09-669-271A-9	Sequence 9, Appli
452	14	58.3	10	2	US-08-751-300-38	Sequence 38, Appl	525	14	58.3	11	3	US-09-343-623-9	Sequence 9, Appli
453	14	58.3	10	2	US-08-751-300-41	Sequence 41, Appl	526	14	58.3	11	4	US-09-081-975-21	Sequence 21, Appl
454	14	58.3	10	2	US-08-751-300-44	Sequence 44, Appl	527	14	58.3	11	4	US-09-461-325-504	Sequence 504, App
455	14	58.3	10	2	US-08-751-300-57	Sequence 57, Appl	528	14	58.3	11	4	US-09-881-276-5	Sequence 5, Appli
456	14	58.3	10	2	US-08-751-300-59	Sequence 59, Appl	529	14	58.3	11	4	US-09-881-276-6	Sequence 6, Appli
457	14	58.3	10	2	US-08-751-300-63	Sequence 63, Appl	530	14	58.3	11	4	US-09-881-276-8	Sequence 8, Appli
458	14	58.3	10	2	US-08-751-300-65	Sequence 65, Appl	531	14	58.3	11	4	US-09-881-276-9	Sequence 9, Appli
459	14	58.3	10	2	US-08-751-300-77	Sequence 77, Appl	532	14	58.3	11	4	US-09-756-594-5	Sequence 5, Appli
460	14	58.3	10	2	US-08-751-300-90	Sequence 90, Appl	533	14	58.3	11	4	US-09-069-827A-43	Sequence 43, Appl
461	14	58.3	10	2	US-08-751-300-91	Sequence 91, Appl	534	14	58.3	11	4	US-09-069-827A-44	Sequence 44, Appl
462	14	58.3	10	2	US-08-751-300-92	Sequence 92, Appl	535	14	58.3	11	4	US-09-069-827A-47	Sequence 47, Appl
463	14	58.3	10	2	US-08-751-300-93	Sequence 93, Appl	536	14	58.3	11	4	US-10-012-542-504	Sequence 504, App
464	14	58.3	10	2	US-08-751-300-94	Sequence 94, Appl	537	14	58.3	11	4	US-09-750-754-10	Sequence 10, Appl
465	14	58.3	10	2	US-08-751-300-95	Sequence 95, Appl	538	14	58.3	11	4	US-09-428-082B-325	Sequence 325, App

539	14	58.3	11	4	US-10-115-123-504	Sequence 504, App	Sequence 504, App	14	58.3	15	4	US-09-072-596-118	Sequence 118, App
540	14	58.3	12	1	US-08-487-568-113	Sequence 113, App	Sequence 113, App	14	58.3	15	4	US-08-634-332A-64	Sequence 64, Appl
541	14	58.3	12	3	US-09-188-579-45	Sequence 45, Appl	Sequence 45, Appl	14	58.3	15	4	US-09-441-992-50	Sequence 50, Appl
542	14	58.3	12	3	US-09-315-444-45	Sequence 45, Appl	Sequence 45, Appl	14	58.3	15	4	US-09-441-992-51	Sequence 51, Appl
543	14	58.3	12	3	US-09-186-958-13	Sequence 13, Appl	Sequence 13, Appl	14	58.3	15	4	US-09-574-749B-54	Sequence 54, Appl
544	14	58.3	12	3	US-09-669-271A-13	Sequence 13, Appl	Sequence 13, Appl	14	58.3	15	4	US-09-644-442-7	Sequence 7, Appl
545	14	58.3	12	4	US-09-721-362-45	Sequence 45, Appl	Sequence 45, Appl	14	58.3	15	4	US-09-072-967-57	Sequence 57, Appl
546	14	58.3	12	4	US-09-752-165-65	Sequence 65, Appl	Sequence 65, Appl	14	58.3	15	4	US-09-072-967-123	Sequence 123, App
547	14	58.3	12	4	US-09-881-276-13	Sequence 13, Appl	Sequence 13, Appl	14	58.3	15	4	US-09-428-082B-138	Sequence 138, App
548	14	58.3	12	4	US-09-716-129-87	Sequence 87, Appl	Sequence 87, Appl	14	58.3	15	4	US-09-689-097-53	Sequence 53, Appl
549	14	58.3	12	4	US-09-440-772C-28	Sequence 28, Appl	Sequence 28, Appl	14	58.3	15	5	PCT-US93-06751-28	Sequence 28, Appl
550	14	58.3	12	4	US-09-428-082B-135	Sequence 135, App	Sequence 135, App	14	58.3	15	5	PCT-US94-02465-51	Sequence 51, Appl
551	14	58.3	13	1	US-09-487-568-87	Sequence 87, App	Sequence 87, App	14	58.3	15	5	PCT-US94-10356-2	Sequence 2, Appl
552	14	58.3	13	1	US-08-487-568-87	Sequence 87, Appl	Sequence 87, Appl	14	58.3	15	5	PCT-US94-10356-3	Sequence 3, Appl
553	14	58.3	13	3	US-08-702-054B-35	Sequence 35, Appl	Sequence 35, Appl	14	58.3	15	5	PCT-US94-10356-6	Sequence 6, Appl
554	14	58.3	13	3	US-09-236-415-5	Sequence 5, Appl	Sequence 5, Appl	14	58.3	15	5	PCT-US94-10356-7	Sequence 7, Appl
555	14	58.3	13	4	US-09-081-975-9	Sequence 9, Appl	Sequence 9, Appl	14	58.3	15	5	PCT-US94-10356-20	Sequence 20, Appl
556	14	58.3	13	4	US-09-700-993-26	Sequence 26, Appl	Sequence 26, Appl	14	58.3	15	5	PCT-US94-10356-22	Sequence 22, Appl
557	14	58.3	13	5	PCT-US94-01234-47	Sequence 47, Appl	Sequence 47, Appl	14	58.3	15	5	PCT-US95-00498-51	Sequence 51, Appl
558	14	58.3	14	1	US-08-534-975-10	Sequence 10, Appl	Sequence 10, Appl	14	58.3	15	5	PCT-US95-00656-51	Sequence 51, Appl
559	14	58.3	14	2	US-08-449-933-11	Sequence 11, Appl	Sequence 11, Appl	14	58.3	16	1	US-07-959-946-5	Sequence 5, Appl
560	14	58.3	14	2	US-08-392-816-12	Sequence 12, Appl	Sequence 12, Appl	14	58.3	16	1	US-08-321-625-18	Sequence 18, Appl
561	14	58.3	14	2	US-08-954-470-10	Sequence 10, Appl	Sequence 10, Appl	14	58.3	16	1	US-08-321-625-20	Sequence 20, Appl
562	14	58.3	14	2	US-08-750-359-3	Sequence 3, Appl	Sequence 3, Appl	14	58.3	16	1	US-08-321-625-21	Sequence 21, Appl
563	14	58.3	14	2	US-08-750-359-4	Sequence 4, Appl	Sequence 4, Appl	14	58.3	16	1	US-08-321-625-22	Sequence 22, Appl
564	14	58.3	14	3	US-08-564-225-10	Sequence 10, Appl	Sequence 10, Appl	14	58.3	16	1	US-08-321-625-23	Sequence 23, Appl
565	14	58.3	14	3	US-09-129-855A-10	Sequence 10, Appl	Sequence 10, Appl	14	58.3	16	1	US-08-321-625-24	Sequence 24, Appl
566	14	58.3	14	3	US-09-247-154-10	Sequence 10, Appl	Sequence 10, Appl	14	58.3	16	1	US-08-321-625-25	Sequence 25, Appl
567	14	58.3	14	3	US-08-786-455B-4	Sequence 4, Appl	Sequence 4, Appl	14	58.3	16	1	US-08-321-625-53	Sequence 53, Appl
568	14	58.3	14	3	US-07-966-049A-11	Sequence 11, Appl	Sequence 11, Appl	14	58.3	16	1	US-08-321-625-63	Sequence 63, Appl
569	14	58.3	14	3	US-08-687-590-49	Sequence 49, Appl	Sequence 49, Appl	14	58.3	16	1	US-08-321-625-64	Sequence 64, Appl
570	14	58.3	14	4	US-09-480-718-10	Sequence 10, Appl	Sequence 10, Appl	14	58.3	16	1	US-08-321-625-65	Sequence 65, Appl
571	14	58.3	14	4	US-09-461-325-508	Sequence 508, App	Sequence 508, App	14	58.3	16	1	US-08-321-625-68	Sequence 68, Appl
572	14	58.3	14	4	US-09-129-855A-10	Sequence 10, Appl	Sequence 10, Appl	14	58.3	16	1	US-08-321-625-80	Sequence 80, Appl
573	14	58.3	14	4	US-09-610-833-10	Sequence 10, Appl	Sequence 10, Appl	14	58.3	16	1	US-08-077-797A-43	Sequence 43, Appl
574	14	58.3	14	4	US-10-012-542-508	Sequence 508, App	Sequence 508, App	14	58.3	16	1	US-08-473-344-51	Sequence 51, Appl
575	14	58.3	14	4	US-10-115-123-508	Sequence 508, App	Sequence 508, App	14	58.3	16	1	US-08-333-577-5	Sequence 5, Appl
576	14	58.3	15	1	US-08-311-611A-51	Sequence 51, Appl	Sequence 51, Appl	14	58.3	16	3	US-09-181-083-18	Sequence 18, Appl
577	14	58.3	15	1	US-08-372-783-51	Sequence 51, Appl	Sequence 51, Appl	14	58.3	16	3	US-09-181-083-20	Sequence 20, Appl
578	14	58.3	15	1	US-08-372-105-51	Sequence 51, Appl	Sequence 51, Appl	14	58.3	16	3	US-09-181-083-21	Sequence 21, Appl
579	14	58.3	15	1	US-08-148-160-2	Sequence 2, Appl	Sequence 2, Appl	14	58.3	16	3	US-09-181-083-22	Sequence 22, Appl
580	14	58.3	15	1	US-08-306-473A-51	Sequence 51, Appl	Sequence 51, Appl	14	58.3	16	3	US-09-181-083-23	Sequence 23, Appl
581	14	58.3	15	1	US-08-209-762-51	Sequence 51, Appl	Sequence 51, Appl	14	58.3	16	3	US-09-181-083-24	Sequence 24, Appl
582	14	58.3	15	1	US-08-625-691-10	Sequence 10, Appl	Sequence 10, Appl	14	58.3	16	3	US-09-181-083-25	Sequence 25, Appl
583	14	58.3	15	1	US-08-487-568-112	Sequence 112, App	Sequence 112, App	14	58.3	16	3	US-09-181-083-53	Sequence 53, Appl
584	14	58.3	15	2	US-08-621-803-9	Sequence 9, Appl	Sequence 9, Appl	14	58.3	16	3	US-09-181-083-63	Sequence 63, Appl
585	14	58.3	15	2	US-08-485-445A-51	Sequence 51, Appl	Sequence 51, Appl	14	58.3	16	3	US-09-181-083-64	Sequence 64, Appl
586	14	58.3	15	2	US-08-553-257A-50	Sequence 50, Appl	Sequence 50, Appl	14	58.3	16	3	US-09-181-083-65	Sequence 65, Appl
587	14	58.3	15	2	US-08-553-257A-51	Sequence 51, Appl	Sequence 51, Appl	14	58.3	16	3	US-09-181-083-68	Sequence 68, Appl
588	14	58.3	15	3	US-09-119-263-51	Sequence 51, Appl	Sequence 51, Appl	14	58.3	16	3	US-09-181-083-80	Sequence 80, Appl
589	14	58.3	15	3	US-08-657-162-51	Sequence 51, Appl	Sequence 51, Appl	14	58.3	16	3	US-09-093-539-51	Sequence 51, Appl
590	14	58.3	15	3	US-09-224-480-51	Sequence 51, Appl	Sequence 51, Appl	14	58.3	16	4	US-09-009-953-39	Sequence 39, Appl
591	14	58.3	15	3	US-09-217-352-9	Sequence 9, Appl	Sequence 9, Appl	14	58.3	16	4	US-09-009-953-230	Sequence 230, App
592	14	58.3	15	3	US-08-818-112-57	Sequence 57, Appl	Sequence 57, Appl	14	58.3	16	4	US-09-081-975-23	Sequence 23, Appl
593	14	58.3	15	3	US-08-818-112-123	Sequence 123, App	Sequence 123, App	14	58.3	16	4	US-09-790-230-51	Sequence 51, Appl
594	14	58.3	15	3	US-08-818-111-57	Sequence 57, Appl	Sequence 57, Appl	14	58.3	16	4	US-09-311-784A-308	Sequence 308, App
595	14	58.3	15	3	US-08-818-111-118	Sequence 118, App	Sequence 118, App	14	58.3	16	4	US-09-546-013-72	Sequence 72, Appl
596	14	58.3	15	3	US-09-056-556-57	Sequence 57, Appl	Sequence 57, Appl	14	58.3	16	4	US-09-750-754-18	Sequence 18, Appl
597	14	58.3	15	3	US-09-056-556-123	Sequence 123, App	Sequence 123, App	14	58.3	16	4	US-09-750-754-20	Sequence 20, Appl
598	14	58.3	15	3	US-09-063-733A-28	Sequence 28, Appl	Sequence 28, Appl	14	58.3	16	4	US-09-750-754-21	Sequence 21, Appl
599	14	58.3	15	4	US-09-009-953-247	Sequence 247, App	Sequence 247, App	14	58.3	16	4	US-09-750-754-22	Sequence 22, Appl
600	14	58.3	15	4	US-08-487-795A-2	Sequence 2, Appl	Sequence 2, Appl	14	58.3	16	4	US-09-750-754-23	Sequence 23, Appl
601	14	58.3	15	4	US-08-487-795A-3	Sequence 3, Appl	Sequence 3, Appl	14	58.3	16	4	US-09-750-754-24	Sequence 24, Appl
602	14	58.3	15	4	US-08-487-795A-16	Sequence 16, Appl	Sequence 16, Appl	14	58.3	16	4	US-09-750-754-25	Sequence 25, Appl
603	14	58.3	15	4	US-08-487-795A-17	Sequence 17, Appl	Sequence 17, Appl	14	58.3	16	4	US-09-750-754-53	Sequence 53, Appl
604	14	58.3	15	4	US-08-487-795A-19	Sequence 19, Appl	Sequence 19, Appl	14	58.3	16	4	US-09-750-754-63	Sequence 63, Appl
605	14	58.3	15	4	US-08-121-105B-3	Sequence 3, Appl	Sequence 3, Appl	14	58.3	16	4	US-09-750-754-64	Sequence 64, Appl
606	14	58.3	15	4	US-08-121-105B-13	Sequence 13, Appl	Sequence 13, Appl	14	58.3	16	4	US-09-750-754-65	Sequence 65, Appl
607	14	58.3	15	4	US-08-121-105B-16	Sequence 16, Appl	Sequence 16, Appl	14	58.3	16	4	US-09-750-754-68	Sequence 68, Appl
608	14	58.3	15	4	US-08-121-105B-17	Sequence 17, Appl	Sequence 17, Appl	14	58.3	16	4	US-09-750-754-80	Sequence 80, Appl
609	14	58.3	15	4	US-08-121-105B-19	Sequence 19, Appl	Sequence 19, Appl	14	58.3	16	4	US-09-854-133-587	Sequence 587, App
610	14	58.3	15	4	US-09-081-975-24	Sequence 24, Appl	Sequence 24, Appl	14	58.3	16	4	US-09-541-345-4	Sequence 4, Appl
611	14	58.3	15	4	US-09-072-596-57	Sequence 57, Appl	Sequence 57, Appl	14	58.3	16	4	US-09-541-345-20	Sequence 20, Appl



685	14	58.3	16	4	US-09-541-345-35	Sequence 35, Appl	758	14	58.3	17	4	US-09-350-641C-814	Sequence 814, App
686	14	58.3	16	4	US-09-541-345-37	Sequence 37, Appl	759	14	58.3	17	4	US-09-428-082B-209	Sequence 209, App
687	14	58.3	16	4	US-09-541-345-38	Sequence 38, Appl	760	14	58.3	17	4	US-08-077-255A-123	Sequence 123, App
688	14	58.3	16	4	US-09-541-345-39	Sequence 39, Appl	761	14	58.3	17	4	US-09-490-070A-222	Sequence 222, App
689	14	58.3	16	4	US-09-541-345-40	Sequence 40, Appl	762	14	58.3	17	4	US-09-490-070A-228	Sequence 228, App
690	14	58.3	16	4	US-09-541-345-41	Sequence 41, Appl	763	14	58.3	17	4	US-09-490-070A-254	Sequence 254, App
691	14	58.3	16	4	US-09-541-345-42	Sequence 42, Appl	764	14	58.3	17	4	US-09-490-070A-262	Sequence 262, App
692	14	58.3	16	4	US-09-541-345-43	Sequence 43, Appl	765	14	58.3	17	4	US-09-490-153-222	Sequence 222, App
693	14	58.3	16	4	US-09-541-345-44	Sequence 44, Appl	766	14	58.3	17	4	US-09-490-153-228	Sequence 228, App
694	14	58.3	16	4	US-09-541-345-45	Sequence 45, Appl	767	14	58.3	17	4	US-09-490-153-254	Sequence 254, App
695	14	58.3	16	4	US-09-541-345-46	Sequence 46, Appl	768	14	58.3	17	4	US-09-490-153-262	Sequence 262, App
696	14	58.3	16	4	US-09-541-345-47	Sequence 47, Appl	769	14	58.3	17	4	US-09-350-841A-814	Sequence 814, App
697	14	58.3	16	4	US-09-541-345-48	Sequence 48, Appl	770	14	58.3	17	4	US-09-695-437A-40	Sequence 40, Appl
698	14	58.3	16	4	US-09-541-345-50	Sequence 50, Appl	771	14	58.3	17	4	US-09-490-324-222	Sequence 222, App
699	14	58.3	16	4	US-09-541-345-51	Sequence 51, Appl	772	14	58.3	17	4	US-09-490-324-228	Sequence 228, App
700	14	58.3	16	4	US-09-541-345-52	Sequence 52, Appl	773	14	58.3	17	4	US-09-490-324-254	Sequence 254, App
701	14	58.3	16	4	US-09-541-345-53	Sequence 53, Appl	774	14	58.3	17	4	US-09-490-324-262	Sequence 262, App
702	14	58.3	16	4	US-09-541-345-55	Sequence 55, Appl	775	14	58.3	17	5	PCT-US93-07545-123	Sequence 123, App
703	14	58.3	16	4	US-09-541-345-57	Sequence 57, Appl	776	14	58.3	17	5	PCT-US94-05684-7	Sequence 7, Appl
704	14	58.3	16	4	US-09-541-345-58	Sequence 58, Appl	777	14	58.3	17	5	PCT-US94-10356-19	Sequence 19, Appl
705	14	58.3	16	4	US-09-541-345-59	Sequence 59, Appl	778	14	58.3	17	5	PCT-US94-10356-21	Sequence 21, Appl
706	14	58.3	16	4	US-09-541-345-61	Sequence 61, Appl	779	14	58.3	18	1	US-08-218-025A-3	Sequence 3, Appl
707	14	58.3	16	4	US-09-541-345-62	Sequence 62, Appl	780	14	58.3	18	1	US-08-375-100-3	Sequence 3, Appl
708	14	58.3	16	4	US-09-541-345-63	Sequence 63, Appl	781	14	58.3	18	2	US-08-448-603A-24	Sequence 24, Appl
709	14	58.3	16	4	US-09-541-345-64	Sequence 64, Appl	782	14	58.3	18	2	US-08-484-905-36	Sequence 36, Appl
710	14	58.3	16	4	US-09-541-345-66	Sequence 66, Appl	783	14	58.3	18	3	US-08-940-095-199	Sequence 199, App
711	14	58.3	16	4	US-09-541-345-69	Sequence 69, Appl	784	14	58.3	18	3	US-08-940-095-224	Sequence 224, App
712	14	58.3	16	4	US-09-541-345-71	Sequence 71, Appl	785	14	58.3	18	3	US-08-481-985B-36	Sequence 36, Appl
713	14	58.3	16	4	US-09-541-345-73	Sequence 73, Appl	786	14	58.3	18	3	US-08-940-093-199	Sequence 199, App
714	14	58.3	16	4	US-09-541-345-74	Sequence 74, Appl	787	14	58.3	18	3	US-08-940-093-224	Sequence 224, App
715	14	58.3	16	4	US-09-541-345-75	Sequence 75, Appl	788	14	58.3	18	3	US-09-134-075-24	Sequence 24, Appl
716	14	58.3	16	4	US-09-541-345-76	Sequence 76, Appl	789	14	58.3	18	3	US-08-940-096-199	Sequence 199, App
717	14	58.3	16	4	US-09-541-345-77	Sequence 77, Appl	790	14	58.3	18	3	US-08-940-096-224	Sequence 224, App
718	14	58.3	16	4	US-09-541-345-79	Sequence 79, Appl	791	14	58.3	18	3	US-08-370-476-36	Sequence 36, Appl
719	14	58.3	16	4	US-09-541-345-81	Sequence 81, Appl	792	14	58.3	18	3	US-09-082-279B-1147	Sequence 1147, Ap
720	14	58.3	16	4	US-09-541-345-83	Sequence 83, Appl	793	14	58.3	18	3	US-09-465-719-199	Sequence 199, App
721	14	58.3	16	4	US-09-541-345-84	Sequence 84, Appl	794	14	58.3	18	3	US-09-465-719-224	Sequence 224, App
722	14	58.3	16	4	US-09-541-345-85	Sequence 85, Appl	795	14	58.3	18	3	US-09-453-605-199	Sequence 199, App
723	14	58.3	16	4	US-09-541-345-86	Sequence 86, Appl	796	14	58.3	18	3	US-09-453-605-224	Sequence 224, App
724	14	58.3	16	4	US-09-541-345-89	Sequence 89, Appl	797	14	58.3	18	3	US-09-492-739-24	Sequence 24, Appl
725	14	58.3	16	4	US-09-541-345-91	Sequence 91, Appl	798	14	58.3	18	3	US-08-992-877-16	Sequence 16, Appl
726	14	58.3	16	4	US-09-541-345-92	Sequence 92, Appl	799	14	58.3	18	3	US-09-315-304B-1147	Sequence 1147, Ap
727	14	58.3	16	4	US-09-541-345-96	Sequence 96, Appl	800	14	58.3	18	3	US-09-453-838-199	Sequence 199, App
728	14	58.3	16	4	US-09-541-345-98	Sequence 98, Appl	801	14	58.3	18	3	US-09-453-838-224	Sequence 224, App
729	14	58.3	16	4	US-09-541-345-99	Sequence 99, Appl	802	14	58.3	18	4	US-09-081-975-22	Sequence 22, Appl
730	14	58.3	16	4	US-09-541-345-106	Sequence 106, App	803	14	58.3	18	4	US-08-940-136-199	Sequence 199, App
731	14	58.3	16	5	PCT-US92-08634-5	Sequence 5, Appl	804	14	58.3	18	4	US-08-940-136-224	Sequence 224, App
732	14	58.3	16	5	PCT-US92-01238-43	Sequence 43, Appl	805	14	58.3	18	4	US-08-634-332A-12	Sequence 12, Appl
733	14	58.3	17	1	US-08-321-625-35	Sequence 35, Appl	806	14	58.3	18	4	US-08-634-332A-13	Sequence 13, Appl
734	14	58.3	17	1	US-08-370-567-7	Sequence 7, Appl	807	14	58.3	18	4	US-09-834-784-1147	Sequence 1147, Ap
735	14	58.3	17	1	US-08-438-759-7	Sequence 7, Appl	808	14	58.3	18	4	US-09-453-841-199	Sequence 199, App
736	14	58.3	17	2	US-08-480-190-123	Sequence 123, App	809	14	58.3	18	4	US-09-453-841-224	Sequence 224, App
737	14	58.3	17	2	US-08-488-379-123	Sequence 123, App	810	14	58.3	18	4	US-10-158-847-78	Sequence 78, Appl
738	14	58.3	17	3	US-09-181-083-35	Sequence 35, Appl	811	14	58.3	18	4	US-09-453-833-199	Sequence 199, App
739	14	58.3	17	3	US-08-990-823-88	Sequence 88, Appl	812	14	58.3	18	4	US-09-453-833-224	Sequence 224, App
740	14	58.3	17	3	US-08-990-823-89	Sequence 89, Appl	813	14	58.3	18	4	US-09-515-965A-1147	Sequence 1147, Ap
741	14	58.3	17	3	US-09-082-279B-814	Sequence 814, App	814	14	58.3	18	4	US-09-453-826-199	Sequence 199, App
742	14	58.3	17	3	US-09-025-769B-222	Sequence 222, App	815	14	58.3	18	4	US-09-453-826-224	Sequence 224, App
743	14	58.3	17	3	US-09-025-769B-228	Sequence 228, App	816	14	58.3	18	4	US-09-385-328-90	Sequence 90, Appl
744	14	58.3	17	3	US-09-025-769B-254	Sequence 254, App	817	14	58.3	18	4	US-09-350-641C-1147	Sequence 1147, Ap
745	14	58.3	17	3	US-09-025-769B-262	Sequence 262, App	818	14	58.3	18	4	US-09-620-091-195	Sequence 195, App
746	14	58.3	17	3	US-09-315-304B-814	Sequence 814, App	819	14	58.3	18	4	US-09-453-840-199	Sequence 199, App
747	14	58.3	17	4	US-08-487-795A-15	Sequence 15, Appl	820	14	58.3	18	4	US-09-453-840-224	Sequence 224, App
748	14	58.3	17	4	US-08-487-795A-18	Sequence 18, Appl	821	14	58.3	18	4	US-09-865-989-199	Sequence 199, App
749	14	58.3	17	4	US-08-121-105B-15	Sequence 15, Appl	822	14	58.3	18	4	US-09-865-989-224	Sequence 224, App
750	14	58.3	17	4	US-08-121-105B-18	Sequence 18, Appl	823	14	58.3	18	4	US-09-350-841A-1147	Sequence 1147, Ap
751	14	58.3	17	4	US-08-475-399A-123	Sequence 123, App	824	14	58.3	18	4	US-09-453-834-199	Sequence 199, App
752	14	58.3	17	4	US-09-205-258-363	Sequence 363, App	825	14	58.3	18	4	US-09-453-834-224	Sequence 224, App
753	14	58.3	17	4	US-09-834-784-814	Sequence 814, App	826	14	58.3	18	4	US-09-966-931A-24	Sequence 24, Appl
754	14	58.3	17	4	US-09-477-135A-88	Sequence 88, Appl	827	14	58.3	19	4	US-09-461-325-298	Sequence 298, App
755	14	58.3	17	4	US-09-477-135A-89	Sequence 89, Appl	828	14	58.3	19	4	US-09-489-847-359	Sequence 359, App
756	14	58.3	17	4	US-09-515-965A-814	Sequence 814, App	829	14	58.3	19	4	US-09-489-847-360	Sequence 360, App
757	14	58.3	17	4	US-09-750-754-35	Sequence 35, Appl	830	14	58.3	19	4	US-10-012-542-298	Sequence 298, App



831	14	58.3	19	4	US-10-080-505-51	Sequence 51, Appl	904	14	58.3	20	3	US-09-119-263-54	Sequence 54, Appl
832	14	58.3	19	4	US-09-620-091-382	Sequence 382, App	905	14	58.3	20	3	US-09-119-263-57	Sequence 57, Appl
833	14	58.3	19	4	US-10-115-123-298	Sequence 298, App	906	14	58.3	20	3	US-09-119-263-58	Sequence 58, Appl
834	14	58.3	19	4	US-09-700-993-34	Sequence 34, Appl	907	14	58.3	20	3	US-09-119-263-59	Sequence 59, Appl
835	14	58.3	20	1	US-08-311-611A-54	Sequence 54, Appl	908	14	58.3	20	3	US-09-119-263-101	Sequence 101, App
836	14	58.3	20	1	US-08-311-611A-57	Sequence 57, Appl	909	14	58.3	20	3	US-09-119-263-150	Sequence 150, App
837	14	58.3	20	1	US-08-311-611A-58	Sequence 58, Appl	910	14	58.3	20	3	US-09-119-263-151	Sequence 151, App
838	14	58.3	20	1	US-08-311-611A-59	Sequence 59, Appl	911	14	58.3	20	3	US-09-119-263-152	Sequence 152, App
839	14	58.3	20	1	US-08-311-611A-101	Sequence 101, App	912	14	58.3	20	3	US-09-119-263-159	Sequence 159, App
840	14	58.3	20	1	US-08-311-611A-150	Sequence 150, App	913	14	58.3	20	3	US-09-119-263-160	Sequence 160, App
841	14	58.3	20	1	US-08-311-611A-151	Sequence 151, App	914	14	58.3	20	3	US-08-658-136-25	Sequence 25, Appl
842	14	58.3	20	1	US-08-311-611A-152	Sequence 152, App	915	14	58.3	20	3	US-08-658-136-27	Sequence 27, Appl
843	14	58.3	20	1	US-08-311-611A-159	Sequence 159, App	916	14	58.3	20	3	US-08-657-162-54	Sequence 54, Appl
844	14	58.3	20	1	US-08-311-611A-160	Sequence 160, App	917	14	58.3	20	3	US-08-657-162-57	Sequence 57, Appl
845	14	58.3	20	1	US-08-372-783-54	Sequence 54, Appl	918	14	58.3	20	3	US-08-657-162-58	Sequence 58, Appl
846	14	58.3	20	1	US-08-372-783-57	Sequence 57, Appl	919	14	58.3	20	3	US-08-657-162-59	Sequence 59, Appl
847	14	58.3	20	1	US-08-372-783-58	Sequence 58, Appl	920	14	58.3	20	3	US-08-657-162-101	Sequence 101, App
848	14	58.3	20	1	US-08-372-783-59	Sequence 59, Appl	921	14	58.3	20	3	US-08-657-162-150	Sequence 150, App
849	14	58.3	20	1	US-08-372-783-101	Sequence 101, App	922	14	58.3	20	3	US-08-657-162-151	Sequence 151, App
850	14	58.3	20	1	US-08-372-783-150	Sequence 150, App	923	14	58.3	20	3	US-08-657-162-152	Sequence 152, App
851	14	58.3	20	1	US-08-372-783-151	Sequence 151, App	924	14	58.3	20	3	US-08-657-162-159	Sequence 159, App
852	14	58.3	20	1	US-08-372-783-152	Sequence 152, App	925	14	58.3	20	3	US-08-657-162-159	Sequence 159, App
853	14	58.3	20	1	US-08-372-783-159	Sequence 159, App	926	14	58.3	20	3	US-08-657-162-160	Sequence 160, App
854	14	58.3	20	1	US-08-372-783-160	Sequence 160, App	927	14	58.3	20	3	US-08-612-973-76	Sequence 76, Appl
855	14	58.3	20	1	US-08-372-105-54	Sequence 54, Appl	928	14	58.3	20	3	US-08-612-973-77	Sequence 77, Appl
856	14	58.3	20	1	US-08-372-105-57	Sequence 57, Appl	929	14	58.3	20	3	US-08-612-973-83	Sequence 83, Appl
857	14	58.3	20	1	US-08-372-105-58	Sequence 58, Appl	930	14	58.3	20	3	US-09-224-480-54	Sequence 54, Appl
858	14	58.3	20	1	US-08-372-105-59	Sequence 59, Appl	931	14	58.3	20	3	US-09-224-480-57	Sequence 57, Appl
859	14	58.3	20	1	US-08-372-105-101	Sequence 101, App	932	14	58.3	20	3	US-09-224-480-58	Sequence 58, Appl
860	14	58.3	20	1	US-08-372-105-150	Sequence 150, App	933	14	58.3	20	3	US-09-224-480-59	Sequence 59, Appl
861	14	58.3	20	1	US-08-372-105-151	Sequence 151, App	934	14	58.3	20	3	US-09-224-480-101	Sequence 101, App
862	14	58.3	20	1	US-08-372-105-152	Sequence 152, App	935	14	58.3	20	3	US-09-224-480-150	Sequence 150, App
863	14	58.3	20	1	US-08-372-105-159	Sequence 159, App	936	14	58.3	20	3	US-09-224-480-151	Sequence 151, App
864	14	58.3	20	1	US-08-372-105-160	Sequence 160, App	937	14	58.3	20	3	US-09-224-480-152	Sequence 152, App
865	14	58.3	20	1	US-08-321-625-36	Sequence 36, Appl	938	14	58.3	20	3	US-09-224-480-159	Sequence 159, App
866	14	58.3	20	1	US-08-321-625-50	Sequence 50, Appl	939	14	58.3	20	3	US-09-224-480-160	Sequence 160, App
867	14	58.3	20	1	US-08-306-473A-54	Sequence 54, Appl	940	14	58.3	20	3	US-09-181-083-36	Sequence 36, Appl
868	14	58.3	20	1	US-08-306-473A-57	Sequence 57, Appl	941	14	58.3	20	3	US-09-181-083-50	Sequence 50, Appl
869	14	58.3	20	1	US-08-306-473A-58	Sequence 58, Appl	942	14	58.3	20	3	US-09-093-539-54	Sequence 54, Appl
870	14	58.3	20	1	US-08-306-473A-59	Sequence 59, Appl	943	14	58.3	20	3	US-08-927-597-76	Sequence 76, Appl
871	14	58.3	20	1	US-08-306-473A-101	Sequence 101, App	944	14	58.3	20	3	US-08-927-597-77	Sequence 77, Appl
872	14	58.3	20	1	US-08-306-473A-150	Sequence 150, App	945	14	58.3	20	3	US-08-927-597-83	Sequence 83, Appl
873	14	58.3	20	1	US-08-306-473A-151	Sequence 151, App	946	14	58.3	20	3	US-09-400-208B-1	Sequence 1, Appli
874	14	58.3	20	1	US-08-306-473A-152	Sequence 152, App	947	14	58.3	20	3	US-09-217-352-7	Sequence 7, Appli
875	14	58.3	20	1	US-08-306-473A-159	Sequence 159, App	948	14	58.3	20	3	US-09-217-352-47	Sequence 47, Appl
876	14	58.3	20	1	US-08-306-473A-160	Sequence 160, App	949	14	58.3	20	3	US-09-217-352-48	Sequence 48, Appl
877	14	58.3	20	1	US-08-209-762-54	Sequence 54, Appl	950	14	58.3	20	3	US-09-217-352-49	Sequence 49, Appl
878	14	58.3	20	1	US-08-209-762-57	Sequence 57, Appl	951	14	58.3	20	3	US-09-217-352-120	Sequence 120, App
879	14	58.3	20	1	US-08-209-762-58	Sequence 58, Appl	952	14	58.3	20	3	US-09-217-352-148	Sequence 148, App
880	14	58.3	20	1	US-08-209-762-59	Sequence 59, Appl	953	14	58.3	20	3	US-08-860-656B-12	Sequence 12, Appl
881	14	58.3	20	1	US-08-473-344-54	Sequence 54, Appl	954	14	58.3	20	3	US-08-525-539A-71	Sequence 71, Appl
882	14	58.3	20	2	US-08-493-235-33	Sequence 33, Appl	955	14	58.3	20	3	US-09-011-922A-7	Sequence 7, Appli
883	14	58.3	20	2	US-08-621-803-7	Sequence 7, Appli	956	14	58.3	20	4	US-09-201-945-294	Sequence 294, App
884	14	58.3	20	2	US-08-621-803-47	Sequence 47, Appl	957	14	58.3	20	4	US-09-155-613A-6	Sequence 6, Appli
885	14	58.3	20	2	US-08-621-803-48	Sequence 48, Appl	958	14	58.3	20	4	US-08-487-795A-13	Sequence 13, Appl
886	14	58.3	20	2	US-08-621-803-49	Sequence 49, Appl	959	14	58.3	20	4	US-08-121-105B-13	Sequence 13, Appl
887	14	58.3	20	2	US-08-621-803-120	Sequence 120, App	960	14	58.3	20	4	US-09-081-975-18	Sequence 18, Appl
888	14	58.3	20	2	US-08-485-445A-54	Sequence 54, Appl	961	14	58.3	20	4	US-09-790-230-54	Sequence 54, Appl
889	14	58.3	20	2	US-08-485-445A-57	Sequence 57, Appl	962	14	58.3	20	4	US-08-635-886C-32	Sequence 32, Appl
890	14	58.3	20	2	US-08-485-445A-58	Sequence 58, Appl	963	14	58.3	20	4	US-08-635-886C-33	Sequence 33, Appl
891	14	58.3	20	2	US-08-485-445A-59	Sequence 59, Appl	964	14	58.3	20	4	US-08-635-886C-39	Sequence 39, Appl
892	14	58.3	20	2	US-08-485-445A-101	Sequence 101, App	965	14	58.3	20	4	US-09-889-136-7	Sequence 7, Appli
893	14	58.3	20	2	US-08-485-445A-150	Sequence 150, App	966	14	58.3	20	4	US-08-974-690C-32	Sequence 32, Appl
894	14	58.3	20	2	US-08-485-445A-151	Sequence 151, App	967	14	58.3	20	4	US-08-974-690C-33	Sequence 33, Appl
895	14	58.3	20	2	US-08-485-445A-152	Sequence 152, App	968	14	58.3	20	4	US-08-974-690C-39	Sequence 39, Appl
896	14	58.3	20	2	US-08-485-445A-159	Sequence 159, App	969	14	58.3	20	4	US-09-750-754-36	Sequence 36, Appl
897	14	58.3	20	2	US-08-485-445A-160	Sequence 160, App	970	14	58.3	20	4	US-09-750-754-50	Sequence 50, Appl
898	14	58.3	20	2	US-08-714-677-17	Sequence 17, Appl	971	14	58.3	20	4	US-09-498-134A-3	Sequence 3, Appli
899	14	58.3	20	2	US-08-393-540-17	Sequence 17, Appl	972	14	58.3	20	4	US-09-664-945-23	Sequence 23, Appl
900	14	58.3	20	2	US-08-714-537-17	Sequence 17, Appl	973	14	58.3	20	4	US-09-689-097-56	Sequence 56, Appl
901	14	58.3	20	2	US-08-637-759B-294	Sequence 17, Appl	974	14	58.3	20	4	US-09-689-097-59	Sequence 59, Appl
902	14	58.3	20	2	US-08-637-759B-294	Sequence 294, App	975	14	58.3	20	4	US-09-689-097-61	Sequence 61, Appl
903	14	58.3	20	3	US-08-871-355A-294	Sequence 294, App	976	14	58.3	20	4	US-09-689-097-100	Sequence 100, App

977 14 58.3 20 4 US-09-689-097-147 Sequence 147, App  
978 14 58.3 20 4 US-09-689-097-148 Sequence 148, App  
979 14 58.3 20 4 US-09-689-097-149 Sequence 149, App  
980 14 58.3 20 4 US-09-689-097-156 Sequence 156, App  
981 14 58.3 20 4 US-09-689-097-157 Sequence 157, App  
982 14 58.3 20 4 US-08-974-685-32 Sequence 32, Appl  
983 14 58.3 20 4 US-08-974-685-33 Sequence 33, Appl  
984 14 58.3 20 4 US-08-974-685-39 Sequence 39, Appl  
985 14 58.3 20 4 US-09-674-973A-459 Sequence 459, App  
986 14 58.3 20 4 US-09-400-122A-1 Sequence 1, Appli  
987 14 58.3 20 4 US-09-695-437A-45 Sequence 45, Appl  
988 14 58.3 20 4 US-09-171-432A-61 Sequence 61, Appl  
989 14 58.3 20 5 PCT-US94-02465-54 Sequence 54, Appl  
990 14 58.3 20 5 PCT-US94-02465-57 Sequence 57, Appl  
991 14 58.3 20 5 PCT-US94-02465-58 Sequence 58, Appl  
992 14 58.3 20 5 PCT-US94-02465-59 Sequence 59, Appl  
993 14 58.3 20 5 PCT-US94-10356-17 Sequence 17, Appl  
994 14 58.3 20 5 PCT-US95-00498-54 Sequence 54, Appl  
995 14 58.3 20 5 PCT-US95-00498-57 Sequence 57, Appl  
996 14 58.3 20 5 PCT-US95-00498-58 Sequence 58, Appl  
997 14 58.3 20 5 PCT-US95-00498-59 Sequence 59, Appl  
998 14 58.3 20 5 PCT-US95-00498-101 Sequence 101, App  
999 14 58.3 20 5 PCT-US95-00498-150 Sequence 150, App  
1000 14 58.3 20 5 PCT-US95-00498-151 Sequence 151, App

ALIGNMENTS

RESULT 1  
US-09-085-072-7  
; Sequence 7, Application US/09085072  
; Patent No. 6265150  
; GENERAL INFORMATION:  
; APPLICANT: L. Terstappen et al.  
; TITLE OF INVENTION: PHAGE ANTIBODIES  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hoffmann & Baron, LLP  
; STREET: 350 Jericho Turnpike  
; CITY: Jericho  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 11753  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/085,072  
; FILING DATE: 26-MAY-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Feit, Irving N.  
; REGISTRATION NUMBER: 28,601  
; REFERENCE/DOCKET NUMBER: 890-2 FWC/CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 822-3550  
; TELEFAX: (516) 822-3582  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-085-072-7

Query Match 70.8%; Score 17; DB 3; Length 13;  
Best Local Similarity 40.0%; Pred. No. 1.9e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Sequence 147, App  
Sequence 148, App  
Sequence 149, App  
Sequence 156, App  
Sequence 157, App  
Sequence 32, Appl  
Sequence 33, Appl  
Sequence 39, Appl  
Sequence 459, App  
Sequence 1, Appli  
Sequence 45, Appl  
Sequence 61, Appl  
Sequence 54, Appl  
Sequence 57, Appl  
Sequence 58, Appl  
Sequence 59, Appl  
Sequence 17, Appl  
Sequence 54, Appl  
Sequence 57, Appl  
Sequence 58, Appl  
Sequence 59, Appl  
Sequence 101, App  
Sequence 150, App  
Sequence 151, App

QY 2 FXXXW 6  
Db 6 FASSW 10

RESULT 2

US-09-142-524D-87  
; Sequence 87, Application US/09142524D  
; Patent No. 6719976  
; GENERAL INFORMATION:  
; APPLICANT: Sone, Toshio  
; APPLICANT: Kume, Akinori  
; APPLICANT: Dairiki, Kazuo  
; APPLICANT: Iwama, Akiko  
; APPLICANT: Kino, Kohsuke  
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease  
; FILE REFERENCE: SPO-103  
; CURRENT APPLICATION NUMBER: US/09/142,524D  
; CURRENT FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: PCT/JP97/00740  
; PRIOR FILING DATE: 1997-03-10  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 87  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Cryptomeria japonica  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(15)  
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 4  
US-09-142-524D-87

Query Match 70.8%; Score 17; DB 4; Length 15;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
Db 9 FSTAW 13

RESULT 3

US-09-142-524D-88  
; Sequence 88, Application US/09142524D  
; Patent No. 6719976  
; GENERAL INFORMATION:  
; APPLICANT: Sone, Toshio  
; APPLICANT: Kume, Akinori  
; APPLICANT: Dairiki, Kazuo  
; APPLICANT: Iwama, Akiko  
; APPLICANT: Kino, Kohsuke  
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease  
; FILE REFERENCE: SPO-103  
; CURRENT APPLICATION NUMBER: US/09/142,524D  
; CURRENT FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: PCT/JP97/00740  
; PRIOR FILING DATE: 1997-03-10  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 88  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Cryptomeria japonica  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(15)  
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 5  
US-09-142-524D-88

Query Match 70.8%; Score 17; DB 4; Length 15;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
|  
Db 4 FSTW 8

RESULT 4

US-07-920-519-10  
; Sequence 10, Application US/07920519  
; Patent No. 5382518  
; GENERAL INFORMATION:  
; APPLICANT: CAPUT, DANIEL  
; APPLICANT: FERRARA, PASCUAL  
; APPLICANT: GUILLEMOT, JEAN-CLAUDE  
; APPLICANT: KAGHAD, MOURAD  
; APPLICANT: LEGOUX, RICHARD  
; APPLICANT: LOISON, GERARD  
; APPLICANT: LARBRE, ELIZABETH  
; APPLICANT: LUPKER, JOHANNES  
; APPLICANT: LEPLATOIS, PASCUAL  
; APPLICANT: SALOME, MARK  
; TITLE OF INVENTION: URATE OXIDASE ACTIVITY PROTEIN,  
; RECOMBINANT GENE CODING THEREFOR, EXPRESSION VECTOR,  
; TITLE OF INVENTION: MICRO-ORGANISMS AND TRANSFORMED CELLS  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/07920,519  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/659,408  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 16781/276 BEDL  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; IMMEDIATE SOURCE:  
; CLONE: Hydrolysis product T 23  
US-07-920-519-10

Query Match 66.7%; Score 16; DB 1; Length 6;  
Best Local Similarity 40.0%; Pred. No. 4.1e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
|  
Db 1 FSTW 8

RESULT 5

US-08-086-410-7  
; Sequence 7, Application US/08086410  
; Patent No. 5407822  
; GENERAL INFORMATION:  
; APPLICANT: LEPLATOIS, Pascal  
; APPLICANT: LOISON, Gerard  
; APPLICANT: PESSEGUE, Bernard  
; APPLICANT: SHIRE, David  
; TITLE OF INVENTION: Artificial promoter for the expression  
; of proteins in yeast  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY & LARDNER  
; STREET: King Street Station, Suite 500, 1800 Diagonal  
; STREET: Road, PO Box 299  
; CITY: ALEXANDRIA  
; STATE: VIRGINIA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/086,410  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/768,083  
; FILING DATE: 02-OCT-1991  
; APPLICATION NUMBER: FR 89 17467  
; FILING DATE: 29-DEC-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAXE, Bernhard D  
; REGISTRATION NUMBER: 28,665  
; REFERENCE/DOCKET NUMBER: 16781/318  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-9300  
; TELEFAX: (703) 683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; CLONE: hydrolysis product T23  
US-08-086-410-7

Query Match 66.7%; Score 16; DB 1; Length 6;  
Best Local Similarity 40.0%; Pred. No. 4.1e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
|  
Db 1 FSTW 8

RESULT 6

US-08-314-586-10  
; Sequence 10, Application US/08314586  
; Patent No. 5541098  
; GENERAL INFORMATION:  
; APPLICANT: CAPUT, DANIEL  
; APPLICANT: FERRARA, PASCUAL  
; APPLICANT: GUILLEMOT, JEAN-CLAUDE  
; APPLICANT: KAGHAD, MOURAD  
; APPLICANT: LEGOUX, RICHARD  
; APPLICANT: LOISON, GERARD  
; APPLICANT: LARBRE, ELIZABETH

```
; APPLICANT: LUPKER, JOHANNES
; APPLICANT: LEPLATOIS, PASCUAL
; APPLICANT: SALOME, MARK
; APPLICANT: LAURENT, PATRICK
; TITLE OF INVENTION: URATE OXIDASE ACTIVITY PROTEIN,
; TITLE OF INVENTION: RECOMBINANT GENE CODING THEREFOR, EXPRESSION VECTOR,
; TITLE OF INVENTION: MICROORGANISMS AND TRANSFORMED CELLS
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/314,586
; FILING DATE: 28-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/659,408
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16781/509/BEDL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; IMMEDIATE SOURCE:
; CLONE: Hydrolysis product T 23
;
US-08-314-586-10

Query Match 66.7%; Score 16; DB 1; Length 6;
Best Local Similarity 40.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
| |
Db 1 FDATW 5

RESULT 7
US-09-774-639-284
; Sequence 284, Application US/09774639
; Patent No. 6806351
; GENERAL INFORMATION:
; APPLICANT: Roben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: PZ013P1
; CURRENT APPLICATION NUMBER: US/09/774,639
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 284
; LENGTH: 7
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-774-639-284

Query Match 66.7%; Score 16; DB 4; Length 7;
Best Local Similarity 40.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
| |
Db 2 FGTSW 6

RESULT 8
US-09-702-114A-28
; Sequence 28, Application US/09702114A
; Patent No. 6566078
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Aya Jakobovits
; APPLICANT: Mary Paris
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Steve Chappell Mitchell
; TITLE OF INVENTION: 36P6D5; SECRETED TUMOR ANTIGEN
; FILE REFERENCE: 129.22-US-U1
; CURRENT APPLICATION NUMBER: US/09/702,114A
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/162,417
; PRIOR FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-702-114A-28

Query Match 66.7%; Score 16; DB 4; Length 9;
Best Local Similarity 40.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
| |
Db 4 FRSSW 8

RESULT 9
US-08-208-886C-87
; Sequence 87, Application US/08208886C
; Patent No. 5597710
; GENERAL INFORMATION:
; APPLICANT: Dalie, Barbara
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Tindall, Stephen
; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,886C
; FILING DATE: March 10, 1994
; CLASSIFICATION: 424
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: JB0429
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908 298 2987
; TELEFAX: 908 298 5388
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-208-886C-87

Query Match 66.7%; Score 16; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
Db 4 FSSYW 8

RESULT 10
US-08-704-744-89
; Sequence 89, Application US/08704744
; Patent No. 5705154
; GENERAL INFORMATION:
; APPLICANT: Dalie, Barbara
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Tindall, Stephen
; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5.3
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,744
; FILING DATE: 06-SEPT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/208886
; FILING DATE: 10-MAR-1994
; APPLICATION NUMBER: PCT/US/95/02400
; FILING DATE: 08-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: JB0429K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 298-2987
; TELEFAX: (908) 298-5388
; TELEX:
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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US-08-704-744-89

Query Match 66.7%; Score 16; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
Db 4 FSSYW 8

RESULT 11
US-08-469-557-68
; Sequence 68, Application US/08469557
; Patent No. 5770403
; GENERAL INFORMATION:
; APPLICANT: Dalie, Barbara
; APPLICANT: Le, Hung
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Nguyen, Hanh
; APPLICANT: Tindall, Stephen
; APPLICANT: Zavodny, Paul
; TITLE OF INVENTION: Cloning and Expression of
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; TITLE OF INVENTION: Against Human Interleukin-4
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,557
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/290,793
; FILING DATE: August 16, 1994
; APPLICATION NUMBER: PCT/US93/01301
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: US 07/841,659
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: US 07/782,784
; FILING DATE: 24-OCT-1991
; APPLICATION NUMBER: US 07/499,327
; FILING DATE: 21-MAY-1990
; APPLICATION NUMBER: PCT/US88/03631
; FILING DATE: 21-OCT-1988
; APPLICATION NUMBER: US 07/655,966
; FILING DATE: 14-FEB-1991
; APPLICATION NUMBER: US 07/113,623
; FILING DATE: 26-OCT-1987
; APPLICATION NUMBER: US 06/881,553
; FILING DATE: 03-JUL-1986
; APPLICATION NUMBER: US 06/843,958
; FILING DATE: 25-MAR-1986
; APPLICATION NUMBER: US 06/799,668
; FILING DATE: 19-NOV-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: 2409K7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908 298-2987
; TELEFAX: 908-298-5388
```

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; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-469-557-68

Query Match          66.7%; Score 16; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 FXXW 6
Db      4 FSSW 8

RESULT 12
US-08-290-793B-68
; Sequence 68, Application US/08290793B
; Patent No. 5863537
; GENERAL INFORMATION:
; APPLICANT: Dalie, Barbara
; APPLICANT: Le, Hung
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Nguyen, Hanh
; APPLICANT: Tindall, Stephen
; APPLICANT: Zavodny, Paul
; TITLE OF INVENTION: Cloning and Expression of
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; TITLE OF INVENTION: Against Human Interleukin-4
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,793B
; FILING DATE: August 16, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/01301
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: US 07/841,659
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: US 07/782,784
; FILING DATE: 24-OCT-1991
; APPLICATION NUMBER: US 07/499,327
; FILING DATE: 21-MAY-1990
; APPLICATION NUMBER: PCT/US88/03631
; FILING DATE: 21-OCT-1988
; APPLICATION NUMBER: US 07/655,966
; FILING DATE: 14-FEB-1991
; APPLICATION NUMBER: US 07/113,623
; FILING DATE: 26-OCT-1987
; APPLICATION NUMBER: US 06/881,553
; FILING DATE: 03-JUL-1986
; APPLICATION NUMBER: US 06/843,958
; FILING DATE: 25-MAR-1986
; APPLICATION NUMBER: US 06/799,668
; FILING DATE: 19-NOV-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: 2409K7

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908 298-2987
; TELEFAX: 908-298-5388
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-290-793B-68

Query Match          66.7%; Score 16; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 FXXW 6
Db      4 FSSW 8

RESULT 13
US-08-277-660A-16
; Sequence 16, Application US/08277660A
; Patent No. 5702908
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,660A
; FILING DATE: 20-JUL-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-60244/WHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-277-660A-16

Query Match          66.7%; Score 16; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 FXXW 6
Db      5 FSALW 9

RESULT 14
US-08-277-660A-17
```

; Sequence 17, Application US/08277660A  
; Patent No. 5702908  
; GENERAL INFORMATION:  
; APPLICANT: Picksley, Steven M.  
; APPLICANT: Lane, David P.  
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/277,660A  
; FILING DATE: 20-JUL-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Walter H.  
; REGISTRATION NUMBER: 24,190  
; REFERENCE/DOCKET NUMBER: A-60244/WHd  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; US-08-277-660A-17  
  
Query Match 66.7%; Score 16; DB 1; Length 11;  
Best Local Similarity 40.0%; Pred. No. 2.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXW 6  
Db 5 FSDAW 9  
  
RESULT 15  
US-08-424-957-29  
; Sequence 29, Application US/08424957  
; Patent No. 5770377  
; GENERAL INFORMATION:  
; APPLICANT: Picksley, Steven M.  
; APPLICANT: Lane, David P.  
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/424,957  
; FILING DATE: 19-APR-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/277,660  
; FILING DATE: 20-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Walter H.  
; REGISTRATION NUMBER: 24,190  
; REFERENCE/DOCKET NUMBER: A-61228/WHd  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; US/08/424,957

; FILING DATE: 19-APR-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/277,660  
; FILING DATE: 20-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Walter H.  
; REGISTRATION NUMBER: 24,190  
; REFERENCE/DOCKET NUMBER: A-61228/WHd  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; US-08-424-957-29  
  
Query Match 66.7%; Score 16; DB 1; Length 11;  
Best Local Similarity 40.0%; Pred. No. 2.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXW 6  
Db 5 FSALW 9  
  
RESULT 16  
US-08-424-957-30  
; Sequence 30, Application US/08424957  
; Patent No. 5770377  
; GENERAL INFORMATION:  
; APPLICANT: Picksley, Steven M.  
; APPLICANT: Lane, David P.  
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/424,957  
; FILING DATE: 19-APR-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/277,660  
; FILING DATE: 20-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Walter H.  
; REGISTRATION NUMBER: 24,190  
; REFERENCE/DOCKET NUMBER: A-61228/WHd  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown



US-08-424-957-30

Query Match 66.7%; Score 16; DB 1; Length 11;  
Best Local Similarity 40.0%; Pred. No. 2.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6  
|  
Db 5 FSDAW 9

RESULT 17

US-09-035-686-29  
; Sequence 29, Application US/09035686  
; Patent No. 6153391  
; GENERAL INFORMATION:

; APPLICANT: Pickaley, Steven M.  
; APPLICANT: Lane, David P.  
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111-4187

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/035,686  
; FILING DATE:

; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/424,957  
; FILING DATE: 19-APR-1995  
; APPLICATION NUMBER: US 08/277,660  
; FILING DATE: 20-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Walter H.  
; REGISTRATION NUMBER: 24,190  
; REFERENCE/DOCKET NUMBER: A-61228/WH  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299

; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; US-09-035-686-29

Query Match 66.7%; Score 16; DB 3; Length 11;  
Best Local Similarity 40.0%; Pred. No. 2.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6  
|  
Db 5 FSLW 9

RESULT 18

US-09-035-686-30  
; Sequence 30, Application US/09035686  
; Patent No. 6153391  
; GENERAL INFORMATION:  
; APPLICANT: Pickaley, Steven M.

; APPLICANT: Lane, David P.  
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111-4187

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/035,686  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/424,957  
; FILING DATE: 19-APR-1995  
; APPLICATION NUMBER: US 08/277,660  
; FILING DATE: 20-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Walter H.  
; REGISTRATION NUMBER: 24,190  
; REFERENCE/DOCKET NUMBER: A-61228/WH  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299

; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; US-09-035-686-30

Query Match 66.7%; Score 16; DB 3; Length 11;  
Best Local Similarity 40.0%; Pred. No. 2.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6  
|  
Db 5 FSDAW 9

RESULT 19

US-08-406-330-32  
; Sequence 32, Application US/08406330  
; Patent No. 5817748  
; GENERAL INFORMATION:

; APPLICANT: Miller, Jonathan L.  
; APPLICANT: Lyle, Vicki A.  
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF  
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
; STREET: Clinton Square, P.O. Box 1051  
; CITY: Rochester  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 14603

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/406,330  
FILING DATE: 530  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Timian, Susan J.  
REGISTRATION NUMBER: 34,103  
REFERENCE/DOCKET NUMBER: 20884/100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1636  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-406-330-32

Query Match 66.7%; Score 16; DB 2; Length 12;  
Best Local Similarity 40.0%; Pred. No. 2.8e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
| |  
Db 3 FSSVW 7

RESULT 20  
US-08-556-597-32  
Sequence 32, Application US/08556597  
Patent No. 5877155  
GENERAL INFORMATION:  
APPLICANT: Miller, Jonathan L.  
APPLICANT: Lyle, Vicki A.  
TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF  
TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: New York  
COUNTRY: USA  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/556,597  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/406,330  
FILING DATE: 17-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Timian, Susan J.  
REGISTRATION NUMBER: 34,103  
REFERENCE/DOCKET NUMBER: 20884/101  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1636  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-556-597-32

Query Match 66.7%; Score 16; DB 2; Length 12;  
Best Local Similarity 40.0%; Pred. No. 2.8e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
| |  
Db 3 FSSVW 7

RESULT 21  
US-08-305-871A-23  
Sequence 23, Application US/08305871A  
Patent No. 5736142  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Gaeta, Federico  
APPLICANT: Grey, Howard M.  
APPLICANT: Sidney, John  
APPLICANT: Alexander, Jeffrey L.  
TITLE OF INVENTION: Alteration of Immune Response Using Pan  
TITLE OF INVENTION: DR-Binding Peptides  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/305,871A  
FILING DATE: 14-SEP-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/121,101  
FILING DATE: 14-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 14137-0062-10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1..13  
OTHER INFORMATION: /note= "Peptide wherein X is  
OTHER INFORMATION: tyrosine or phenylalanine."  
US-08-305-871A-23

Query Match 66.7%; Score 16; DB 1; Length 13;  
Best Local Similarity 40.0%; Pred. No. 2.9e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
| |  
Db 3 FVAW 7

RESULT 22  
US-08-912-560-11



QY 2 FXXXW 6  
| |  
Db 3 FVAAW 7

RESULT 26  
5185431-25  
; Patent No. 5185431  
; APPLICANT: YOSHIMATSU, KENTARO; SHIKATA, YASUSHI; TANAKA, ISAO;  
; HASEGAWA, YOSHIKAZU; SETO, TOSHIO; OSAWA, TOSHIO  
; TITLE OF INVENTION: RECOMBINANT NATURAL KILLER CELL ACTIVATOR  
; NUMBER OF SEQUENCES: 31  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/392,841  
; FILING DATE: 11-AUG-1989  
; SEQ ID NO: 25:  
; LENGTH: 13  
5185431-25

Query Match 66.7%; Score 16; DB 6; Length 13;  
Best Local Similarity 40.0%; Pred. No. 2.9e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |  
Db 5 FSQAW 9

RESULT 27  
5185431-25  
; Patent No. 5185431  
; APPLICANT: YOSHIMATSU, KENTARO; SHIKATA, YASUSHI; TANAKA, ISAO;  
; HASEGAWA, YOSHIKAZU; SETO, TOSHIO; OSAWA, TOSHIO  
; TITLE OF INVENTION: RECOMBINANT NATURAL KILLER CELL ACTIVATOR  
; NUMBER OF SEQUENCES: 31  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/392,841  
; FILING DATE: 11-AUG-1989  
; SEQ ID NO: 25:  
; LENGTH: 13  
5185431-25

Query Match 66.7%; Score 16; DB 6; Length 13;  
Best Local Similarity 40.0%; Pred. No. 2.9e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |  
Db 5 FSQAW 9

RESULT 28  
US-08-218-025A-139  
; Sequence 139, Application US/08218025A  
; Patent No. 5556744  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, David B.  
; APPLICANT: Ugen, Kenneth E.  
; APPLICANT: Williams, William V.  
; TITLE OF INVENTION: Methods and Compositions for Diagnosing  
; TITLE OF INVENTION: and Treating Certain HIV Infected Patients  
; NUMBER OF SEQUENCES: 197  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Howson and Howson  
; STREET: P.O. Box 457, 321 No. 5556744ristown Road  
; CITY: Spring House  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19477  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/218,025A  
; FILING DATE: 24-MAR-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/891,451  
; FILING DATE: 29-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bak, Mary E.  
; REGISTRATION NUMBER: 31,215  
; REFERENCE/DOCKET NUMBER: WST33A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 540-9206  
; TELEFAX: (215) 540-5818  
; INFORMATION FOR SEQ ID NO: 139:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-218-025A-139

Query Match 66.7%; Score 16; DB 1; Length 15;  
Best Local Similarity 40.0%; Pred. No. 3.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |  
Db 1 FNSTW 5

RESULT 29  
US-08-847-844A-22  
; Sequence 22, Application US/08847844A  
; Patent No. 6150160  
; GENERAL INFORMATION:  
; APPLICANT: KAZAZIAN JR., HAIG H.  
; APPLICANT: BOEKE, JEF D.  
; APPLICANT: MORAN, JOHN V.  
; APPLICANT: DOMBROSKI, BETH A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF  
; TITLE OF INVENTION: MAMMALIAN RETROTRANSPOSONS  
; NUMBER OF SEQUENCES: 137  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.  
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND FL.  
; CITY: PHILADELPHIA  
; STATE: PA  
; COUNTRY: U.S.A.  
; ZIP: 19103-7086  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/847,844A  
; FILING DATE: 28-APR-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/749,805  
; FILING DATE: 16-NOV-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/006,831  
; FILING DATE: 16-NOV-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DOYLE LEARY Ph.D., KATHRYN  
; REGISTRATION NUMBER: 36,317  
; REFERENCE/DOCKET NUMBER: 9596-23U2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-567-2020

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; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-847-844A-22

Query Match 66.7%; Score 16; DB 3; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 6 FIATW 10

RESULT 30
PCT-US93-08699-1
; Sequence 1, Application PC/TUS9308699
; GENERAL INFORMATION:
; APPLICANT: JOHNSON & JOHNSON and GEORGETOWN UNIVERSITY
; TITLE OF INVENTION: IMMUNOREACTIVE PEPTIDES FROM
; TITLE OF INVENTION: EPSTEIN-BARR VIRUS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East - Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08699
; FILING DATE: 15-SEP-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John R.,
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: FD-3033
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
; PCT-US93-08699-1

Query Match 66.7%; Score 16; DB 5; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 3 FTETW 7

RESULT 31
; US-09-330-914A-11
; Sequence 11, Application US/09330914A
; Patent No. 6432671
; GENERAL INFORMATION:
; APPLICANT: Flohe, Leopold
; No. 6432671ecke, Everson
; Kalisz, Henryk
; Montemartini, Marisa
; TITLE OF INVENTION: TRYPAREDOXIN, EXPRESSION PLASMID, PROCESS OF
; PRODUCTION, METHOD OF USE, TEST KIT, AND
; PHARMACEUTICAL COMPOSITION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshhall, O'Toole, Gerstein, Murray & Broun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: Unites States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/330,914A
; FILING DATE: 11-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP97/06983
; FILING DATE: 12-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, James P.
; REGISTRATION NUMBER: 28,491
; REFERENCE/DOCKET NUMBER: 29473/35678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
; US-09-330-914A-11

Query Match 66.7%; Score 16; DB 4; Length 16;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 8 FAQSW 12

RESULT 32
US-08-413-233-3
; Sequence 3, Application US/08413233
; Patent No. 6506553
; GENERAL INFORMATION:
; APPLICANT: Smith, Richard S.
; APPLICANT: Parks, D. Ellio
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS OF EPSTEIN-BARR
; TITLE OF INVENTION: VIRUS ASSOCIATED DISEASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOEB AND LOEB
; STREET: 1880 Century Park East, 5th Floor
; CITY: Los Angeles
; STATE: California
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; COUNTRY: USA  
; ZIP: 90067  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/413,233  
; FILING DATE: 30-MAR-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Yang, Wei-ning  
; REGISTRATION NUMBER: 38,690  
; REFERENCE/DOCKET NUMBER: 7586D.4007  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (310) 553-5050  
; TELEFAX: (310) 553-4619  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..16  
; US-08-413-233-3

Query Match 66.7%; Score 16; DB 4; Length 16;  
Best Local Similarity 40.0%; Pred. No. 3.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
Db 3 FTETW 7

RESULT 33  
US-09-690-454-88  
; Sequence 88, Application US/09690454  
; Patent No. 6531447  
; GENERAL INFORMATION:  
; APPLICANT: Steven M. Ruben, et al.  
; TITLE OF INVENTION: 32 Human Secreted Proteins  
; FILE REFERENCE: PZ006P1  
; CURRENT APPLICATION NUMBER: US/09/690,454  
; CURRENT FILING DATE: 2000-10-18  
; PRIOR APPLICATION NUMBER: 09/189,144  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: 60/044,039  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,093  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,190  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/050,935  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,101  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,356  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/056,250  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,296  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,293  
; PRIOR FILING DATE: August 29, 1997  
; NUMBER OF SEQ ID NOS: 229  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 88  
; LENGTH: 16

; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-690-454-88  
Query Match 66.7%; Score 16; DB 4; Length 16;  
Best Local Similarity 40.0%; Pred. No. 3.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 FXXXW 6  
Db 8 FRSW 12  
RESULT 34  
US-09-170-496D-285  
; Sequence 285, Application US/09170496D  
; Patent No. 6555339  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: AREN-0040  
; CURRENT APPLICATION NUMBER: US/09/170,496D  
; CURRENT FILING DATE: 1998-10-13  
; NUMBER OF SEQ ID NOS: 294  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 285  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: No. 6555339el Sequence  
; US-09-170-496D-285

Query Match 66.7%; Score 16; DB 4; Length 16;  
Best Local Similarity 40.0%; Pred. No. 3.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
Db 5 FMSTW 9

RESULT 35  
US-08-218-025A-115  
; Sequence 115, Application US/08218025A  
; Patent No. 5556744  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, David B.  
; APPLICANT: Ugen, Kenneth E.  
; APPLICANT: Williams, William V.  
; TITLE OF INVENTION: Methods and Compositions for Diagnosing  
; TITLE OF INVENTION: and Treating Certain HIV Infected Patients  
; NUMBER OF SEQUENCES: 197  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Howson and Howson  
; STREET: P.O. Box 457, 321 No. 5556744ristown Road  
; CITY: Spring House  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19477  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/218,025A  
; FILING DATE: 24-MAR-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 07/891,451  
/ FILING DATE: 29-MAY-1992  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Bak, Mary E.  
/ REGISTRATION NUMBER: 31,215  
/ REFERENCE/DOCKET NUMBER: WST33A  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (215) 540-9206  
/ TELEFAX: (215) 540-5818  
/ INFORMATION FOR SEQ ID NO: 115:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 17 amino acids  
/ TYPE: amino acid  
/ TOPOLOGY: unknown  
/ MOLECULE TYPE: peptide  
/ US-08-218-025A-115

Query Match 66.7%; Score 16; DB 1; Length 17;  
Best Local Similarity 40.0%; Pred. No. 3.5e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
| |  
Db 13 FNSTW 17

RESULT 36  
US-08-746-283-7  
; Sequence 7, Application US/08746283  
; Patent No. 5834280  
; GENERAL INFORMATION:  
; APPLICANT: Oxenboll, Karen M.  
; APPLICANT: Si, Joan O.  
; APPLICANT: Aagaard, Jesper  
; TITLE OF INVENTION: Glucose Oxidases  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5834280o No. 5834280disk of No. 5834280th America  
; STREET: 405 Lexington Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10174  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/746,283  
; FILING DATE: 07-NOV-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Agis, Dr. Cheryl H.  
; REGISTRATION NUMBER: 34,086  
; REFERENCE/DOCKET NUMBER: 4158.214-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 867-0123  
; TELEFAX: (212) 878-9655  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 5834280e  
/ US-08-746-283-7

Query Match 66.7%; Score 16; DB 2; Length 17;  
Best Local Similarity 40.0%; Pred. No. 3.5e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
| |  
Db 13 FNSTW 17

Db 3 FTSVW 7

RESULT 37  
US-08-746-257A-5  
; Sequence 5, Application US/08746257A  
; Patent No. 5879921  
; GENERAL INFORMATION:  
; APPLICANT: Cherry, Joel  
; APPLICANT: Berka, Randy  
; APPLICANT: Halkier, Torben  
; TITLE OF INVENTION: Glucose Oxidases  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5879921o No. 5879921disk of No. 5879921th America  
; STREET: 405 Lexington Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10174  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/746,257A  
; FILING DATE: 07-NOV-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Starnes, Robert L.  
; REGISTRATION NUMBER: 41,324  
; REFERENCE/DOCKET NUMBER: 4700.000-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-867-0123  
; TELEFAX: 212-878-9655  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 5879921e  
/ US-08-746-257A-5

Query Match 66.7%; Score 16; DB 2; Length 17;  
Best Local Similarity 40.0%; Pred. No. 3.5e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
| |  
Db 3 FTSVW 7

RESULT 38  
US-08-987-743-11  
; Sequence 11, Application US/08987743  
; Patent No. 6123938  
; GENERAL INFORMATION:  
; APPLICANT: Stern, Robert  
; APPLICANT: Csoka, Anthony  
; APPLICANT: Frost, Gregory I.  
; APPLICANT: Wong, Tim M.  
; TITLE OF INVENTION: Purification and Microsequencing of  
; FILE REFERENCE: 9076/088CIP2  
; CURRENT APPLICATION NUMBER: US/08/987,743  
; CURRENT FILING DATE: 1997-12-09  
; EARLIER APPLICATION NUMBER: 08/733,360  
; EARLIER FILING DATE: 1996-10-17  
; NUMBER OF SEQ ID NOS: 16



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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 17
; TYPE: PRT
; ORGANISM: H. sapiens
US-08-987-743-11

Query Match      66.7%; Score 16; DB 3; Length 17;
Best Local Similarity 40.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
Db      11 FTTW 15

RESULT 39
US-09-170-496D-286
; Sequence 286, Application US/09170496D
; Patent No. 655339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 655339-Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 286
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 655339e1 Sequence
US-09-170-496D-286

Query Match      66.7%; Score 16; DB 4; Length 17;
Best Local Similarity 40.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
Db      5 FMSTW 9

RESULT 40
US-08-934-915-125
; Sequence 125, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-125

Query Match      66.7%; Score 16; DB 2; Length 18;
Best Local Similarity 40.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
Db      7 FSRTW 11

Search completed: October 18, 2005, 16:00:26
Job time : 32.2353 secs
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:58:45 ; Search time 115.412 Seconds  
(without alignments)  
32.505 Million cell updates/sec

Title: US-09-214-371-11  
Perfect score: 24  
Sequence: 1 XFXXXWXXX 9

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Maximum Match 100%  
Listing first 1000 summaries

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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
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14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*  
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18: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep:\*  
20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	17	70.8	8	18	US-10-818-036-27
3	17	70.8	8	18	US-10-818-036-28
4	17	70.8	8	18	US-10-818-036-30
5	17	70.8	9	14	US-10-072-419-3
6	17	70.8	9	14	US-10-072-419-8
7	17	70.8	9	16	US-10-869-768-3
8	17	70.8	9	16	US-10-869-768-8
9	17	70.8	9	18	US-10-818-036-14
10	17	70.8	9	18	US-10-818-036-15
11	17	70.8	9	18	US-10-818-036-23
					Sequence 24, Appl
					Sequence 27, Appl
					Sequence 28, Appl
					Sequence 30, Appl
					Sequence 3, Appl
					Sequence 8, Appl
					Sequence 3, Appl
					Sequence 8, Appl
					Sequence 14, Appl
					Sequence 15, Appl
					Sequence 23, Appl

85	16	66.7	10	15	US-10-264-309-128	Sequence 128, App	158	16	66.7	16	14	US-10-193-795-11	Sequence 11, Appl
86	16	66.7	10	15	US-10-436-782-6	Sequence 6, Appli	159	16	66.7	16	14	US-10-251-385-285	Sequence 285, App
87	16	66.7	10	15	US-10-239-656-14	Sequence 14, Appl	160	16	66.7	16	14	US-10-062-831-88	Sequence 88, Appl
88	16	66.7	10	15	US-10-128-520-367	Sequence 367, App	161	16	66.7	16	14	US-10-224-356-36	Sequence 36, Appl
89	16	66.7	10	16	US-10-468-250A-109	Sequence 109, App	162	16	66.7	16	14	US-10-062-599-88	Sequence 88, Appl
90	16	66.7	10	16	US-10-863-768-34	Sequence 34, Appl	163	16	66.7	16	18	US-10-962-760-11	Sequence 11, Appl
91	16	66.7	10	16	US-10-869-768-36	Sequence 36, Appl	164	16	66.7	17	14	US-10-059-271-20	Sequence 20, Appl
92	16	66.7	10	16	US-10-729-441-53	Sequence 53, Appl	165	16	66.7	17	14	US-10-251-385-286	Sequence 286, App
93	16	66.7	10	17	US-10-769-308-30	Sequence 30, Appl	166	16	66.7	17	14	US-10-031-874A-59	Sequence 59, Appl
94	16	66.7	10	17	US-10-723-962-62	Sequence 62, Appl	167	16	66.7	17	14	US-10-029-386-29993	Sequence 29993, A
95	16	66.7	10	17	US-10-725-962-65	Sequence 65, Appl	168	16	66.7	17	14	US-10-029-386-31536	Sequence 31536, A
96	16	66.7	10	17	US-10-638-265-89	Sequence 89, Appl	169	16	66.7	17	16	US-10-450-036A-59	Sequence 59, Appl
97	16	66.7	10	17	US-10-879-994-19	Sequence 19, Appl	170	16	66.7	18	9	US-09-205-658-283	Sequence 283, Appl
98	16	66.7	10	17	US-10-726-332-54	Sequence 54, Appl	171	16	66.7	18	9	US-09-205-658-285	Sequence 285, App
99	16	66.7	10	17	US-10-726-332-72	Sequence 72, Appl	172	16	66.7	18	10	US-09-963-693-283	Sequence 283, App
100	16	66.7	10	17	US-10-726-332-87	Sequence 87, Appl	173	16	66.7	18	10	US-09-963-693-285	Sequence 285, App
101	16	66.7	10	17	US-10-726-332-90	Sequence 90, Appl	174	16	66.7	18	11	US-09-833-245-1958	Sequence 1958, Ap
102	16	66.7	10	17	US-10-726-332-107	Sequence 107, App	175	16	66.7	18	11	US-09-833-245-1959	Sequence 1959, Ap
103	16	66.7	10	17	US-10-769-074-30	Sequence 30, Appl	176	16	66.7	18	14	US-10-224-356-17	Sequence 17, Appl
104	16	66.7	10	17	US-10-867-506-55	Sequence 55, Appl	177	16	66.7	19	9	US-09-864-761-41546	Sequence 41546, A
105	16	66.7	10	18	US-10-981-738-17	Sequence 17, Appl	178	16	66.7	20	9	US-09-812-528-19	Sequence 19, Appl
106	16	66.7	10	18	US-10-727-737-20	Sequence 20, Appl	179	16	66.7	20	9	US-09-884-441-411	Sequence 411, App
107	16	66.7	10	18	US-10-727-737-23	Sequence 23, Appl	180	16	66.7	20	9	US-09-884-441-412	Sequence 412, App
108	16	66.7	10	18	US-10-727-737-24	Sequence 24, Appl	181	16	66.7	20	10	US-09-907-969-411	Sequence 411, App
109	16	66.7	10	18	US-10-264-309-128	Sequence 128, App	182	16	66.7	20	10	US-09-907-969-412	Sequence 412, App
110	16	66.7	10	18	US-10-897-406-53	Sequence 53, Appl	183	16	66.7	20	10	US-09-827-271-411	Sequence 411, App
111	16	66.7	10	20	US-11-004-795A-6	Sequence 6, Appli	184	16	66.7	20	10	US-09-827-271-412	Sequence 412, App
112	16	66.7	10	20	US-11-004-794A-6	Sequence 6, Appli	185	16	66.7	20	10	US-09-933-767-744	Sequence 744, App
113	16	66.7	11	14	US-10-097-175-70	Sequence 70, Appl	186	16	66.7	20	14	US-10-004-860-744	Sequence 744, App
114	16	66.7	11	14	US-10-097-175-90	Sequence 90, Appl	187	16	66.7	20	14	US-10-023-282-744	Sequence 744, App
115	16	66.7	11	14	US-10-193-651-11	Sequence 11, Appl	188	16	66.7	20	14	US-10-174-613-14	Sequence 14, Appl
116	16	66.7	11	15	US-10-398-104-238	Sequence 238, App	189	16	66.7	20	14	US-10-198-053-411	Sequence 411, App
117	16	66.7	11	17	US-10-879-994-83	Sequence 83, Appl	190	16	66.7	20	14	US-10-198-053-412	Sequence 412, App
118	16	66.7	11	17	US-10-879-994-99	Sequence 99, Appl	191	16	66.7	20	14	US-10-198-053-617	Sequence 617, App
119	16	66.7	12	10	US-09-954-385-391	Sequence 391, App	192	16	66.7	20	14	US-10-198-053-618	Sequence 618, App
120	16	66.7	12	14	US-10-092-908-22	Sequence 22, Appl	193	16	66.7	20	14	US-10-280-066-400	Sequence 400, App
121	16	66.7	12	14	US-10-092-908-42	Sequence 42, Appl	194	16	66.7	20	15	US-10-023-339-26	Sequence 26, Appl
122	16	66.7	12	14	US-10-075-869-36	Sequence 36, Appl	195	16	66.7	20	16	US-10-725-952-19	Sequence 19, Appl
123	16	66.7	12	15	US-10-366-493-36	Sequence 36, Appl	196	16	66.7	20	17	US-10-860-790-411	Sequence 411, App
124	16	66.7	12	16	US-10-467-758-26	Sequence 26, Appl	197	16	66.7	20	17	US-10-860-790-412	Sequence 412, App
125	16	66.7	12	17	US-10-912-512-391	Sequence 391, App	198	16	66.7	20	17	US-10-860-790-617	Sequence 617, App
126	16	66.7	12	17	US-10-235-043-391	Sequence 391, App	199	16	66.7	20	17	US-10-860-790-618	Sequence 618, App
127	16	66.7	12	17	US-10-926-893-36	Sequence 36, Appl	200	15	62.5	5	10	US-09-594-594-11	Sequence 11, Appl
128	16	66.7	12	20	US-11-003-951-32	Sequence 32, Appl	201	15	62.5	5	20	US-11-081-198-114	Sequence 114, App
129	16	66.7	13	9	US-09-894-018-69	Sequence 69, Appl	202	15	62.5	6	9	US-09-214-371-83	Sequence 83, Appl
130	16	66.7	13	9	US-09-949-375A-18	Sequence 18, Appl	203	15	62.5	6	9	US-09-732-384-4	Sequence 4, Appli
131	16	66.7	13	9	US-09-785-215-19	Sequence 19, Appl	204	15	62.5	6	9	US-09-732-384-5	Sequence 5, Appli
132	16	66.7	13	14	US-10-116-118-36	Sequence 36, Appl	205	15	62.5	6	9	US-09-486-734A-34	Sequence 34, Appl
133	16	66.7	13	14	US-10-223-809A-17	Sequence 17, Appl	206	15	62.5	6	13	US-10-155-059-1	Sequence 1, Appli
134	16	66.7	13	14	US-10-295-074-7	Sequence 7, Appli	207	15	62.5	6	15	US-10-609-217-130	Sequence 130, App
135	16	66.7	13	14	US-10-295-074-20	Sequence 20, Appl	208	15	62.5	6	15	US-10-632-388-130	Sequence 130, App
136	16	66.7	13	14	US-10-295-069-52	Sequence 52, Appl	209	15	62.5	6	15	US-10-651-723-130	Sequence 130, App
137	16	66.7	13	15	US-10-371-069-52	Sequence 52, Appl	210	15	62.5	6	15	US-10-645-761-130	Sequence 130, App
138	16	66.7	13	15	US-10-371-260-52	Sequence 52, Appl	211	15	62.5	6	15	US-10-666-696-130	Sequence 130, App
139	16	66.7	13	16	US-10-441-779C-33	Sequence 33, Appl	212	15	62.5	6	15	US-10-653-048-130	Sequence 130, App
140	16	66.7	13	16	US-10-363-954A-18	Sequence 18, Appl	213	15	62.5	6	18	US-10-645-784-130	Sequence 130, App
141	16	66.7	13	16	US-10-643-103-3	Sequence 3, Appli	214	15	62.5	6	18	US-10-927-262A-83	Sequence 83, Appl
142	16	66.7	13	16	US-10-474-960A-69	Sequence 69, Appl	215	15	62.5	7	9	US-09-096-749A-36	Sequence 36, Appl
143	16	66.7	13	16	US-10-846-911-7	Sequence 7, Appli	216	15	62.5	7	10	US-09-912-414-28	Sequence 28, Appl
144	16	66.7	13	16	US-10-846-911-20	Sequence 20, Appl	217	15	62.5	7	10	US-09-903-412-36	Sequence 36, Appl
145	16	66.7	13	17	US-10-893-018-15	Sequence 15, Appl	218	15	62.5	7	14	US-10-174-717A-36	Sequence 36, Appl
146	16	66.7	13	18	US-10-732-862A-233	Sequence 233, App	219	15	62.5	7	14	US-10-165-155-36	Sequence 36, Appl
147	16	66.7	13	18	US-10-783-317A-17	Sequence 17, Appl	220	15	62.5	7	14	US-10-190-082-27	Sequence 27, Appl
148	16	66.7	13	18	US-10-939-107-7	Sequence 7, Appli	221	15	62.5	7	14	US-10-190-082-30	Sequence 30, Appl
149	16	66.7	13	18	US-10-939-107-20	Sequence 20, Appl	222	15	62.5	7	14	US-10-190-082-81	Sequence 81, Appl
150	16	66.7	14	16	US-10-387-955-49	Sequence 49, Appl	223	15	62.5	7	14	US-10-190-082-98	Sequence 98, Appl
151	16	66.7	15	9	US-09-205-658-284	Sequence 284, App	224	15	62.5	7	14	US-10-190-082-128	Sequence 128, App
152	16	66.7	15	10	US-09-963-693-284	Sequence 284, App	225	15	62.5	7	14	US-10-190-082-179	Sequence 179, App
153	16	66.7	15	14	US-10-216-122-22	Sequence 22, Appl	226	15	62.5	7	14	US-10-197-927-5	Sequence 5, Appli
154	16	66.7	15	15	US-10-442-456-1	Sequence 1, Appli	227	15	62.5	7	14	US-10-190-162-36	Sequence 36, Appl
155	16	66.7	15	18	US-10-946-647-790	Sequence 790, App	228	15	62.5	7	18	US-10-953-901-680	Sequence 680, App
156	16	66.7	15	18	US-10-946-647-957	Sequence 957, App	229	15	62.5	8	8	US-08-424-550B-252	Sequence 252, App
157	16	66.7	15	18	US-10-705-165-9	Sequence 9, Appli	230	15	62.5	8	9	US-09-214-371-12	Sequence 12, Appl

231	15	62.5	8	9	US-09-214-371-13	Sequence 13, Appl	304	15	62.5	8	18	US-10-927-262A-22	Sequence 22, Appl
232	15	62.5	8	9	US-09-214-371-21	Sequence 21, Appl	305	15	62.5	8	18	US-10-927-262A-46	Sequence 46, Appl
233	15	62.5	8	9	US-09-214-371-22	Sequence 22, Appl	306	15	62.5	8	18	US-10-927-262A-47	Sequence 47, Appl
234	15	62.5	8	9	US-09-214-371-46	Sequence 46, Appl	307	15	62.5	8	18	US-10-927-262A-48	Sequence 48, Appl
235	15	62.5	8	9	US-09-214-371-47	Sequence 47, Appl	308	15	62.5	8	18	US-10-927-262A-49	Sequence 49, Appl
236	15	62.5	8	9	US-09-214-371-48	Sequence 48, Appl	309	15	62.5	8	18	US-10-927-262A-52	Sequence 52, Appl
237	15	62.5	8	9	US-09-214-371-49	Sequence 49, Appl	310	15	62.5	8	18	US-10-946-647-346	Sequence 346, Appl
238	15	62.5	8	9	US-09-214-371-52	Sequence 52, Appl	311	15	62.5	8	18	US-10-946-647-621	Sequence 621, Appl
239	15	62.5	8	9	US-09-908-322-83	Sequence 83, Appl	312	15	62.5	8	18	US-10-776-521B-338	Sequence 338, Appl
240	15	62.5	8	10	US-09-783-931-83	Sequence 83, Appl	313	15	62.5	8	18	US-10-820-067A-848	Sequence 848, Appl
241	15	62.5	8	14	US-10-209-372-31	Sequence 31, Appl	314	15	62.5	8	20	US-11-051-411-203	Sequence 203, Appl
242	15	62.5	8	14	US-10-190-082-265	Sequence 265, Appl	315	15	62.5	8	20	US-11-051-411-345	Sequence 345, Appl
243	15	62.5	8	14	US-10-072-419-16	Sequence 16, Appl	316	15	62.5	8	20	US-11-051-411-475	Sequence 475, Appl
244	15	62.5	8	14	US-10-072-419-17	Sequence 17, Appl	317	15	62.5	8	20	US-11-051-411-690	Sequence 690, Appl
245	15	62.5	8	15	US-10-325-810-154	Sequence 154, Appl	318	15	62.5	8	20	US-11-051-411-902	Sequence 902, Appl
246	15	62.5	8	15	US-10-387-957-36	Sequence 36, Appl	319	15	62.5	8	20	US-11-051-411-1052	Sequence 1052, Appl
247	15	62.5	8	15	US-10-387-957-37	Sequence 37, Appl	320	15	62.5	8	20	US-11-013-537-39	Sequence 39, Appl
248	15	62.5	8	15	US-10-387-957-38	Sequence 38, Appl	321	15	62.5	9	8	US-08-821-739A-49	Sequence 49, Appl
249	15	62.5	8	15	US-10-387-957-39	Sequence 39, Appl	322	15	62.5	9	8	US-08-821-739A-53	Sequence 53, Appl
250	15	62.5	8	15	US-10-387-934-36	Sequence 36, Appl	323	15	62.5	9	9	US-09-214-371-37	Sequence 37, Appl
251	15	62.5	8	15	US-10-387-934-37	Sequence 37, Appl	324	15	62.5	9	9	US-09-214-371-38	Sequence 38, Appl
252	15	62.5	8	15	US-10-387-934-37	Sequence 38, Appl	325	15	62.5	9	9	US-09-764-304-12	Sequence 12, Appl
253	15	62.5	8	15	US-10-387-934-38	Sequence 39, Appl	326	15	62.5	9	9	US-09-862-260A-13	Sequence 13, Appl
254	15	62.5	8	16	US-10-387-934-39	Sequence 2, Appli	327	15	62.5	9	9	US-09-780-053-130	Sequence 130, Appl
255	15	62.5	8	16	US-10-340-179-2	Sequence 3, Appli	328	15	62.5	9	9	US-09-771-415-16	Sequence 16, Appl
256	15	62.5	8	16	US-10-340-179-3	Sequence 3, Appli	329	15	62.5	9	10	US-09-884-456-5	Sequence 5, Appli
257	15	62.5	8	16	US-10-387-955-36	Sequence 36, Appl	330	15	62.5	9	10	US-09-884-456-8	Sequence 8, Appli
258	15	62.5	8	16	US-10-387-955-37	Sequence 37, Appl	331	15	62.5	9	10	US-09-884-456-11	Sequence 11, Appl
259	15	62.5	8	16	US-10-387-955-38	Sequence 38, Appl	332	15	62.5	9	10	US-09-884-456-14	Sequence 14, Appl
260	15	62.5	8	16	US-10-387-955-39	Sequence 39, Appl	333	15	62.5	9	10	US-09-809-638-117	Sequence 117, Appl
261	15	62.5	8	16	US-10-869-768-16	Sequence 16, Appl	334	15	62.5	9	10	US-09-809-638-255	Sequence 255, Appl
262	15	62.5	8	16	US-10-869-768-17	Sequence 17, Appl	335	15	62.5	9	10	US-09-809-638-347	Sequence 347, Appl
263	15	62.5	8	16	US-10-877-022-154	Sequence 154, Appl	336	15	62.5	9	10	US-09-884-455-5	Sequence 5, Appli
264	15	62.5	8	16	US-10-877-022-154	Sequence 154, Appl	337	15	62.5	9	10	US-09-884-455-8	Sequence 8, Appli
265	15	62.5	8	16	US-10-488-219-36	Sequence 36, Appl	338	15	62.5	9	10	US-09-884-455-11	Sequence 11, Appl
266	15	62.5	8	16	US-10-488-219-37	Sequence 37, Appl	339	15	62.5	9	10	US-09-884-455-14	Sequence 14, Appl
267	15	62.5	8	16	US-10-488-219-38	Sequence 38, Appl	340	15	62.5	9	10	US-09-865-548A-186	Sequence 186, Appl
268	15	62.5	8	16	US-10-488-219-39	Sequence 39, Appl	341	15	62.5	9	11	US-09-920-480B-3	Sequence 3, Appli
269	15	62.5	8	17	US-10-877-146-154	Sequence 154, Appl	342	15	62.5	9	12	US-09-957-806A-62	Sequence 62, Appl
270	15	62.5	8	17	US-10-480-954-49	Sequence 49, Appl	343	15	62.5	9	12	US-09-957-806A-69	Sequence 69, Appl
271	15	62.5	8	17	US-10-480-954-84	Sequence 84, Appl	344	15	62.5	9	13	US-10-047-539-13	Sequence 13, Appl
272	15	62.5	8	17	US-10-480-954-86	Sequence 86, Appl	345	15	62.5	9	14	US-10-265-713-12	Sequence 12, Appl
273	15	62.5	8	17	US-10-480-954-88	Sequence 88, Appl	346	15	62.5	9	14	US-10-190-082-169	Sequence 169, Appl
274	15	62.5	8	17	US-10-480-954-90	Sequence 90, Appl	347	15	62.5	9	14	US-10-190-082-180	Sequence 180, Appl
275	15	62.5	8	17	US-10-480-954-92	Sequence 92, Appl	348	15	62.5	9	14	US-10-190-082-212	Sequence 212, Appl
276	15	62.5	8	17	US-10-480-954-94	Sequence 94, Appl	349	15	62.5	9	14	US-10-166-626-12	Sequence 12, Appl
277	15	62.5	8	17	US-10-480-954-96	Sequence 96, Appl	350	15	62.5	9	15	US-10-245-871-297	Sequence 297, Appl
278	15	62.5	8	17	US-10-480-954-98	Sequence 98, Appl	351	15	62.5	9	15	US-10-447-161-83	Sequence 83, Appl
279	15	62.5	8	17	US-10-480-954-113	Sequence 113, Appl	352	15	62.5	9	15	US-10-398-104-22	Sequence 22, Appl
280	15	62.5	8	17	US-10-480-954-115	Sequence 115, Appl	353	15	62.5	9	15	US-10-363-208-237	Sequence 237, Appl
281	15	62.5	8	17	US-10-480-954-117	Sequence 117, Appl	354	15	62.5	9	15	US-10-253-286-297	Sequence 297, Appl
282	15	62.5	8	17	US-10-480-954-119	Sequence 119, Appl	355	15	62.5	9	16	US-10-657-363-16	Sequence 16, Appl
283	15	62.5	8	17	US-10-480-954-121	Sequence 121, Appl	356	15	62.5	9	16	US-10-340-179-1	Sequence 1, Appli
284	15	62.5	8	17	US-10-480-954-123	Sequence 123, Appl	357	15	62.5	9	16	US-10-363-204-198	Sequence 198, Appl
285	15	62.5	8	17	US-10-480-954-125	Sequence 125, Appl	358	15	62.5	9	16	US-10-793-943-7	Sequence 7, Appli
286	15	62.5	8	17	US-10-480-954-143	Sequence 143, Appl	359	15	62.5	9	17	US-10-705-459-186	Sequence 186, Appl
287	15	62.5	8	17	US-10-480-954-145	Sequence 145, Appl	360	15	62.5	9	17	US-10-654-601-2374	Sequence 2374, Appl
288	15	62.5	8	17	US-10-480-954-147	Sequence 147, Appl	361	15	62.5	9	18	US-10-927-262A-37	Sequence 37, Appl
289	15	62.5	8	17	US-10-480-954-149	Sequence 149, Appl	362	15	62.5	9	18	US-10-927-262A-38	Sequence 38, Appl
290	15	62.5	8	17	US-10-480-954-151	Sequence 151, Appl	363	15	62.5	9	18	US-10-149-137A-540	Sequence 540, Appl
291	15	62.5	8	17	US-10-480-954-153	Sequence 153, Appl	364	15	62.5	9	18	US-10-953-901-690	Sequence 690, Appl
292	15	62.5	8	17	US-10-480-954-155	Sequence 155, Appl	365	15	62.5	9	18	US-10-510-523-33	Sequence 33, Appl
293	15	62.5	8	17	US-10-480-954-157	Sequence 157, Appl	366	15	62.5	9	18	US-10-510-523-34	Sequence 34, Appl
294	15	62.5	8	17	US-10-480-954-166	Sequence 166, Appl	367	15	62.5	9	20	US-11-051-411-73	Sequence 73, Appl
295	15	62.5	8	17	US-10-480-954-168	Sequence 168, Appl	368	15	62.5	9	20	US-11-051-411-281	Sequence 281, Appl
296	15	62.5	8	17	US-10-480-954-170	Sequence 170, Appl	369	15	62.5	9	20	US-11-051-411-346	Sequence 346, Appl
297	15	62.5	8	17	US-10-480-954-172	Sequence 172, Appl	370	15	62.5	9	20	US-11-051-411-473	Sequence 473, Appl
298	15	62.5	8	17	US-10-480-954-174	Sequence 174, Appl	371	15	62.5	9	20	US-11-051-411-607	Sequence 607, Appl
299	15	62.5	8	17	US-10-480-954-176	Sequence 176, Appl	372	15	62.5	9	20	US-11-051-411-1053	Sequence 1053, Appl
300	15	62.5	8	17	US-10-480-954-178	Sequence 178, Appl	373	15	62.5	10	9	US-09-214-371-35	Sequence 35, Appl
301	15	62.5	8	17	US-10-480-954-180	Sequence 180, Appl	374	15	62.5	10	9	US-09-214-371-36	Sequence 36, Appl
302	15	62.5	8	18	US-10-927-262A-12	Sequence 12, Appl	375	15	62.5	10	9	US-09-767-460-53	Sequence 53, Appl
303	15	62.5	8	18	US-10-927-262A-13	Sequence 13, Appl	376	15	62.5	10	9	US-09-767-460-72	Sequence 72, Appl

377	15	62.5	10	9	US-09-780-053-175	Sequence 175, App	450	15	62.5	10	18	US-10-818-036-20	Sequence 20, Appl
378	15	62.5	10	9	US-09-826-290-390	Sequence 390, App	451	15	62.5	10	20	US-11-003-951-93	Sequence 93, Appl
379	15	62.5	10	10	US-09-809-638-187	Sequence 187, App	452	15	62.5	10	20	US-11-009-443-85	Sequence 85, Appl
380	15	62.5	10	10	US-09-809-638-273	Sequence 273, App	453	15	62.5	10	20	US-11-051-411-15	Sequence 15, Appl
381	15	62.5	10	10	US-09-995-529-26	Sequence 26, Appl	454	15	62.5	10	20	US-11-051-411-74	Sequence 74, Appl
382	15	62.5	10	10	US-09-995-529-43	Sequence 43, Appl	455	15	62.5	10	20	US-11-051-411-282	Sequence 282, App
383	15	62.5	10	10	US-09-995-529-44	Sequence 44, Appl	456	15	62.5	10	20	US-11-051-411-474	Sequence 474, App
384	15	62.5	10	10	US-09-995-529-45	Sequence 45, Appl	457	15	62.5	10	20	US-11-051-411-502	Sequence 502, App
385	15	62.5	10	10	US-09-995-529-46	Sequence 46, Appl	458	15	62.5	11	10	US-09-840-085-31	Sequence 31, Appl
386	15	62.5	10	10	US-09-995-529-47	Sequence 47, Appl	459	15	62.5	11	14	US-10-014-340-216	Sequence 216, App
387	15	62.5	10	10	US-09-795-798-10	Sequence 10, Appl	460	15	62.5	11	15	US-10-398-104-162	Sequence 162, App
388	15	62.5	10	11	US-09-995-529-26	Sequence 26, Appl	461	15	62.5	11	16	US-10-793-943-5	Sequence 5, Appli
389	15	62.5	10	11	US-09-995-529-43	Sequence 43, Appl	462	15	62.5	11	17	US-10-659-207-444	Sequence 444, App
390	15	62.5	10	11	US-09-995-529-44	Sequence 44, Appl	463	15	62.5	11	17	US-10-656-250-46	Sequence 46, Appl
391	15	62.5	10	11	US-09-995-529-45	Sequence 45, Appl	464	15	62.5	11	17	US-10-656-250-171	Sequence 171, App
392	15	62.5	10	11	US-09-995-529-46	Sequence 46, Appl	465	15	62.5	11	20	US-11-051-411-21	Sequence 21, Appl
393	15	62.5	10	11	US-09-995-529-47	Sequence 47, Appl	466	15	62.5	11	20	US-11-051-411-162	Sequence 162, App
394	15	62.5	10	14	US-10-094-401-172	Sequence 172, App	467	15	62.5	11	20	US-11-051-411-222	Sequence 222, App
395	15	62.5	10	14	US-10-190-082-167	Sequence 167, App	468	15	62.5	11	20	US-11-051-411-325	Sequence 325, App
396	15	62.5	10	14	US-10-190-082-170	Sequence 170, App	469	15	62.5	11	20	US-11-051-411-584	Sequence 584, App
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399	15	62.5	10	14	US-10-190-082-276	Sequence 276, App	472	15	62.5	12	9	US-09-214-371-7	Sequence 7, Appli
400	15	62.5	10	14	US-10-190-082-290	Sequence 290, App	473	15	62.5	12	9	US-09-214-371-17	Sequence 17, Appl
401	15	62.5	10	14	US-10-160-506-29	Sequence 29, Appl	474	15	62.5	12	9	US-09-214-371-18	Sequence 18, Appl
402	15	62.5	10	14	US-10-072-419-32	Sequence 32, Appl	475	15	62.5	12	9	US-09-214-371-20	Sequence 20, Appl
403	15	62.5	10	14	US-10-031-874A-16	Sequence 16, Appl	476	15	62.5	12	9	US-09-214-371-24	Sequence 24, Appl
404	15	62.5	10	15	US-10-462-262-140	Sequence 140, App	477	15	62.5	12	9	US-09-214-371-25	Sequence 25, Appl
405	15	62.5	10	15	US-10-264-309-407	Sequence 407, App	478	15	62.5	12	9	US-09-214-371-26	Sequence 26, Appl
406	15	62.5	10	16	US-10-449-379-29	Sequence 29, Appl	479	15	62.5	12	9	US-09-214-371-31	Sequence 31, Appl
407	15	62.5	10	16	US-10-338-552-35	Sequence 35, Appl	480	15	62.5	12	9	US-09-214-371-64	Sequence 64, Appl
408	15	62.5	10	16	US-10-338-552-37	Sequence 37, Appl	481	15	62.5	12	10	US-09-820-053A-98	Sequence 98, Appl
409	15	62.5	10	16	US-10-338-552-39	Sequence 39, Appl	482	15	62.5	12	14	US-10-032-818-31	Sequence 31, Appl
410	15	62.5	10	16	US-10-338-552-41	Sequence 41, Appl	483	15	62.5	12	14	US-10-109-171-98	Sequence 98, Appl
411	15	62.5	10	16	US-10-338-627-35	Sequence 35, Appl	484	15	62.5	12	14	US-10-190-082-252	Sequence 252, App
412	15	62.5	10	16	US-10-338-627-37	Sequence 37, Appl	485	15	62.5	12	15	US-10-180-648-18	Sequence 18, Appl
413	15	62.5	10	16	US-10-338-627-39	Sequence 39, Appl	486	15	62.5	12	15	US-10-609-217-131	Sequence 131, App
414	15	62.5	10	16	US-10-338-627-41	Sequence 41, Appl	487	15	62.5	12	15	US-10-609-217-132	Sequence 132, App
415	15	62.5	10	16	US-10-688-015-29	Sequence 29, Appl	488	15	62.5	12	15	US-10-609-217-133	Sequence 133, App
416	15	62.5	10	16	US-10-450-036A-16	Sequence 16, Appl	489	15	62.5	12	15	US-10-609-217-134	Sequence 134, App
417	15	62.5	10	16	US-10-361-275-42	Sequence 42, Appl	490	15	62.5	12	15	US-10-609-217-137	Sequence 137, App
418	15	62.5	10	16	US-10-327-598-450	Sequence 450, App	491	15	62.5	12	15	US-10-609-217-143	Sequence 143, App
419	15	62.5	10	16	US-10-327-598-457	Sequence 457, App	492	15	62.5	12	15	US-10-609-217-144	Sequence 144, App
420	15	62.5	10	16	US-10-327-598-458	Sequence 458, App	493	15	62.5	12	15	US-10-609-217-145	Sequence 145, App
421	15	62.5	10	16	US-10-160-505-29	Sequence 29, Appl	494	15	62.5	12	15	US-10-609-217-146	Sequence 146, App
422	15	62.5	10	16	US-10-869-768-32	Sequence 32, Appl	495	15	62.5	12	15	US-10-632-388-131	Sequence 131, App
423	15	62.5	10	16	US-10-451-315A-8	Sequence 8, Appli	496	15	62.5	12	15	US-10-632-388-132	Sequence 132, App
424	15	62.5	10	17	US-10-823-253-1	Sequence 1, Appli	497	15	62.5	12	15	US-10-632-388-133	Sequence 133, App
425	15	62.5	10	17	US-10-823-253-11	Sequence 11, Appl	498	15	62.5	12	15	US-10-632-388-134	Sequence 134, App
426	15	62.5	10	17	US-10-823-253-19	Sequence 19, Appl	499	15	62.5	12	15	US-10-632-388-137	Sequence 137, App
427	15	62.5	10	17	US-10-823-253-19	Sequence 26, Appl	500	15	62.5	12	15	US-10-632-388-143	Sequence 143, App
428	15	62.5	10	17	US-10-823-253-26	Sequence 29, Appl	501	15	62.5	12	15	US-10-632-388-144	Sequence 144, App
429	15	62.5	10	17	US-10-769-308-29	Sequence 61, Appl	502	15	62.5	12	15	US-10-632-388-145	Sequence 145, App
430	15	62.5	10	17	US-10-777-829-51	Sequence 53, Appl	503	15	62.5	12	15	US-10-632-388-146	Sequence 146, App
431	15	62.5	10	17	US-10-777-829-72	Sequence 72, Appl	504	15	62.5	12	15	US-10-651-723-131	Sequence 131, App
432	15	62.5	10	17	US-10-879-994-67	Sequence 67, Appl	505	15	62.5	12	15	US-10-651-723-132	Sequence 132, App
433	15	62.5	10	17	US-10-726-332-128	Sequence 128, App	506	15	62.5	12	15	US-10-651-723-133	Sequence 133, App
434	15	62.5	10	17	US-10-769-074-29	Sequence 29, Appl	507	15	62.5	12	15	US-10-651-723-134	Sequence 134, App
435	15	62.5	10	17	US-10-818-067-53	Sequence 53, Appl	508	15	62.5	12	15	US-10-651-723-137	Sequence 137, App
436	15	62.5	10	17	US-10-818-067-72	Sequence 72, Appl	509	15	62.5	12	15	US-10-651-723-143	Sequence 143, App
437	15	62.5	10	18	US-10-996-316-138	Sequence 138, App	510	15	62.5	12	15	US-10-651-723-144	Sequence 144, App
438	15	62.5	10	18	US-10-996-316-147	Sequence 147, App	511	15	62.5	12	15	US-10-651-723-145	Sequence 145, App
439	15	62.5	10	18	US-10-996-316-148	Sequence 148, App	512	15	62.5	12	15	US-10-651-723-146	Sequence 146, App
440	15	62.5	10	18	US-10-927-262A-35	Sequence 35, Appl	513	15	62.5	12	15	US-10-645-761-131	Sequence 131, App
441	15	62.5	10	18	US-10-927-262A-36	Sequence 36, Appl	514	15	62.5	12	15	US-10-645-761-132	Sequence 132, App
442	15	62.5	10	18	US-10-823-810-1	Sequence 1, Appli	515	15	62.5	12	15	US-10-645-761-133	Sequence 133, App
443	15	62.5	10	18	US-10-823-810-11	Sequence 11, Appl	516	15	62.5	12	15	US-10-645-761-134	Sequence 134, App
444	15	62.5	10	18	US-10-823-810-19	Sequence 19, Appl	517	15	62.5	12	15	US-10-645-761-137	Sequence 137, App
445	15	62.5	10	18	US-10-823-810-26	Sequence 26, Appl	518	15	62.5	12	15	US-10-645-761-143	Sequence 143, App
446	15	62.5	10	18	US-10-727-737-19	Sequence 19, Appl	519	15	62.5	12	15	US-10-645-761-144	Sequence 144, App
447	15	62.5	10	18	US-10-727-737-21	Sequence 21, Appl	520	15	62.5	12	15	US-10-645-761-145	Sequence 145, App
448	15	62.5	10	18	US-10-727-737-22	Sequence 22, Appl	521	15	62.5	12	15	US-10-645-761-146	Sequence 146, App
449	15	62.5	10	18	US-10-261-309-407	Sequence 407, App	522	15	62.5	12	15	US-10-666-696-131	Sequence 131, App



523	15	62.5	12	15	US-10-666-696-132	Sequence 132, App	596	15	62.5	14	15	US-10-632-388-68	Sequence 68, Appl
524	15	62.5	12	15	US-10-666-696-133	Sequence 133, App	597	15	62.5	14	15	US-10-651-723-68	Sequence 68, Appl
525	15	62.5	12	15	US-10-666-696-134	Sequence 134, App	598	15	62.5	14	15	US-10-645-761-68	Sequence 68, Appl
526	15	62.5	12	15	US-10-666-696-137	Sequence 137, App	599	15	62.5	14	15	US-10-275-427A-13	Sequence 13, Appl
527	15	62.5	12	15	US-10-666-696-143	Sequence 143, App	600	15	62.5	14	15	US-10-666-696-68	Sequence 68, Appl
528	15	62.5	12	15	US-10-666-696-144	Sequence 144, App	601	15	62.5	14	15	US-10-653-048-68	Sequence 68, Appl
529	15	62.5	12	15	US-10-666-696-145	Sequence 145, App	602	15	62.5	14	16	US-10-387-955-61	Sequence 61, Appl
530	15	62.5	12	15	US-10-666-696-146	Sequence 146, App	603	15	62.5	14	16	US-10-712-447-158	Sequence 158, App
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532	15	62.5	12	15	US-10-653-048-132	Sequence 132, App	605	15	62.5	14	16	US-10-712-447-160	Sequence 160, App
533	15	62.5	12	15	US-10-653-048-133	Sequence 133, App	606	15	62.5	14	16	US-10-712-447-194	Sequence 194, App
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535	15	62.5	12	15	US-10-653-048-137	Sequence 137, App	608	15	62.5	14	16	US-10-712-447-196	Sequence 196, App
536	15	62.5	12	15	US-10-653-048-143	Sequence 143, App	609	15	62.5	14	16	US-10-712-447-204	Sequence 204, App
537	15	62.5	12	15	US-10-653-048-144	Sequence 144, App	610	15	62.5	14	16	US-10-865-478-854	Sequence 854, App
538	15	62.5	12	15	US-10-653-048-145	Sequence 145, App	611	15	62.5	14	17	US-10-808-187-1052	Sequence 1052, Ap
539	15	62.5	12	15	US-10-653-048-146	Sequence 146, App	612	15	62.5	14	18	US-10-645-784-68	Sequence 68, Appl
540	15	62.5	12	16	US-10-467-758-27	Sequence 27, Appl	613	15	62.5	14	18	US-10-853-973A-80	Sequence 80, Appl
541	15	62.5	12	16	US-10-467-758-31	Sequence 31, Appl	614	15	62.5	14	18	US-10-927-262A-33	Sequence 33, Appl
542	15	62.5	12	16	US-10-467-758-33	Sequence 33, Appl	615	15	62.5	14	18	US-10-927-262A-34	Sequence 34, Appl
543	15	62.5	12	16	US-10-467-758-36	Sequence 36, Appl	616	15	62.5	14	18	US-10-807-807-1052	Sequence 1052, Ap
544	15	62.5	12	16	US-10-363-204-228	Sequence 228, App	617	15	62.5	14	20	US-11-093-103-45	Sequence 45, Appl
545	15	62.5	12	16	US-10-649-873-61	Sequence 61, Appl	618	15	62.5	15	9	US-09-214-371-8	Sequence 8, Appli
546	15	62.5	12	16	US-10-839-525-98	Sequence 98, Appl	619	15	62.5	15	9	US-09-214-371-29	Sequence 29, Appl
547	15	62.5	12	17	US-10-873-848B-1	Sequence 1, Appli	620	15	62.5	15	9	US-09-214-371-30	Sequence 30, Appl
548	15	62.5	12	18	US-10-645-784-131	Sequence 131, App	621	15	62.5	15	9	US-09-214-371-66	Sequence 66, Appl
549	15	62.5	12	18	US-10-645-784-132	Sequence 132, App	622	15	62.5	15	9	US-09-829-549A-23	Sequence 23, Appl
550	15	62.5	12	18	US-10-645-784-133	Sequence 133, App	623	15	62.5	15	9	US-09-258-981-3	Sequence 3, Appli
551	15	62.5	12	18	US-10-645-784-134	Sequence 134, App	624	15	62.5	15	9	US-09-950-692-6	Sequence 6, Appli
552	15	62.5	12	18	US-10-645-784-137	Sequence 137, App	625	15	62.5	15	9	US-09-953-510-51	Sequence 51, Appl
553	15	62.5	12	18	US-10-645-784-143	Sequence 143, App	626	15	62.5	15	9	US-09-953-510-52	Sequence 52, Appl
554	15	62.5	12	18	US-10-645-784-144	Sequence 144, App	627	15	62.5	15	9	US-09-732-384-6	Sequence 6, Appli
555	15	62.5	12	18	US-10-645-784-145	Sequence 145, App	628	15	62.5	15	10	US-09-894-594-31	Sequence 31, Appl
556	15	62.5	12	18	US-10-645-784-146	Sequence 146, App	629	15	62.5	15	10	US-09-894-594-43	Sequence 43, Appl
557	15	62.5	12	18	US-10-927-262A-7	Sequence 7, Appli	630	15	62.5	15	10	US-09-952-680A-55	Sequence 55, Appl
558	15	62.5	12	18	US-10-927-262A-17	Sequence 17, Appl	631	15	62.5	15	10	US-09-840-085-33	Sequence 33, Appl
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561	15	62.5	12	18	US-10-927-262A-24	Sequence 24, Appl	634	15	62.5	15	11	US-09-953-413-52	Sequence 52, Appl
562	15	62.5	12	18	US-10-927-262A-25	Sequence 25, Appl	635	15	62.5	15	14	US-10-067-649-90	Sequence 90, Appl
563	15	62.5	12	18	US-10-927-262A-26	Sequence 26, Appl	636	15	62.5	15	14	US-10-186-867-28	Sequence 28, Appl
564	15	62.5	12	18	US-10-927-262A-31	Sequence 31, Appl	637	15	62.5	15	14	US-10-186-867-29	Sequence 29, Appl
565	15	62.5	12	18	US-10-927-262A-64	Sequence 64, Appl	638	15	62.5	15	14	US-10-211-088-141	Sequence 141, App
566	15	62.5	12	18	US-10-312-637-1	Sequence 1, Appli	639	15	62.5	15	14	US-10-147-255-51	Sequence 51, Appl
567	15	62.5	12	20	US-11-136-186-98	Sequence 98, Appl	640	15	62.5	15	14	US-10-147-255-52	Sequence 52, Appl
568	15	62.5	13	14	US-10-058-053A-275	Sequence 275, App	641	15	62.5	15	14	US-10-147-255-52	Sequence 52, Appl
569	15	62.5	13	14	US-10-300-694A-18	Sequence 18, Appl	642	15	62.5	15	14	US-10-239-313A-667	Sequence 667, App
570	15	62.5	13	14	US-10-113-512-1	Sequence 1, Appli	643	15	62.5	15	14	US-10-080-608A-165	Sequence 165, App
571	15	62.5	13	16	US-10-838-226-275	Sequence 275, App	644	15	62.5	15	15	US-10-370-685-74	Sequence 74, Appl
572	15	62.5	13	16	US-10-468-496-692	Sequence 692, App	645	15	62.5	15	15	US-10-375-157-64	Sequence 64, Appl
573	15	62.5	13	16	US-10-468-496-693	Sequence 693, App	646	15	62.5	15	15	US-10-609-217-139	Sequence 139, App
574	15	62.5	13	16	US-10-468-496-694	Sequence 694, App	647	15	62.5	15	15	US-10-609-217-140	Sequence 140, App
575	15	62.5	13	16	US-10-468-496-695	Sequence 695, App	648	15	62.5	15	15	US-10-609-217-141	Sequence 141, App
576	15	62.5	13	16	US-10-468-496-1718	Sequence 1718, Ap	649	15	62.5	15	15	US-10-425-970-4	Sequence 4, Appli
577	15	62.5	13	16	US-10-468-496-1719	Sequence 1719, Ap	650	15	62.5	15	15	US-10-632-388-139	Sequence 139, App
578	15	62.5	13	16	US-10-468-496-1720	Sequence 1720, Ap	651	15	62.5	15	15	US-10-632-388-140	Sequence 140, App
579	15	62.5	13	16	US-10-468-496-1721	Sequence 1721, Ap	652	15	62.5	15	15	US-10-632-388-141	Sequence 141, App
580	15	62.5	13	16	US-10-495-146-185	Sequence 185, App	653	15	62.5	15	15	US-10-651-723-139	Sequence 139, App
581	15	62.5	13	16	US-10-495-146-186	Sequence 186, App	654	15	62.5	15	15	US-10-651-723-140	Sequence 140, App
582	15	62.5	13	16	US-10-495-146-187	Sequence 187, App	655	15	62.5	15	15	US-10-651-723-141	Sequence 141, App
583	15	62.5	13	16	US-10-495-146-188	Sequence 188, App	656	15	62.5	15	15	US-10-645-761-139	Sequence 139, App
584	15	62.5	13	16	US-10-793-943-4	Sequence 4, Appli	657	15	62.5	15	15	US-10-645-761-140	Sequence 140, App
585	15	62.5	13	16	US-10-948-707-1379	Sequence 1379, Ap	658	15	62.5	15	15	US-10-645-761-141	Sequence 141, App
586	15	62.5	13	20	US-11-093-103-7	Sequence 7, Appli	659	15	62.5	15	15	US-10-666-696-139	Sequence 139, App
587	15	62.5	14	9	US-09-214-371-33	Sequence 33, Appl	660	15	62.5	15	15	US-10-666-696-140	Sequence 140, App
588	15	62.5	14	9	US-09-214-371-34	Sequence 34, Appl	661	15	62.5	15	15	US-10-666-696-141	Sequence 141, App
589	15	62.5	14	14	US-10-186-867-7	Sequence 7, Appli	662	15	62.5	15	15	US-10-653-048-139	Sequence 139, App
590	15	62.5	14	14	US-10-083-768-33	Sequence 33, Appl	663	15	62.5	15	15	US-10-653-048-140	Sequence 140, App
591	15	62.5	14	14	US-10-083-768-213	Sequence 213, App	664	15	62.5	15	15	US-10-653-048-141	Sequence 141, App
592	15	62.5	14	15	US-10-435-766-80	Sequence 80, Appl	665	15	62.5	15	16	US-10-775-965-74	Sequence 74, Appl
593	15	62.5	14	15	US-10-436-715-430	Sequence 430, App	666	15	62.5	15	16	US-10-215-982-55	Sequence 55, Appl
594	15	62.5	14	15	US-10-436-715-442	Sequence 442, App	667	15	62.5	15	16	US-10-695-155-51	Sequence 51, Appl
595	15	62.5	14	15	US-10-609-217-68	Sequence 68, Appl	668	15	62.5	15	16	US-10-695-155-52	Sequence 52, Appl



669	15	62.5	15	16	US-10-695-155-110	Sequence 110, App	742	15	62.5	18	20	US-11-093-103-47	Sequence 47, Appl
670	15	62.5	15	16	US-10-695-155-111	Sequence 111, App	743	15	62.5	18	20	US-11-093-103-48	Sequence 48, Appl
671	15	62.5	15	16	US-10-495-146-23	Sequence 23, Appl	744	15	62.5	19	9	US-09-214-371-1	Sequence 1, Appli
672	15	62.5	15	16	US-10-495-146-24	Sequence 24, Appl	745	15	62.5	19	9	US-09-732-357A-9	Sequence 9, Appli
673	15	62.5	15	16	US-10-495-146-25	Sequence 25, Appl	746	15	62.5	19	9	US-09-732-384-7	Sequence 7, Appli
674	15	62.5	15	16	US-10-495-146-26	Sequence 26, Appl	747	15	62.5	19	10	US-09-774-639-342	Sequence 342, App
675	15	62.5	15	16	US-10-793-943-3	Sequence 3, Appli	748	15	62.5	19	10	US-09-229-173-45	Sequence 45, Appl
676	15	62.5	15	17	US-10-182-613A-6	Sequence 6, Appli	749	15	62.5	19	10	US-09-977-797A-116	Sequence 116, App
677	15	62.5	15	17	US-10-182-613A-7	Sequence 7, Appli	750	15	62.5	19	10	US-09-969-730-289	Sequence 289, App
678	15	62.5	15	18	US-10-645-784-139	Sequence 139, App	751	15	62.5	19	13	US-10-155-059-13	Sequence 13, Appl
679	15	62.5	15	18	US-10-645-784-140	Sequence 140, App	752	15	62.5	19	14	US-10-144-929-231	Sequence 231, App
680	15	62.5	15	18	US-10-645-784-141	Sequence 141, App	753	15	62.5	19	14	US-10-225-567A-1318	Sequence 1318, Ap
681	15	62.5	15	18	US-10-645-784-142	Sequence 8, Appli	754	15	62.5	19	14	US-10-300-694A-42	Sequence 42, Appl
682	15	62.5	15	18	US-10-927-262A-8	Sequence 29, Appl	755	15	62.5	19	14	US-10-029-386-28258	Sequence 28258, A
683	15	62.5	15	18	US-10-927-262A-29	Sequence 30, Appl	756	15	62.5	19	14	US-10-029-386-33510	Sequence 33510, A
684	15	62.5	15	18	US-10-927-262A-66	Sequence 66, Appl	757	15	62.5	19	15	US-10-120-885A-45	Sequence 45, Appl
685	15	62.5	15	18	US-10-862-195-2239	Sequence 2239, Ap	758	15	62.5	19	15	US-10-144-929-231	Sequence 231, App
686	15	62.5	15	18	US-10-754-473-30	Sequence 30, Appl	759	15	62.5	19	15	US-10-621-363-289	Sequence 289, App
687	15	62.5	15	20	US-11-051-411-1069	Sequence 1069, Ap	760	15	62.5	19	15	US-10-616-279-9	Sequence 9, Appli
688	15	62.5	15	20	US-11-051-411-1109	Sequence 1109, Ap	761	15	62.5	19	15	US-10-257-864A-100	Sequence 100, App
689	15	62.5	15	20	US-11-051-411-1469	Sequence 1469, Ap	762	15	62.5	19	15	US-10-328-953-14	Sequence 14, Appl
690	15	62.5	16	9	US-09-214-371-39	Sequence 39, Appl	763	15	62.5	19	15	US-10-399-518-129	Sequence 129, App
691	15	62.5	16	9	US-09-214-371-40	Sequence 40, Appl	764	15	62.5	19	16	US-10-624-884-9	Sequence 9, Appli
692	15	62.5	16	9	US-09-214-371-41	Sequence 41, Appl	765	15	62.5	19	16	US-10-754-457-9	Sequence 9, Appli
693	15	62.5	16	9	US-09-019-679-3	Sequence 3, Appli	766	15	62.5	19	16	US-10-399-585-128	Sequence 128, App
694	15	62.5	16	9	US-09-962-805-13	Sequence 13, Appl	767	15	62.5	19	16	US-10-645-085A-100	Sequence 100, App
695	15	62.5	16	9	US-09-813-333-20	Sequence 20, Appl	768	15	62.5	19	17	US-10-895-183-9	Sequence 9, Appli
696	15	62.5	16	10	US-09-825-517A-56	Sequence 56, Appl	769	15	62.5	19	17	US-10-637-317-58	Sequence 58, Appl
697	15	62.5	16	10	US-09-825-517A-105	Sequence 105, App	770	15	62.5	19	17	US-10-866-831-231	Sequence 231, App
698	15	62.5	16	10	US-09-825-517A-130	Sequence 130, App	771	15	62.5	19	17	US-10-947-352-37	Sequence 37, Appl
699	15	62.5	16	10	US-09-825-517A-137	Sequence 137, App	772	15	62.5	19	18	US-10-927-262A-1	Sequence 1, Appli
700	15	62.5	16	13	US-10-044-703-20	Sequence 20, Appl	773	15	62.5	20	9	US-09-735-705-234	Sequence 234, App
701	15	62.5	16	14	US-10-223-047-19	Sequence 19, Appl	774	15	62.5	20	9	US-09-735-705-381	Sequence 234, App
702	15	62.5	16	14	US-10-094-401-220	Sequence 220, App	775	15	62.5	20	9	US-09-850-716A-234	Sequence 234, App
703	15	62.5	16	15	US-10-462-262-188	Sequence 188, App	776	15	62.5	20	9	US-09-850-716A-381	Sequence 381, App
704	15	62.5	16	15	US-10-239-103-20	Sequence 20, Appl	777	15	62.5	20	9	US-09-897-778-234	Sequence 234, App
705	15	62.5	16	16	US-10-467-758-14	Sequence 14, Appl	778	15	62.5	20	9	US-09-897-778-381	Sequence 381, App
706	15	62.5	16	18	US-10-927-262A-39	Sequence 39, Appl	779	15	62.5	20	10	US-09-764-891-4348	Sequence 4348, Ap
707	15	62.5	16	18	US-10-927-262A-40	Sequence 40, Appl	780	15	62.5	20	13	US-10-155-059-8	Sequence 8, Appli
708	15	62.5	16	18	US-10-927-262A-41	Sequence 41, Appl	781	15	62.5	20	13	US-10-155-059-10	Sequence 10, Appl
709	15	62.5	16	20	US-11-045-477-56	Sequence 56, Appl	782	15	62.5	20	13	US-10-155-059-11	Sequence 11, Appl
710	15	62.5	16	20	US-11-045-477-105	Sequence 105, App	783	15	62.5	20	13	US-10-155-059-14	Sequence 14, Appl
711	15	62.5	16	20	US-11-045-477-130	Sequence 130, App	784	15	62.5	20	13	US-10-155-059-15	Sequence 15, Appl
712	15	62.5	16	20	US-11-045-477-137	Sequence 137, App	785	15	62.5	20	13	US-10-155-059-16	Sequence 16, Appl
713	15	62.5	16	20	US-10-280-066-83	Sequence 83, Appl	786	15	62.5	20	13	US-10-155-059-19	Sequence 19, Appl
714	15	62.5	17	14	US-10-029-386-27504	Sequence 27504, A	787	15	62.5	20	13	US-10-155-059-20	Sequence 20, Appl
715	15	62.5	17	14	US-10-029-386-28133	Sequence 28133, A	788	15	62.5	20	14	US-10-007-700-234	Sequence 234, App
716	15	62.5	17	15	US-10-120-885A-44	Sequence 44, Appl	789	15	62.5	20	14	US-10-007-700-381	Sequence 381, App
717	15	62.5	17	16	US-10-258-144-248	Sequence 248, App	790	15	62.5	20	14	US-10-205-428-377	Sequence 377, App
718	15	62.5	17	16	US-10-258-144-258	Sequence 258, App	791	15	62.5	20	14	US-10-162-538-11	Sequence 11, Appl
719	15	62.5	17	16	US-10-258-144-442	Sequence 442, App	792	15	62.5	20	14	US-10-117-982-234	Sequence 234, App
720	15	62.5	17	16	US-10-695-155-155	Sequence 155, App	793	15	62.5	20	14	US-10-117-982-381	Sequence 381, App
721	15	62.5	17	17	US-10-661-156-93	Sequence 93, Appl	794	15	62.5	20	14	US-10-280-066-286	Sequence 286, App
722	15	62.5	17	18	US-10-946-647-66	Sequence 66, Appl	795	15	62.5	20	14	US-10-280-066-316	Sequence 316, App
723	15	62.5	18	9	US-09-214-371-74	Sequence 74, Appl	796	15	62.5	20	14	US-10-280-066-343	Sequence 343, App
724	15	62.5	18	10	US-09-896-841A-48	Sequence 48, Appl	797	15	62.5	20	14	US-10-029-386-33058	Sequence 33058, A
725	15	62.5	18	10	US-09-896-841A-49	Sequence 49, Appl	798	15	62.5	20	15	US-10-329-087-26	Sequence 26, Appl
726	15	62.5	18	14	US-10-225-567A-2147	Sequence 2147, Ap	799	15	62.5	20	15	US-10-329-087-31	Sequence 31, Appl
727	15	62.5	18	14	US-10-187-215-48	Sequence 48, Appl	800	15	62.5	20	15	US-10-313-986-234	Sequence 234, App
728	15	62.5	18	14	US-10-187-215-49	Sequence 49, Appl	801	15	62.5	20	15	US-10-313-986-381	Sequence 381, App
729	15	62.5	18	15	US-10-273-386-48	Sequence 48, Appl	802	15	62.5	20	15	US-10-644-703-14	Sequence 14, Appl
730	15	62.5	18	15	US-10-273-386-49	Sequence 49, Appl	803	15	62.5	20	16	US-10-666-480-5	Sequence 5, Appli
731	15	62.5	18	16	US-10-258-144-268	Sequence 268, App	804	15	62.5	20	16	US-10-467-758-8	Sequence 8, Appli
732	15	62.5	18	16	US-10-258-144-358	Sequence 358, App	805	15	62.5	20	16	US-10-467-758-9	Sequence 9, Appli
733	15	62.5	18	16	US-10-742-379-68	Sequence 68, Appl	806	15	62.5	20	16	US-10-329-087-31	Sequence 31, Appl
734	15	62.5	18	16	US-10-468-655-28	Sequence 28, Appl	807	15	62.5	20	16	US-10-775-972-234	Sequence 234, App
735	15	62.5	18	16	US-10-649-378A-51	Sequence 51, Appl	808	15	62.5	20	16	US-10-775-972-381	Sequence 381, App
736	15	62.5	18	16	US-10-649-378A-52	Sequence 52, Appl	809	15	62.5	20	17	US-10-660-370-154	Sequence 154, App
737	15	62.5	18	16	US-10-423-830-48	Sequence 48, Appl	810	15	62.5	20	17	US-10-661-156-181	Sequence 181, App
738	15	62.5	18	16	US-10-423-830-49	Sequence 49, Appl	811	15	62.5	20	17	US-10-661-156-182	Sequence 182, App
739	15	62.5	18	17	US-10-913-937-8	Sequence 8, Appli	812	15	62.5	20	17	US-10-926-683-1481	Sequence 1481, Ap
740	15	62.5	18	17	US-10-661-156-107	Sequence 107, App	813	15	62.5	20	17	US-10-690-276-394	Sequence 394, App
741	15	62.5	18	18	US-10-927-262A-74	Sequence 74, Appl	814	15	62.5	20	17	US-10-690-276-443	Sequence 443, App

815	15	62.5	20	18	US-10-922-124-234	Sequence 234, App	888	14	58.3	8	15	US-10-260-937-89	Sequence 89, Appl
816	15	62.5	20	18	US-10-922-124-381	Sequence 381, App	889	14	58.3	8	15	US-10-367-580-156	Sequence 156, App
817	15	62.5	20	18	US-10-792-582-456	Sequence 456, App	890	14	58.3	8	15	US-10-367-580-211	Sequence 211, App
818	15	62.5	20	18	US-10-518-358-1	Sequence 1, Appli	891	14	58.3	8	15	US-10-367-593-156	Sequence 156, App
819	15	62.5	20	18	US-10-518-358-2	Sequence 2, Appli	892	14	58.3	8	15	US-10-367-593-211	Sequence 211, App
820	15	62.5	20	18	US-10-518-358-3	Sequence 3, Appli	893	14	58.3	8	15	US-10-367-594-156	Sequence 156, App
821	15	62.5	20	20	US-11-066-697-1366	Sequence 1366, Ap	894	14	58.3	8	15	US-10-367-594-211	Sequence 211, App
822	15	62.5	20	20	US-11-065-970-27	Sequence 27, Appl	895	14	58.3	8	15	US-10-367-654-156	Sequence 156, App
823	15	62.5	20	20	US-11-075-234-257	Sequence 257, App	896	14	58.3	8	15	US-10-367-654-211	Sequence 211, App
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825	14	58.3	5	9	US-09-214-371-2	Sequence 2, Appli	898	14	58.3	8	15	US-10-367-668-156	Sequence 156, App
826	14	58.3	5	9	US-09-281-717-3	Sequence 3, Appli	899	14	58.3	8	15	US-10-367-668-211	Sequence 211, App
827	14	58.3	5	12	US-09-957-806A-226	Sequence 226, App	900	14	58.3	8	15	US-10-440-390-52	Sequence 52, Appl
828	14	58.3	5	15	US-10-436-549-16	Sequence 16, Appl	901	14	58.3	8	16	US-10-440-390-89	Sequence 89, Appl
829	14	58.3	5	15	US-10-126-962-3	Sequence 3, Appli	902	14	58.3	8	16	US-10-367-674-156	Sequence 156, App
830	14	58.3	5	16	US-10-777-053-801	Sequence 801, App	903	14	58.3	8	16	US-10-367-674-211	Sequence 211, App
831	14	58.3	5	16	US-10-337-105-3	Sequence 3, Appli	904	14	58.3	8	16	US-10-712-425-1325	Sequence 1325, Ap
832	14	58.3	5	16	US-10-337-105-4	Sequence 4, Appli	905	14	58.3	8	16	US-10-869-768-5	Sequence 5, Appli
833	14	58.3	5	16	US-10-837-217-801	Sequence 16, Appl	906	14	58.3	8	16	US-10-869-768-6	Sequence 6, Appli
834	14	58.3	5	16	US-10-773-032-16	Sequence 801, App	907	14	58.3	8	16	US-10-869-768-7	Sequence 7, Appli
835	14	58.3	5	17	US-10-927-262A-2	Sequence 16, Appl	908	14	58.3	8	16	US-10-869-768-9	Sequence 9, Appli
836	14	58.3	5	18	US-10-705-165-21	Sequence 21, Appl	909	14	58.3	8	16	US-10-869-768-12	Sequence 12, Appl
837	14	58.3	5	18	US-09-813-153-232	Sequence 232, App	910	14	58.3	8	16	US-10-869-768-14	Sequence 14, Appl
838	14	58.3	6	10	US-09-750-754-27	Sequence 27, Appl	911	14	58.3	8	16	US-10-869-768-18	Sequence 18, Appl
839	14	58.3	6	10	US-09-750-754-28	Sequence 28, Appl	912	14	58.3	8	16	US-10-869-768-19	Sequence 19, Appl
840	14	58.3	6	10	US-09-750-754-30	Sequence 29, Appl	913	14	58.3	8	16	US-10-869-768-20	Sequence 20, Appl
841	14	58.3	6	10	US-09-750-754-29	Sequence 30, Appl	914	14	58.3	8	16	US-10-869-768-21	Sequence 21, Appl
842	14	58.3	6	10	US-09-750-754-30	Sequence 225, App	915	14	58.3	8	16	US-10-869-768-22	Sequence 22, Appl
843	14	58.3	6	12	US-09-957-806A-225	Sequence 2, Appli	916	14	58.3	8	16	US-10-869-768-23	Sequence 23, Appl
844	14	58.3	6	13	US-10-155-059-2	Sequence 84, Appl	917	14	58.3	8	16	US-10-869-768-26	Sequence 26, Appl
845	14	58.3	6	13	US-10-156-820-84	Sequence 30, Appl	918	14	58.3	8	16	US-10-869-768-38	Sequence 38, Appl
846	14	58.3	6	14	US-10-127-691-30	Sequence 249, App	919	14	58.3	8	16	US-10-771-232-1	Sequence 1, Appli
847	14	58.3	6	15	US-10-139-794-249	Sequence 47, Appl	920	14	58.3	8	16	US-10-480-954-2	Sequence 2, Appli
848	14	58.3	6	15	US-10-374-466-47	Sequence 30, Appl	921	14	58.3	8	17	US-10-480-954-4	Sequence 4, Appli
849	14	58.3	6	17	US-10-643-627-30	Sequence 40, Appl	922	14	58.3	8	17	US-10-480-954-6	Sequence 6, Appli
850	14	58.3	6	18	US-10-776-521B-190	Sequence 190, App	923	14	58.3	8	17	US-10-480-954-17	Sequence 17, Appl
851	14	58.3	6	18	US-10-820-067A-696	Sequence 696, App	924	14	58.3	8	17	US-10-480-954-19	Sequence 19, Appl
852	14	58.3	7	9	US-09-884-767A-93	Sequence 93, Appl	925	14	58.3	8	17	US-10-480-954-21	Sequence 21, Appl
853	14	58.3	7	10	US-09-750-754-26	Sequence 26, Appl	926	14	58.3	8	17	US-10-480-954-23	Sequence 23, Appl
854	14	58.3	7	10	US-09-750-754-70	Sequence 79, Appl	927	14	58.3	8	17	US-10-480-954-25	Sequence 25, Appl
855	14	58.3	7	10	US-09-750-754-79	Sequence 61, Appl	928	14	58.3	8	17	US-10-480-954-27	Sequence 27, Appl
856	14	58.3	7	14	US-10-190-082-61	Sequence 253, App	929	14	58.3	8	17	US-10-480-954-31	Sequence 31, Appl
857	14	58.3	7	15	US-10-363-208-253	Sequence 7, Appli	930	14	58.3	8	17	US-10-480-954-58	Sequence 58, Appl
858	14	58.3	7	15	US-10-126-962-7	Sequence 15, Appl	931	14	58.3	8	17	US-10-480-954-60	Sequence 60, Appl
859	14	58.3	7	16	US-10-789-450-15	Sequence 6, Appli	932	14	58.3	8	17	US-10-480-954-62	Sequence 62, Appl
860	14	58.3	7	17	US-10-935-254-6	Sequence 402, App	933	14	58.3	8	17	US-10-480-954-64	Sequence 64, Appl
861	14	58.3	7	17	US-10-607-595-402	Sequence 182, App	934	14	58.3	8	17	US-10-480-954-66	Sequence 66, Appl
862	14	58.3	7	18	US-10-989-462-182	Sequence 93, Appl	935	14	58.3	8	17	US-10-659-207-484	Sequence 484, App
863	14	58.3	7	20	US-11-030-348-93	Sequence 10, Appl	936	14	58.3	8	17	US-10-773-032-1325	Sequence 1325, Ap
864	14	58.3	8	9	US-09-214-371-10	Sequence 14, Appl	937	14	58.3	8	17	US-10-886-165-39	Sequence 39, Appl
865	14	58.3	8	9	US-09-214-371-14	Sequence 16, Appl	938	14	58.3	8	17	US-10-886-165-68	Sequence 68, Appl
866	14	58.3	8	9	US-09-214-371-16	Sequence 23, Appl	939	14	58.3	8	18	US-10-927-262A-10	Sequence 10, Appl
867	14	58.3	8	9	US-09-214-371-23	Sequence 50, Appl	940	14	58.3	8	18	US-10-927-262A-14	Sequence 14, Appl
868	14	58.3	8	9	US-09-214-371-50	Sequence 51, Appl	941	14	58.3	8	18	US-10-927-262A-16	Sequence 16, Appl
869	14	58.3	8	9	US-09-214-371-51	Sequence 53, Appl	942	14	58.3	8	18	US-10-927-262A-23	Sequence 23, Appl
870	14	58.3	8	9	US-09-214-371-53	Sequence 12, Appl	943	14	58.3	8	18	US-10-927-262A-23	Sequence 23, Appl
871	14	58.3	8	14	US-10-209-372-12	Sequence 37, Appl	944	14	58.3	8	18	US-10-927-262A-50	Sequence 50, Appl
872	14	58.3	8	14	US-10-209-372-37	Sequence 43, Appl	945	14	58.3	8	18	US-10-927-262A-51	Sequence 51, Appl
873	14	58.3	8	14	US-10-209-372-43	Sequence 5, Appli	946	14	58.3	8	18	US-10-927-262A-53	Sequence 53, Appl
874	14	58.3	8	14	US-10-072-419-5	Sequence 6, Appli	947	14	58.3	8	18	US-10-927-262A-54	Sequence 54, Appl
875	14	58.3	8	14	US-10-072-419-6	Sequence 7, Appli	948	14	58.3	8	18	US-10-927-262A-57	Sequence 57, Appl
876	14	58.3	8	14	US-10-072-419-7	Sequence 9, Appli	949	14	58.3	8	18	US-10-927-262A-58	Sequence 58, Appl
877	14	58.3	8	14	US-10-072-419-9	Sequence 12, Appl	950	14	58.3	8	18	US-10-927-262A-60	Sequence 60, Appl
878	14	58.3	8	14	US-10-072-419-12	Sequence 14, Appl	951	14	58.3	8	18	US-10-927-262A-61	Sequence 61, Appl
879	14	58.3	8	14	US-10-072-419-14	Sequence 18, Appl	952	14	58.3	8	18	US-10-927-262A-62	Sequence 62, Appl
880	14	58.3	8	14	US-10-072-419-18	Sequence 19, Appl	953	14	58.3	8	18	US-10-938-135A-1	Sequence 1, Appli
881	14	58.3	8	14	US-10-072-419-19	Sequence 20, Appl	954	14	58.3	8	18	US-10-894-106-192	Sequence 192, App
882	14	58.3	8	14	US-10-072-419-20	Sequence 21, Appl	955	14	58.3	8	18	US-10-776-521B-228	Sequence 228, App
883	14	58.3	8	14	US-10-072-419-21	Sequence 22, Appl	956	14	58.3	8	18	US-10-776-521B-237	Sequence 237, App
884	14	58.3	8	14	US-10-072-419-22	Sequence 23, Appl	957	14	58.3	8	18	US-10-776-521B-264	Sequence 264, App
885	14	58.3	8	14	US-10-072-419-23	Sequence 26, Appl	958	14	58.3	8	18	US-10-776-521B-329	Sequence 329, App
886	14	58.3	8	14	US-10-072-419-26	Sequence 38, Appl	959	14	58.3	8	18	US-10-820-067A-135	Sequence 135, App
887	14	58.3	8	14	US-10-072-419-38		960	14	58.3	8	18		

961	14	58.3	8	18	US-10-820-067A-190	Sequence 190, Appl
962	14	58.3	8	18	US-10-820-067A-738	Sequence 738, Appl
963	14	58.3	8	18	US-10-820-067A-747	Sequence 747, Appl
964	14	58.3	8	18	US-10-820-067A-774	Sequence 774, Appl
965	14	58.3	8	18	US-10-820-067A-839	Sequence 839, Appl
966	14	58.3	8	18	US-10-989-462-179	Sequence 179, Appl
967	14	58.3	9	9	US-09-214-371-11	Sequence 11, Appl
968	14	58.3	9	9	US-09-214-371-15	Sequence 15, Appl
969	14	58.3	9	9	US-09-214-371-55	Sequence 55, Appl
970	14	58.3	9	9	US-09-214-371-56	Sequence 56, Appl
971	14	58.3	9	9	US-09-214-371-59	Sequence 59, Appl
972	14	58.3	9	9	US-09-862-260A-9	Sequence 9, Appli
973	14	58.3	9	10	US-09-809-638-42	Sequence 42, Appl
974	14	58.3	9	10	US-09-809-638-427	Sequence 427, App
975	14	58.3	9	10	US-09-938-864-123	Sequence 123, App
976	14	58.3	9	10	US-09-938-864-207	Sequence 207, App
977	14	58.3	9	10	US-09-791-477-123	Sequence 123, App
978	14	58.3	9	10	US-09-791-477-207	Sequence 207, App
979	14	58.3	9	10	US-09-785-019-123	Sequence 123, App
980	14	58.3	9	10	US-09-785-019-207	Sequence 207, App
981	14	58.3	9	10	US-09-898-860-77	Sequence 77, Appl
982	14	58.3	9	10	US-09-870-089B-3	Sequence 3, Appli
983	14	58.3	9	10	US-09-870-089B-7	Sequence 7, Appli
984	14	58.3	9	10	US-09-870-089B-9	Sequence 9, Appli
985	14	58.3	9	13	US-10-046-922-42	Sequence 42, Appl
986	14	58.3	9	13	US-10-114-091-11	Sequence 11, Appl
987	14	58.3	9	14	US-10-125-635A-123	Sequence 123, App
988	14	58.3	9	14	US-10-125-635A-207	Sequence 207, App
989	14	58.3	9	14	US-10-014-340-245	Sequence 245, App
990	14	58.3	9	14	US-10-158-596A-57	Sequence 57, Appl
991	14	58.3	9	14	US-10-157-775B-57	Sequence 57, Appl
992	14	58.3	9	14	US-10-002-603-123	Sequence 123, App
993	14	58.3	9	14	US-10-002-603-207	Sequence 207, App
994	14	58.3	9	14	US-10-281-478-66	Sequence 66, Appl
995	14	58.3	9	14	US-10-254-446A-57	Sequence 57, Appl
996	14	58.3	9	14	US-10-197-954-148	Sequence 148, App
997	14	58.3	9	14	US-10-190-082-613	Sequence 613, App
998	14	58.3	9	14	US-10-155-883B-57	Sequence 57, Appl
999	14	58.3	9	14	US-10-062-109A-372	Sequence 372, App
1000	14	58.3	9	14	US-10-062-109A-380	Sequence 380, App

## ALIGNMENTS

RESULT 1  
 US-10-818-036-24  
 ; Sequence 24, Application US/10818036  
 ; Publication No. US20050222040A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schacter, Bernice Z  
 ; APPLICANT: Schacter, Lee P.  
 ; APPLICANT: Zeldin, Michael H.  
 ; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM  
 ; FILE REFERENCE: 303544.3000-100  
 ; CURRENT APPLICATION NUMBER: US/10/818,036  
 ; CURRENT FILING DATE: 2004-04-05  
 ; NUMBER OF SEQ ID NOS: 38  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 24  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-818-036-24

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RESULT 2
US-10-818-036-27
; Sequence 27, Application US/10818036
; Publication No. US2005022040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)-(8)
; OTHER INFORMATION: AMIDATION
;
US-10-818-036-27

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RESULT 3
US-10-818-036-28
; Sequence 28, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)..(8)
; OTHER INFORMATION: AMIDATION
US-10-818-036-28

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Query Match      70.8%;      Score 17;   DB 18;   Length 8;
Best Local Similarity 40.0%;      Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
      |  |  |
Db      4 FTASW 8

RESULT 4
US-10-818-036-30

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RESULT 4  
US-10-818-036-30

; Sequence 30, Application US/10818036  
; Publication No. US20050222040A1  
; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice Z  
; APPLICANT: Schacter, Lee P.  
; APPLICANT: Zeldin, Michael H.  
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM  
; FILE REFERENCE: 303544.3000-100  
; CURRENT APPLICATION NUMBER: US/10/818,036  
; CURRENT FILING DATE: 2004-04-05  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 30  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-10-818-036-30

Query Match 70.8%; Score 17; DB 18; Length 8;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6  
|  
Db 4 FTASW 8

## RESULT 5

US-10-072-419-3  
; Sequence 3, Application US/10072419  
; Publication No. US20030162717A1  
; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice  
; APPLICANT: Schacter, Lee  
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human  
; FILE REFERENCE: 10739-1  
; CURRENT APPLICATION NUMBER: US/10/072,419  
; CURRENT FILING DATE: 2002-02-07  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Apis mellifera  
US-10-072-419-3

Query Match 70.8%; Score 17; DB 14; Length 9;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6  
|  
Db 4 FTSSW 8

## RESULT 6

US-10-072-419-8  
; Sequence 8, Application US/10072419  
; Publication No. US20030162717A1  
; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice  
; APPLICANT: Schacter, Lee  
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human  
; FILE REFERENCE: 10739-1  
; CURRENT APPLICATION NUMBER: US/10/072,419  
; CURRENT FILING DATE: 2002-02-07  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8

; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Vanessa cardui  
US-10-072-419-8

Query Match 70.8%; Score 17; DB 14; Length 9;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6  
|  
Db 4 FTSSW 8

## RESULT 7

US-10-869-768-3  
; Sequence 3, Application US/10869768  
; Publication No. US20040224898A1  
; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice  
; APPLICANT: Schacter, Lee  
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human  
; FILE REFERENCE: 10739-1  
; CURRENT APPLICATION NUMBER: US/10/869,768  
; CURRENT FILING DATE: 2004-06-16  
; PRIOR APPLICATION NUMBER: US 10/072,419  
; PRIOR FILING DATE: 2002-02-07  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Apis mellifera  
US-10-869-768-3

Query Match 70.8%; Score 17; DB 16; Length 9;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6  
|  
Db 4 FTSSW 8

## RESULT 8

US-10-869-768-8  
; Sequence 8, Application US/10869768  
; Publication No. US20040224898A1  
; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice  
; APPLICANT: Schacter, Lee  
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human  
; FILE REFERENCE: 10739-1  
; CURRENT APPLICATION NUMBER: US/10/869,768  
; CURRENT FILING DATE: 2004-06-16  
; PRIOR APPLICATION NUMBER: US 10/072,419  
; PRIOR FILING DATE: 2002-02-07  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Vanessa cardui  
US-10-869-768-8

Query Match 70.8%; Score 17; DB 16; Length 9;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6  
|  
Db 4 FTSSW 8

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RESULT 9
US-10-818-036-14
; Sequence 14, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-818-036-14

Query Match      70.8%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
Db      4 FTASW 8

RESULT 10
US-10-818-036-15
; Sequence 15, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-818-036-15

Query Match      70.8%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
Db      4 FTASW 8

RESULT 11
US-10-818-036-23
; Sequence 23, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 23
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Manduca sexta
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: AMIDATION
US-10-818-036-23

Query Match      70.8%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
Db      4 FTSSW 8

RESULT 12
US-10-818-036-25
; Sequence 25, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-818-036-25

Query Match      70.8%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
Db      4 FTASW 8

RESULT 13
US-10-818-036-26
; Sequence 26, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 9
; TYPE: PRT
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; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (9)..(9)  
; OTHER INFORMATION: AMIDATION  
US-10-818-036-26

Query Match 70.8%; Score 17; DB 18; Length 9;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |  
Db 4 FTASW 8

## RESULT 14

US-10-818-036-29  
; Sequence 29, Application US/10818036  
; Publication No. US2005022040A1

; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice Z  
; APPLICANT: Schacter, Lee P.  
; APPLICANT: Zeldin, Michael H.  
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM  
; FILE REFERENCE: 303544.3000-100  
; CURRENT APPLICATION NUMBER: US/10/818,036  
; CURRENT FILING DATE: 2004-04-05  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 29

; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID

; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (9)..(9)  
; OTHER INFORMATION: AMIDATION  
US-10-818-036-29

Query Match 70.8%; Score 17; DB 18; Length 9;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |  
Db 4 FTASW 8

## RESULT 15

US-09-842-776A-28  
; Sequence 28, Application US/09842776A  
; Publication No. US20040023316A1

; GENERAL INFORMATION:  
; APPLICANT: CONNEX GMBH  
; TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS  
; TITLE OF INVENTION: IN THE STOOL

; FILE REFERENCE: 41735  
; CURRENT APPLICATION NUMBER: US/09/842,776A  
; CURRENT FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: PCT/EP99/08212  
; PRIOR FILING DATE: 1999-10-29  
; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Complementarity determining region (CDR1) of an  
; OTHER INFORMATION: antibody heavy chain directed to a beta-urease  
; OTHER INFORMATION: epitope (alternative sequence)  
US-09-842-776A-28

Query Match 70.8%; Score 17; DB 11; Length 10;  
Best Local Similarity 40.0%; Pred. No. 6.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |  
Db 4 FSTSW 8

## RESULT 16

US-10-996-316-139  
; Sequence 139, Application US/10996316  
; Publication No. US20050129690A1

; GENERAL INFORMATION:  
; APPLICANT: Alexion Pharmaceuticals, Inc.  
; APPLICANT: Bowdish, Katherine S.  
; APPLICANT: McWhirter, John  
; APPLICANT: Kretz-Rommel, Anke  
; TITLE OF INVENTION: POLYPEPTIDES AND ANTIBODIES DERIVED FROM CHRONIC LYMPHOCYTIC  
; TITLE OF INVENTION: LEUKEMIA CELLS AND USES THEREOF  
; FILE REFERENCE: 60 CIP IV (1087-43 CIP IV)  
; CURRENT APPLICATION NUMBER: US/10/996,316  
; CURRENT FILING DATE: 2004-11-23  
; PRIOR APPLICATION NUMBER: US 10/894,672  
; PRIOR FILING DATE: 2004-07-20  
; PRIOR APPLICATION NUMBER: US 10/736,188  
; PRIOR FILING DATE: 2003-12-15  
; PRIOR APPLICATION NUMBER: US 10/379,151  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: PCT/US01/47931  
; PRIOR FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: US 60/254,113  
; PRIOR FILING DATE: 2000-12-08  
; NUMBER OF SEQ ID NOS: 211  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 139  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: murine  
US-10-996-316-139

Query Match 70.8%; Score 17; DB 18; Length 10;  
Best Local Similarity 40.0%; Pred. No. 6.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |  
Db 4 FSAAW 8

## RESULT 17

US-10-072-419-37  
; Sequence 37, Application US/10072419  
; Publication No. US20030162717A1

; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice  
; APPLICANT: Schacter, Lee  
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Huma

; FILE REFERENCE: 10739-1  
; CURRENT APPLICATION NUMBER: US/10/072,419  
; CURRENT FILING DATE: 2002-02-07  
; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 37  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Vanessa cardui

US-10-072-419-37

Query Match 70.8%; Score 17; DB 14; Length 11;  
Best Local Similarity 40.0%; Pred. No. 6.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
| |  
Db 4 FTSSW 8

RESULT 18

US-10-869-768-37  
; Sequence 37, Application US/10869768  
; Publication No. US20040224898A1  
; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice  
; APPLICANT: Schacter, Lee  
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Huma  
; FILE REFERENCE: 10739-1  
; CURRENT APPLICATION NUMBER: US/10/869,768  
; CURRENT FILING DATE: 2004-06-16  
; PRIOR APPLICATION NUMBER: US 10/072,419  
; PRIOR FILING DATE: 2002-02-07  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 37  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Vanessa cardui  
US-10-869-768-37

Query Match 70.8%; Score 17; DB 16; Length 11;  
Best Local Similarity 40.0%; Pred. No. 6.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
| |  
Db 4 FTSSW 8

RESULT 19

US-10-354-240-87  
; Sequence 87, Application US/10354240  
; Publication No. US20030185847A1  
; GENERAL INFORMATION:  
; APPLICANT: Sone, Toshio  
; APPLICANT: Kume, Akinori  
; APPLICANT: Dairiki, Kazuo  
; APPLICANT: Iwama, Akiko  
; APPLICANT: Kino, Kohsuke  
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disea  
; FILE REFERENCE: SPO-103D1  
; CURRENT APPLICATION NUMBER: US/10/354,240  
; CURRENT FILING DATE: 2003-01-29  
; PRIOR APPLICATION NUMBER: PCT/JP97/00740  
; PRIOR FILING DATE: 1997-03-10  
; PRIOR APPLICATION NUMBER: US 09/142,524  
; PRIOR FILING DATE: 1998-09-09  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 87  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Cryptomeria japonica  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(15)  
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 4  
US-10-354-240-87

Query Match 70.8%; Score 17; DB 14; Length 15;  
Best Local Similarity 40.0%; Pred. No. 8e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
| |  
Db 9 FSTAW 13

RESULT 20

US-10-354-240-88  
; Sequence 88, Application US/10354240  
; Publication No. US20030185847A1  
; GENERAL INFORMATION:  
; APPLICANT: Sone, Toshio  
; APPLICANT: Kume, Akinori  
; APPLICANT: Dairiki, Kazuo  
; APPLICANT: Iwama, Akiko  
; APPLICANT: Kino, Kohsuke  
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disea  
; FILE REFERENCE: SPO-103D1  
; CURRENT APPLICATION NUMBER: US/10/354,240  
; CURRENT FILING DATE: 2003-01-29  
; PRIOR APPLICATION NUMBER: PCT/JP97/00740  
; PRIOR FILING DATE: 1997-03-10  
; PRIOR APPLICATION NUMBER: US 09/142,524  
; PRIOR FILING DATE: 1998-09-09  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 88  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Cryptomeria japonica  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(15)  
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 5  
US-10-354-240-88

Query Match 70.8%; Score 17; DB 14; Length 15;  
Best Local Similarity 40.0%; Pred. No. 8e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
| |  
Db 4 FSTAW 8

RESULT 21

US-09-963-339-10  
; Sequence 10, Application US/09963339  
; Publication No. US20030049700A1  
; GENERAL INFORMATION:  
; APPLICANT: Bandaru, Rajasekhar  
; TITLE OF INVENTION: 22108 AND 47916, NOVEL HUMAN THIOREDOXIN  
; TITLE OF INVENTION: FAMILY MEMBERS AND USES THEREOF  
; FILE REFERENCE: 10448-090001  
; CURRENT APPLICATION NUMBER: US/09/963,339  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 60/235,049  
; PRIOR FILING DATE: 2000-09-25  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-963-339-10

Query Match 70.8%; Score 17; DB 10; Length 19;  
Best Local Similarity 40.0%; Pred. No. 9.3e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
| |



Db 4 FSATW 8

RESULT 22

US-10-145-586-59

Sequence 59, Application US/10145586

Publication No. US20030138890A1

GENERAL INFORMATION:

APPLICANT: Alexandra Glucksmann, Maria

APPLICANT: Silos-Santiago, Inmaculada

APPLICANT: M. Galvin, Katherine

APPLICANT: Weich, Nadine

APPLICANT: Curtis, Rory A.J.

APPLICANT: Bandaru, Rajasekhar

APPLICANT: Kapeller-Libermann, Rosana

TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS,

TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LEUCINE-RICH

TITLE OF INVENTION: REPEAT FAMILY MEMBERS, AND HUMAN RINGFINGER FAMILY MEMBER

FILE REFERENCE: 10448-188001

CURRENT APPLICATION NUMBER: US/10/145,586

CURRENT FILING DATE: 2002-05-14

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 95

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 59

LENGTH: 19

TYPE: PRT

ORGANISM: Homo sapiens

US-10-145-586-59

Query Match 70.8%; Score 17; DB 14; Length 19;

Best Local Similarity 40.0%; Pred. No. 9.3e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6

Db 4 FSATW 8

RESULT 23

US-10-931-260-265

Sequence 265, Application US/10931260

Publication No. US20050152927A1

GENERAL INFORMATION:

APPLICANT: Griffith, Irwin J.;

Pollock, Joanne;

Bond, Julian F.;

Garman, Richard D.;

Kuo, Mei-Chang;

Powers, Stephen P.;

Exley, Mark A.;

Chen, Xian;

Shaked, Ze'ev

TITLE OF INVENTION: Allergenic Proteins And Peptides From

NUMBER OF SEQUENCES: 283

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lahive & Cockfield, LLP

STREET: 28 State St

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/931,260

FILING DATE: 30-Aug-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/240,203

FILING DATE: 29-Jan-1999

APPLICATION NUMBER: 08/467,023

FILING DATE: 1995-JUN-06

APPLICATION NUMBER: 08/350,225

FILING DATE: 1994-DEC-06

APPLICATION NUMBER: 08/226,248

FILING DATE: 1994-APR-08

APPLICATION NUMBER: PCT/US93/00139

FILING DATE: 1993-JAN-15

APPLICATION NUMBER: 07/938,990

FILING DATE: 1992-SEP-01

APPLICATION NUMBER: 07/730,452

FILING DATE: 1991-JUL-15

APPLICATION NUMBER: 07/729,134

FILING DATE: 1991-JUL-12

APPLICATION NUMBER: 07/975,179

FILING DATE: 1992-NOV-12

APPLICATION NUMBER: PCT/US92/05661

FILING DATE: 1992-JUL-10

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras, Esq.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IMI-028CD2CCPA2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 742-4214

INFORMATION FOR SEQ ID NO: 265:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 265:

US-10-931-260-265

Query Match 70.8%; Score 17; DB 18; Length 20;

Best Local Similarity 40.0%; Pred. No. 9.6e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6

Db 12 FSTAW 16

RESULT 24

US-10-190-082-36

Sequence 36, Application US/10190082

Publication No. US20030148264A1

GENERAL INFORMATION:

APPLICANT: Lasky, Lawrence A.

APPLICANT: Sidhu, Sachdev S.

APPLICANT: Held, Heike A.

TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS

FILE REFERENCE: P1905R1

CURRENT APPLICATION NUMBER: US/10/190,082

CURRENT FILING DATE: 2002-07-03

PRIOR APPLICATION NUMBER: US 60/303,634

PRIOR FILING DATE: 2001-07-06

NUMBER OF SEQ ID NOS: 683

SEQ ID NO 36

LENGTH: 6

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: Synthetic

US-10-190-082-36

Query Match 66.7%; Score 16; DB 14; Length 6;

Best Local Similarity 40.0%; Pred. No. 1.6e+06;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
|  
Db 1 FSDTW 5

RESULT 25

US-09-774-639-284  
; Sequence 284, Application US/09774639  
; Publication No. US20030003555A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 90 Human Secreted Proteins  
; FILE REFERENCE: P2013P1  
; CURRENT APPLICATION NUMBER: US/09/774,639  
; CURRENT FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04  
; NUMBER OF SEQ ID NOS: 371  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 284  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-774-639-284

Query Match 66.7%; Score 16; DB 10; Length 7;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
|  
Db 2 FGTSW 6

RESULT 26

US-09-969-730-267  
; Sequence 267, Application US/09969730  
; Publication No. US2003005443A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 90 Human Secreted Proteins  
; FILE REFERENCE: P2013P2  
; CURRENT APPLICATION NUMBER: US/09/969,730  
; CURRENT FILING DATE: 2001-10-04  
; PRIOR APPLICATION NUMBER: 09/774,639  
; PRIOR FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: 60/238,291  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 09/244,112  
; PRIOR FILING DATE: 1999-02-04  
; PRIOR APPLICATION NUMBER: PCT/US98/16235  
; PRIOR FILING DATE: 1998-08-04  
; PRIOR APPLICATION NUMBER: 60/056,371  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,732  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,366  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,364  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,370  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,367  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,365  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,731  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,557  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,563  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/055,970

; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/055,986  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/055,311  
; PRIOR FILING DATE: 1997-08-05  
; PRIOR APPLICATION NUMBER: 60/054,808  
; PRIOR FILING DATE: 1997-08-05  
; PRIOR APPLICATION NUMBER: 60/054,803  
; PRIOR FILING DATE: 1997-08-05  
; PRIOR APPLICATION NUMBER: 60/054,804  
; PRIOR FILING DATE: 1997-08-05  
; PRIOR APPLICATION NUMBER: 60/054,809  
; PRIOR FILING DATE: 1997-08-05  
; PRIOR APPLICATION NUMBER: 60/054,806  
; PRIOR FILING DATE: 1997-08-05  
; PRIOR APPLICATION NUMBER: 60/055,310  
; PRIOR FILING DATE: 1997-08-05  
; PRIOR APPLICATION NUMBER: 60/054,798  
; PRIOR FILING DATE: 1997-08-05  
; PRIOR APPLICATION NUMBER: 60/055,309  
; PRIOR FILING DATE: 1997-08-05  
; PRIOR APPLICATION NUMBER: 60/055,312  
; PRIOR FILING DATE: 1997-08-05  
; PRIOR APPLICATION NUMBER: 60/054,807  
; PRIOR FILING DATE: 1997-08-05  
; PRIOR APPLICATION NUMBER: 60/055,386  
; PRIOR FILING DATE: 1997-08-05  
; NUMBER OF SEQ ID NOS: 373  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 267  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-969-730-267

Query Match 66.7%; Score 16; DB 10; Length 7;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
|  
Db 2 FGTSW 6

RESULT 27

US-10-046-922-48  
; Sequence 48, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Koivunen, Erkki  
; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 48  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: peptide  
US-10-046-922-48

Query Match 66.7%; Score 16; DB 13; Length 7;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
|  
Db 3 FEAW 7

RESULT 28  
US-10-621-363-267  
; Sequence 267, Application US/10621363  
; Publication No. US20040023283A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 90 Human Secreted Proteins  
; FILE REFERENCE: P2013P2C1  
; CURRENT APPLICATION NUMBER: US/10/621,363  
; CURRENT FILING DATE: 2003-07-18  
; PRIOR APPLICATION NUMBER: 09/969,730  
; PRIOR FILING DATE: 2001-10-06  
; PRIOR APPLICATION NUMBER: 09/774,639  
; PRIOR FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: 60/238,291  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 09/244,112  
; PRIOR FILING DATE: 1999-02-04  
; PRIOR APPLICATION NUMBER: PCT/US98/16235  
; PRIOR FILING DATE: 1998-08-04  
; PRIOR APPLICATION NUMBER: 60/056,371  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,732  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,366  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,364  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,370  
; PRIOR FILING DATE: 1997-08-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 373  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 267  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-621-363-267

Query Match 66.7%; Score 16; DB 15; Length 7;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 2 FGTSW 6

RESULT 29  
US-10-072-419-4  
; Sequence 4, Application US/10072419  
; Publication No. US20030162717A1  
; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice  
; APPLICANT: Schacter, Lee  
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human  
; FILE REFERENCE: 10739-1  
; CURRENT APPLICATION NUMBER: US/10/072,419  
; CURRENT FILING DATE: 2002-02-07  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Schistocerca gregaria  
US-10-072-419-4

Query Match 66.7%; Score 16; DB 14; Length 8;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|

Db 4 FSTGW 8  
RESULT 30  
US-10-072-419-11  
; Sequence 11, Application US/10072419  
; Publication No. US20030162717A1  
; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice  
; APPLICANT: Schacter, Lee  
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human  
; FILE REFERENCE: 10739-1  
; CURRENT APPLICATION NUMBER: US/10/072,419  
; CURRENT FILING DATE: 2002-02-07  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 11  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Locusta migratoria  
US-10-072-419-11

Query Match 66.7%; Score 16; DB 14; Length 8;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 4 FSAGW 8

RESULT 31  
US-10-072-419-15  
; Sequence 15, Application US/10072419  
; Publication No. US20030162717A1  
; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice  
; APPLICANT: Schacter, Lee  
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human  
; FILE REFERENCE: 10739-1  
; CURRENT APPLICATION NUMBER: US/10/072,419  
; CURRENT FILING DATE: 2002-02-07  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 15  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Phymateus leprosus  
US-10-072-419-15

Query Match 66.7%; Score 16; DB 14; Length 8;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 4 FSTGW 8

RESULT 32  
US-10-072-419-24  
; Sequence 24, Application US/10072419  
; Publication No. US20030162717A1  
; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice  
; APPLICANT: Schacter, Lee  
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human  
; FILE REFERENCE: 10739-1  
; CURRENT APPLICATION NUMBER: US/10/072,419  
; CURRENT FILING DATE: 2002-02-07  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 24

```
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Gryllobates sigillatus
US-10-072-419-24
Query Match      66.7%; Score 16; DB 14; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 FXXW 6
Db      4 FSTGW 8

RESULT 33
US-10-072-419-25
; Sequence 25, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 25
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Libaniasidus vittatus
US-10-072-419-25
Query Match      66.7%; Score 16; DB 14; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 FXXW 6
Db      4 FSTGW 8

RESULT 34
US-10-072-419-30
; Sequence 30, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 30
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Onitis sp.
US-10-072-419-30
Query Match      66.7%; Score 16; DB 14; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 FXXW 6
Db      4 FSTGW 8

RESULT 35
US-10-367-580-260
; Sequence 260, Application US/10367580
```

```
; Publication No. US20040071720A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461061
; CURRENT APPLICATION NUMBER: US/10/367,580
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/794,832
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 260
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-580-260
```

```
Query Match      66.7%; Score 16; DB 15; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      2 FXXW 6
Db      2 FLSSW 6
```

```
RESULT 36
US-10-367-580-264
; Sequence 264, Application US/10367580
; Publication No. US20040071720A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461061
; CURRENT APPLICATION NUMBER: US/10/367,580
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/794,832
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 264
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: synthetic peptide
US-10-367-580-264

Query Match      66.7%; Score 16; DB 15; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
      |
Db      2 FLSSW 6

RESULT 37
US-10-367-593-260
; Sequence 260, Application US/10367593
; Publication No. US20040071721A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461012
; CURRENT APPLICATION NUMBER: US/10/367,593
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 260
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-593-260

Query Match      66.7%; Score 16; DB 15; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
      |
Db      2 FLSSW 6

RESULT 38
US-10-367-593-264
; Sequence 264, Application US/10367593
; Publication No. US20040071721A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461012
; CURRENT APPLICATION NUMBER: US/10/367,593
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
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; OTHER INFORMATION: synthetic peptide
US-10-367-593-264

Query Match      66.7%; Score 16; DB 15; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
      |
Db      2 FLSSW 6

RESULT 39
US-10-367-594-260
; Sequence 260, Application US/10367594
; Publication No. US20040071722A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461041
; CURRENT APPLICATION NUMBER: US/10/367,594
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/680,806
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 260
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-594-260

Query Match      66.7%; Score 16; DB 15; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXXW 6
      |
Db      2 FLSSW 6

RESULT 40
US-10-367-594-264
; Sequence 264, Application US/10367594
; Publication No. US20040071722A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
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; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461041
; CURRENT APPLICATION NUMBER: US/10/367,594
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/680,806
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: wordPerfect 8.0 for Windows
; SEQ ID NO 264
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-594-264

Query Match      66.7%  Score 16;  DB 15;  Length 8;
Best Local Similarity 40.0%  Pred. No. 1.6e+06;
Matches 2;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;

QY      2 FXXW 6
      |
Db      2 FLSSW 6

Search completed: October 18, 2005, 16:17:19
Job time : 116.412 secs
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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:44:54 ; Search time 24.3529 Seconds  
(without alignments)  
35.558 Million cell updates/sec

Title: US-09-214-371-11  
Perfect score: 24  
Sequence: 1 XFXXXXXXX 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3886

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : PIR\_79:.\*  
1: Pirl:.\*  
2: pirl:.\*  
3: pirl:.\*  
4: pirl:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score		Query		DB	ID	Description
	Match	Length	Match	Length			
1	17	70.8	9	2	A24244		adipokinetic hormo
2	16	66.7	8	2	A28004		adipokinetic hormo
3	16	66.7	10	2	A31571		hypertrehalosemic/
4	15	62.5	8	2	S10596		adipokinetic hormo
5	15	62.5	9	2	D57444		neuropeptide Grb-A
6	15	62.5	10	2	T17063		cytochrome-c oxida
7	15	62.5	10	2	T12325		cytochrome-c oxida
8	15	62.5	10	2	S53789		neuropeptide Pec-H
9	15	62.5	15	2	PH1613		Ig H chain V-D-J r
10	15	62.5	17	2	A34704		protein-tyrosine k
11	15	62.5	20	2	S77981		cytochrome-c oxida
12	15	62.5	20	2	PN0171		peptidylprolyl iso
13	15	62.5	20	2	PH1380		alpha-amylase (EC
14	14	58.3	8	2	A33995		adipokinetic hormo
15	14	58.3	8	2	A44960		neuropeptide Led-C
16	14	58.3	8	2	B44960		neuropeptide Led-C
17	14	58.3	8	2	A58620		adipokinetic hormo
18	14	58.3	8	2	S11545		adipokinetic hormo
19	14	58.3	8	2	S55310		adipokinetic hormo
20	14	58.3	8	2	A61348		red pigment-concen
21	14	58.3	8	2	S08995		hypertrehalosemic
22	14	58.3	8	2	S08996		hypertrehalosemic
23	14	58.3	8	2	A49823		adipokinetic hormo
24	14	58.3	8	2	B49823		adipokinetic hormo
25	14	58.3	8	2	A43976		hypertrehalosemic
26	14	58.3	8	2	B43976		hypertrehalosemic
27	14	58.3	8	2	A05169		neuropeptide M-I -
28	14	58.3	10	2	B33995		hypotrehalosemic h
29	14	58.3	10	2	S08997		hypertrehalosemic

30	14	58.3	10	2	A60421		hypertrehalosemic
31	14	58.3	10	2	S08998		hypertrehalosemic
32	14	58.3	10	2	A26381		hypertrehalosemic
33	14	58.3	10	2	JC1416		hypertrehalosemic
34	14	58.3	10	2	S09138		hypertrehalosemic
35	14	58.3	10	2	C39191		hypothetical prote
36	14	58.3	10	2	PT0322		Ig heavy chain CRD
37	14	58.3	10	2	T17066		cytochrome-c oxida
38	14	58.3	10	2	T17069		cytochrome-c oxida
39	14	58.3	10	2	T12329		cytochrome-c oxida
40	14	58.3	12	2	PT0274		Ig heavy chain CRD
41	14	58.3	12	2	PH1324		Ig heavy chain DJ
42	14	58.3	13	2	PC4391		cysteine proteinas
43	14	58.3	16	2	C37290		homeotic protein G
44	14	58.3	19	2	S32675		nitrogen fixation
45	14	58.3	20	2	PC1240		calcium-binding pr
46	13	54.2	9	2	PT0288		Ig heavy chain CRD
47	13	54.2	9	2	I46023		growth hormone rec
48	13	54.2	11	2	C53652		rhlR protein - pse
49	13	54.2	11	2	PT0302		Ig heavy chain CRD
50	12	50.0	8	2	T13818		cytochrome oxidase
51	12	50.0	10	1	RHLMGS		gonadoliberin - se
52	12	50.0	11	2	S05002		corazonin - Americ
53	12	50.0	18	2	S39009		oviductin - golden
54	11	45.8	3	3	F37196		bradykinin-potenti
55	11	45.8	4	2	A34626		RPH-related neuro
56	11	45.8	4	2	B53284		T-cell receptor be
57	11	45.8	4	2	PT0661		T-cell receptor be
58	11	45.8	5	2	A32516		cholecystokinin-5
59	11	45.8	5	2	A60803		neuropeptide - sea
60	11	45.8	5	2	JH0253		gut pentapeptide -
61	11	45.8	5	2	PT0281		Ig heavy chain CRD
62	11	45.8	5	2	PT0308		Ig heavy chain CRD
63	11	45.8	5	2	PT0729		T-cell receptor be
64	11	45.8	5	2	PT0580		T-cell receptor be
65	11	45.8	5	2	G37196		bradykinin-potenti
66	11	45.8	6	2	S66195		alcohol dehydrogen
67	11	45.8	6	2	B34835		dnaA protein - Pse
68	11	45.8	6	2	A31263		dihydrofolate redu
69	11	45.8	6	2	B31263		dihydrofolate redu
70	11	45.8	6	2	B35640		cerebellar degener
71	11	45.8	6	2	PT0629		T-cell receptor be
72	11	45.8	6	2	PT0532		T-cell receptor be
73	11	45.8	6	2	PT0519		T-cell receptor be
74	11	45.8	6	2	PT0637		T-cell receptor be
75	11	45.8	6	2	PT0641		T-cell receptor be
76	11	45.8	6	2	PT0726		T-cell receptor be
77	11	45.8	6	2	F41946		T-cell receptor ga
78	11	45.8	6	2	PD0028		pev-kinin 2 - pena
79	11	45.8	6	2	A61068		locustakinin - mig
80	11	45.8	6	4	I79564		hypothetical TCL3
81	11	45.8	7	2	S21230		dermorphin (Trp-4,
82	11	45.8	7	2	S09652		hypothetical prote
83	11	45.8	7	2	PQ0727		H2 class I protein
84	11	45.8	7	2	E48394		glycoprotein compo
85	11	45.8	7	2	PH1602		Ig H chain V-D-J r
86	11	45.8	7	2	PT0526		T-cell receptor be
87	11	45.8	7	2	PT0628		T-cell receptor be
88	11	45.8	7	2	PT0642		T-cell receptor be
89	11	45.8	7	2	PT0722		T-cell receptor be
90	11	45.8	7	2	PT0688		T-cell receptor be
91	11	45.8	7	2	PT0586		T-cell receptor be
92	11	45.8	7	2	PT0728		T-cell receptor be
93	11	45.8	7	2	PX0008		glucuronosyltransf
94	11	45.8	7	2	B48394		major fat-globule
95	11	45.8	7	2	PD0029		pev-kinin 1 - pena
96	11	45.8	7	2	PN0649		pullulanase (EC 3.
97	11	45.8	7	2	S57274		triacylglycerol li
98	11	45.8	7	2	S33244		neuromodulatory pe
99	11	45.8	7	2	S33245		neuromodulatory pe
100	11	45.8	7	2	S33246		neuromodulatory pe
101	11	45.8	7	2	S33567		tubulin beta-3 cha
102	11	45.8	7	2	A58512		venom heptapeptide



103	11	45.8	7	2	A61081	tryptophyllin, bas
104	11	45.8	7	4	I55382	hypothetical pepti
105	11	45.8	7	4	A58725	virotaxin - destro
106	11	45.8	8	2	S15422	adipokinetic hormo
107	11	45.8	8	2	A58641	adipokinetic hormo
108	11	45.8	8	2	PQ0012	cholecystokinin -
109	11	45.8	8	2	A43001	cholecystokinin -
110	11	45.8	8	2	PT0724	T-cell receptor be
111	11	45.8	8	2	A38887	T-cell receptor ga
112	11	45.8	8	2	A59495	Vesicle associated
113	11	45.8	8	2	S19288	acylase - Kluyvera
114	11	45.8	8	2	A39308	glycine reductase
115	11	45.8	8	2	C61512	variant surface gl
116	11	45.8	8	2	D61512	variant surface gl
117	11	45.8	8	2	JS0315	leucokinin V - Mad
118	11	45.8	8	2	JS0316	leucokinin VI - Ma
119	11	45.8	8	2	JS0317	leucokinin VII - M
120	11	45.8	8	2	JS0318	leucokinin VIII -
121	11	45.8	8	2	S21663	neuropeptide - flo
122	11	45.8	8	2	A41117	acetylcholinestera
123	11	45.8	8	2	A31570	angiotensin-conver
124	11	45.8	9	1	AKLQIM	locustamyo inhibiti
125	11	45.8	9	2	S07205	litorin 2-Glu - Au
126	11	45.8	9	2	S07204	litorin I - Austr
127	11	45.8	9	2	S07241	litorin - Rohde's
128	11	45.8	9	2	A61357	phyllocaerulein -
129	11	45.8	9	2	JS0302	xenopsin-related p
130	11	45.8	9	2	A60320	xenopsin-related p
131	11	45.8	9	2	PT0231	Ig heavy chain CDR
132	11	45.8	9	2	PT0270	Ig heavy chain CDR
133	11	45.8	9	2	PT0272	Ig heavy chain CDR
134	11	45.8	9	2	PT0299	Ig heavy chain CDR
135	11	45.8	9	2	PT0324	Ig heavy chain CDR
136	11	45.8	9	2	PT0634	T-cell receptor be
137	11	45.8	9	2	PT0562	T-cell receptor be
138	11	45.8	9	2	I58350	gene c-mpl protein
139	11	45.8	9	2	S78426	52.5K protein - sp
140	11	45.8	9	2	S56004	glucan 1,3-beta-gl
141	11	45.8	9	2	A43848	cell surface adhes
142	11	45.8	9	2	A57444	neuropeptide Grb-A
143	11	45.8	9	2	B57444	neuropeptide Grb-A
144	11	45.8	9	2	C57444	neuropeptide Grb-A
145	11	45.8	9	2	A37027	macrophage chemota
146	11	45.8	9	2	QDRB	delta sleep-induci
147	11	45.8	9	2	A60522	sperm-activating p
148	11	45.8	10	1	XASNPC	angiotensin-conver
149	11	45.8	10	1	XAVI6B	angiotensin-conver
150	11	45.8	10	1	RHPGG	gonadoliberin - pi
151	11	45.8	10	1	RHSHG	gonadoliberin - sh
152	11	45.8	10	1	A61126	gonadoliberin - sp
153	11	45.8	10	1	RHAQ1	gonadoliberin I -
154	11	45.8	10	1	RHAQ2	gonadoliberin II -
155	11	45.8	10	2	S71868	glutathione transf
156	11	45.8	10	2	B46030	gonadoliberin II -
157	11	45.8	10	2	JCL367	thyroliberin poten
158	11	45.8	10	2	A60647	neuromedin C - bov
159	11	45.8	10	2	PQ0177	neuromedin C - lau
160	11	45.8	10	2	A61337	caerulein - frog (
161	11	45.8	10	2	A13687	caerulein-like pep
162	11	45.8	10	2	S59625	beta-galactosidase
163	11	45.8	10	2	PQ0753	beta-fructofuranos
164	11	45.8	10	2	S63696	DNA polymerase - Y
165	11	45.8	10	2	A49187	gonadotropin-relea
166	11	45.8	10	2	A35556	hypothetical prote
167	11	45.8	10	2	PT0245	Ig heavy chain CDR
168	11	45.8	10	2	PT0289	Ig heavy chain CDR
169	11	45.8	10	2	PT0310	Ig heavy chain CDR
170	11	45.8	10	2	PH1344	Ig heavy chain DJ
171	11	45.8	10	2	S23370	T-cell receptor al
172	11	45.8	10	2	E49033	T-cell receptor ga
173	11	45.8	10	2	F49033	T-cell receptor ga
174	11	45.8	10	2	E41946	T-cell receptor ga
175	11	45.8	10	2	C41946	T-cell receptor ga

176	11	45.8	10	2	B38887	T-cell receptor ga
177	11	45.8	10	2	PH0916	T-cell receptor be
178	11	45.8	10	2	PH0923	T-cell receptor be
179	11	45.8	10	2	A40753	aldehyde ferredoxi
180	11	45.8	10	2	A59272	peptide-N4-(N-acet
181	11	45.8	10	2	S66248	processing enzyme,
182	11	45.8	10	2	A27617	triose-phosphate i
183	11	45.8	10	2	A46030	gonadoliberin I -
184	11	45.8	10	2	A21114	gonadoliberin - ch
185	11	45.8	10	2	B37196	bradykinin-potent
186	11	45.8	10	2	H37196	bradykinin-potent
187	11	45.8	10	2	F33932	Ig mu chain J regi
188	11	45.8	10	2	T17054	cytochrome-c oxida
189	11	45.8	10	2	T17075	cytochrome-c oxida
190	11	45.8	10	2	T13976	cytochrome-c oxida
191	11	45.8	10	2	T17057	cytochrome-c oxida
192	11	45.8	10	2	T12303	cytochrome-c oxida
193	11	45.8	10	2	T14019	cytochrome-c oxida
194	11	45.8	10	2	T17060	cytochrome-c oxida
195	11	45.8	10	2	T14043	cytochrome-c oxida
196	11	45.8	10	2	T14054	cytochrome-c oxida
197	11	45.8	10	2	T12308	cytochrome-c oxida
198	11	45.8	10	2	T17072	cytochrome-c oxida
199	11	45.8	10	2	T12312	cytochrome-c oxida
200	11	45.8	10	2	T12316	cytochrome-c oxida
201	11	45.8	10	2	T14212	cytochrome-c oxida
202	11	45.8	10	2	T12321	cytochrome-c oxida
203	11	45.8	10	2	T14215	cytochrome-c oxida
204	11	45.8	10	2	T14223	cytochrome-c oxida
205	11	45.8	10	2	T14219	cytochrome-c oxida
206	11	45.8	10	2	A59173	cytochrome-c oxida
207	11	45.8	10	2	S39030	lysyl-bradykinin -
208	11	45.8	11	1	LFTWWE	probable trypsin lea
209	11	45.8	11	2	S66196	alcohol dehydrogen
210	11	45.8	11	2	B49164	chromogranin-B - r
211	11	45.8	11	2	S32575	ribosomal protein
212	11	45.8	11	2	H54346	pyruvate synthase
213	11	45.8	11	2	PT0249	Ig heavy chain CRD
214	11	45.8	11	2	PT0273	Ig heavy chain CRD
215	11	45.8	11	2	PH1343	Ig heavy chain DJ
216	11	45.8	11	2	S68649	spermadhesin AQN-3
217	11	45.8	11	2	A33571	folliculin - bovi
218	11	45.8	11	2	D41946	T-cell receptor ga
219	11	45.8	11	2	B41946	T-cell receptor ga
220	11	45.8	11	2	C38887	T-cell receptor ga
221	11	45.8	11	2	I41946	T-cell receptor ga
222	11	45.8	11	2	A49037	TCR gamma V-J regi
223	11	45.8	11	2	B49037	TCR gamma V-J regi
224	11	45.8	11	2	C49037	TCR gamma V-J regi
225	11	45.8	11	2	S70338	napin small chain
226	11	45.8	11	2	C59151	protein-tyrosine k
227	11	45.8	11	2	JQ2307	hypothetical 1.5K
228	11	45.8	11	2	JQ2317	hypothetical 1.5K
229	11	45.8	11	2	PQ0731	unidentified 5.7/3
230	11	45.8	11	2	S45698	gamma-MSH-like pro
231	11	45.8	11	2	A34662	Achataina cardio-ex
232	11	45.8	11	2	A59146	conotoxin ausa - c
233	11	45.8	11	2	B59146	conotoxin ausb - c
234	11	45.8	11	2	T12264	cytochrome-c oxida
235	11	45.8	11	2	T12253	cytochrome-c oxida
236	11	45.8	11	2	T12244	cytochrome-c oxida
237	11	45.8	11	2	T12248	cytochrome-c oxida
238	11	45.8	11	2	T17081	cytochrome-c oxida
239	11	45.8	11	2	T17078	cytochrome-c oxida
240	11	45.8	12	1	UOGM2	urotensin II - lon
241	11	45.8	12	1	A53709	alpha-conotoxin Im
242	11	45.8	12	2	A29169	phospholipase A2 (
243	11	45.8	12	2	I64829	gene HEXA protein
244	11	45.8	12	2	JS0423	urotensin II-A pep
245	11	45.8	12	2	S42765	urotensin II - tel
246	11	45.8	12	2	PH1675	Ig heavy chain V r
247	11	45.8	12	2	S26548	T-cell receptor be
248	11	45.8	12	2	S26553	T-cell receptor be

249	11	45.8	12	2	A26093	microbial collagen
250	11	45.8	12	2	G54003	hypothetical prote
251	11	45.8	12	2	S69123	proton-translocati
252	11	45.8	12	2	A40763	sucrose-6-phosphat
253	11	45.8	12	2	PH1308	Ig heavy chain DJ
254	11	45.8	12	2	S43957	Ig mu chain V regi
255	11	45.8	12	2	A49033	T-cell receptor de
256	11	45.8	12	2	B49033	T-cell receptor de
257	11	45.8	12	2	S25039	Ig heavy chain V r
258	11	45.8	12	2	H41946	T-cell receptor ga
259	11	45.8	12	2	A42324	cytochrome P450c27
260	11	45.8	12	2	I57678	gene rPLP-A protei
261	11	45.8	12	2	I41235	glutamine-tRNA lig
262	11	45.8	12	2	J50424	urotensin II-B pep
263	11	45.8	12	2	A49637	MHC class II histo
264	11	45.8	12	2	I77529	estrogen receptor
265	11	45.8	12	2	S43170	kinesin light chai
266	11	45.8	12	2	PN0046	ATP synthase D cha
267	11	45.8	12	2	I58273	thyroglobulin - ra
268	11	45.8	12	2	PQ0776	NADH2 dehydrogenas
269	11	45.8	13	1	XAVI9B	angiotensin-conver
270	11	45.8	13	1	MTCMAD	melanotropin alpha
271	11	45.8	13	1	MTHOAD	melanotropin alpha
272	11	45.8	13	2	PQ0445	urotensin II - lau
273	11	45.8	13	2	PH1676	Ig heavy chain V r
274	11	45.8	13	2	B28810	glutathione transf
275	11	45.8	13	2	PT0293	Ig heavy chain CRD
276	11	45.8	13	2	PT0304	Ig heavy chain CRD
277	11	45.8	13	2	S57567	T cell receptor V-
278	11	45.8	13	2	S23372	T-cell receptor al
279	11	45.8	13	2	PH0138	T-cell-specific tr
280	11	45.8	13	2	S61798	dipeptidyl-peptida
281	11	45.8	13	2	B56864	Ig kappa-1 chain,
282	11	45.8	13	2	B25448	Ig H chain V-D-J r
283	11	45.8	13	2	PH1636	Ig H chain V-D-J r
284	11	45.8	13	2	PH1620	Ig heavy chain C r
285	11	45.8	13	2	G37266	Ig heavy chain C r
286	11	45.8	13	2	D37267	Ig heavy chain J r
287	11	45.8	13	2	B26406	Ig kappa chain J r
288	11	45.8	13	2	PH0928	T-cell receptor be
289	11	45.8	13	2	A47630	Ig kappa chain J r
290	11	45.8	13	2	I51905	collecting duct wa
291	11	45.8	13	2	S54344	glyceraldehyde-3-p
292	11	45.8	13	2	A59491	epithelial dog all
293	11	45.8	13	2	I54984	aeg-46.5 protein -
294	11	45.8	13	2	PC2369	unidentified 85K p
295	11	45.8	13	2	S60046	early nodulin 40 -
296	11	45.8	13	2	A61514	glutathione transf
297	11	45.8	13	2	A60379	factor X activator
298	11	45.8	13	2	S32551	glutathione transf
299	11	45.8	13	2	S66558	serine proteinase
300	11	45.8	13	2	A86126	hypothetical prote
301	11	45.8	13	2	A60409	bombesin-like pept
302	11	45.8	13	2	A05174	tryptophyllin-13 -
303	11	45.8	14	1	BSTD	bombesin - fire-be
304	11	45.8	14	1	QMVHXX	mastoparan X - hor
305	11	45.8	14	1	QMWAPP	polistes mastopara
306	11	45.8	14	1	LFEBWC	trp operon leader
307	11	45.8	14	1	LFEBWT	trp operon leader
308	11	45.8	14	1	LFECW	trp operon leader
309	11	45.8	14	2	PC2373	probable IMP dehyd
310	11	45.8	14	2	A60622	somatostatin - spo
311	11	45.8	14	2	A60840	somatostatin I - E
312	11	45.8	14	2	C60414	somatostatin - sli
313	11	45.8	14	2	B60842	somatostatin I - c
314	11	45.8	14	2	S00172	somatostatin I - s
315	11	45.8	14	2	PH1677	Ig heavy chain V r
316	11	45.8	14	2	PH1705	proteochondoitin c
317	11	45.8	14	2	PT0077	trp operon leader
318	11	45.8	14	2	E90858	trp operon leader
319	11	45.8	14	2	B85761	hypothetical prote
320	11	45.8	14	2	A35105	homeotic protein E
321	11	45.8	14	2	PC1215	

322	11	45.8	14	2	S03530	Ig heavy chain J r
323	11	45.8	14	2	I54284	Cl-inhibitor - hum
324	11	45.8	14	2	PT0223	Ig heavy chain CDR
325	11	45.8	14	2	PH1348	Ig heavy chain DJ
326	11	45.8	14	2	PH1327	Ig heavy chain DJ
327	11	45.8	14	2	PH1356	Ig heavy chain DJ
328	11	45.8	14	2	PH1332	Ig heavy chain DJ
329	11	45.8	14	2	PH1322	Ig heavy chain DJ
330	11	45.8	14	2	PH1757	T cell receptor al
331	11	45.8	14	2	PH1758	T cell receptor al
332	11	45.8	14	2	PH1759	T cell receptor al
333	11	45.8	14	2	PH1766	T cell receptor al
334	11	45.8	14	2	PH1767	T cell receptor al
335	11	45.8	14	2	PH1768	T cell receptor al
336	11	45.8	14	2	PH1769	T cell receptor al
337	11	45.8	14	2	S57572	T cell receptor V-
338	11	45.8	14	2	S58426	spermadhesin AWN h
339	11	45.8	14	2	PH1625	Ig H chain V-D-J r
340	11	45.8	14	2	PH1626	Ig H chain V-D-J r
341	11	45.8	14	2	PH1627	Ig H chain V-D-J r
342	11	45.8	14	2	PH1594	Ig H chain V-D-J r
343	11	45.8	14	2	PH0801	T-cell receptor al
344	11	45.8	14	2	PH0747	T-cell receptor be
345	11	45.8	14	2	F49037	TcR delta chain V-
346	11	45.8	14	2	B44854	L-2,4-diaminobutyr
347	11	45.8	14	2	PT0026	calotropin DI - mu
348	11	45.8	14	2	S33801	chaperone, TCPI-re
349	11	45.8	14	2	S33802	chaperone, TCPI-re
350	11	45.8	14	2	PT0029	karatsin - karata
351	11	45.8	14	2	S14336	mastoparan B - hor
352	11	45.8	14	2	A47421	leukotriene B-4 12
353	11	45.8	14	2	S68095	calcium-binding pr
354	11	45.8	14	2	S39931	S-allele-associate
355	11	45.8	14	2	A44515	Trp EG leader pept
356	11	45.8	14	2	JH0328	probursin tetradec
357	11	45.8	15	2	B26997	unspecific monoocy
358	11	45.8	15	2	A26997	unspecific monoocy
359	11	45.8	15	2	PQ0195	Sfli-glycoprotein
360	11	45.8	15	2	PQ0174	stylar glycoprotei
361	11	45.8	15	2	PQ0175	stylar glycoprotei
362	11	45.8	15	2	S21202	glucan 1,4-alpha-g
363	11	45.8	15	2	S21240	alpha-glucosidase
364	11	45.8	15	2	S21241	oligo-1,6-glucosid
365	11	45.8	15	2	S24159	leukocyte elastase
366	11	45.8	15	2	PQ0232	cystatin CI-4a - m
367	11	45.8	15	2	PH1319	Ig heavy chain DJ
368	11	45.8	15	2	S26791	Ig heavy chain V r
369	11	45.8	15	2	PS0382	Ig heavy chain J r
370	11	45.8	15	2	S39012	proteinase - Therm
371	11	45.8	15	2	T46625	hypothetical prote
372	11	45.8	15	2	S08209	hypothetical prote
373	11	45.8	15	2	PQ0750	self-incompatibili
374	11	45.8	15	2	B56891	gamma 2 gliadin -
375	11	45.8	15	2	S10388	Ig heavy chain J r
376	11	45.8	15	2	S10386	Ig heavy chain J r
377	11	45.8	15	2	A47628	Fc gamma receptor
378	11	45.8	15	2	PH1365	Ig heavy chain DJ
379	11	45.8	15	2	PH1366	Ig heavy chain DJ
380	11	45.8	15	2	PH1342	Ig heavy chain DJ
381	11	45.8	15	2	PH1318	Ig heavy chain DJ
382	11	45.8	15	2	PH1320	Ig heavy chain DJ
383	11	45.8	15	2	S43956	Ig mu chain V regi
384	11	45.8	15	2	PH1762	T cell receptor al
385	11	45.8	15	2	PH1788	T cell receptor al
386	11	45.8	15	2	G49655	T-cell-receptor be
387	11	45.8	15	2	PQ0073	T-cell receptor be
388	11	45.8	15	2	A45103	7 alpha-hydroxy-4-
389	11	45.8	15	2	PH1616	Ig H chain V-D-J r
390	11	45.8	15	2	PH1590	Ig H chain V-D-J r
391	11	45.8	15	2	PH1612	Ig H chain V-D-J r
392	11	45.8	15	2	PH0782	T-cell receptor al
393	11	45.8	15	2	E49037	TcR delta chain V-
394	11	45.8	15	2	PL0109	complement factor

395	11	45.8	15	2	S02381	probable membrane	468	11	45.8	17	2	PH1357	Ig heavy chain DJ
396	11	45.8	15	2	PH0216	agarase (EC 3.2.1.1.	469	11	45.8	17	2	PH1630	Ig H chain V-D-J r
397	11	45.8	15	2	S21411	modulation protein	470	11	45.8	17	2	PS0384	Ig heavy chain J r
398	11	45.8	15	2	S33781	acetolactate synth	471	11	45.8	17	2	A46592	lactase-phlorizin
399	11	45.8	15	2	B60763	endo-1,3-beta-gluc	472	11	45.8	17	2	A44560	terephthalate 1,2-
400	11	45.8	15	2	A48372	benzoyl-CoA ligase	473	11	45.8	17	2	A27636	cytotoxin B - Clos
401	11	45.8	15	2	T09463	ribosomal protein	474	11	45.8	17	2	A38824	tachyplesin I - ho
402	11	45.8	15	2	PA0036	glycine cleavage s	475	11	45.8	17	2	JX0125	tachyplesin III -
403	11	45.8	15	2	PA0099	phenotypic variati	476	11	45.8	17	2	PC1318	large granule L6 c
404	11	45.8	15	2	PX0031	mixed lymphocyte r	477	11	45.8	17	2	S10786	enamelin, 26K - bo
405	11	45.8	15	2	C84035	hypothetical prote	478	11	45.8	17	2	I53392	CD33 antigen homol
406	11	45.8	15	4	I38032	hypothetical MN1/T	479	11	45.8	17	2	I67524	CD33 antigen homol
407	11	45.8	16	1	A49761	locustapyrokinin -	480	11	45.8	17	2	I67526	CD33 antigen homol
408	11	45.8	16	1	MTDFBS	melanotropin beta	481	11	45.8	17	2	A61211	anantin - Streptom
409	11	45.8	16	2	E41425	cytochrome P450 IF	482	11	45.8	17	2	B48943	phage antigenic de
410	11	45.8	16	2	S03405	hydrogenase (EC 1.	483	11	45.8	17	2	E59137	protein Pfd3 - gol
411	11	45.8	16	2	I57530	gene c-fms protein	484	11	45.8	17	2	A29834	trp leader peptide
412	11	45.8	16	2	A60551	leukocyte elastase	485	11	45.8	18	1	MTDFBC	melanotropin beta
413	11	45.8	16	2	A29541	little gastrin - C	486	11	45.8	18	1	MTHOB	melanotropin beta
414	11	45.8	16	2	S03532	Ig heavy chain J r	487	11	45.8	18	2	S29379	sorbitol dehydroge
415	11	45.8	16	2	D49021	Ig heavy chain J7	488	11	45.8	18	2	S24780	protein-tyrosine k
416	11	45.8	16	2	A36300	T-cell receptor ga	489	11	45.8	18	2	S74195	epoxide hydrolase
417	11	45.8	16	2	PS0383	Ig heavy chain J r	490	11	45.8	18	2	G02018	proteasome chain L
418	11	45.8	16	2	S26746	Ig heavy chain J r	491	11	45.8	18	2	S04229	N4-(beta-N-acetyl
419	11	45.8	16	2	S66613	protein p12E - Fri	492	11	45.8	18	2	D49570	plasma membrane ca
420	11	45.8	16	2	S28213	glutathione transf	493	11	45.8	18	2	S43834	DNA topoisomerase
421	11	45.8	16	2	PT0237	Ig heavy chain CDR	494	11	45.8	18	2	PH1368	Ig heavy chain DJ
422	11	45.8	16	2	PT0282	Ig heavy chain CDR	495	11	45.8	18	2	PH1323	Ig heavy chain DJ
423	11	45.8	16	2	PT0296	Ig heavy chain CDR	496	11	45.8	18	2	S03528	Ig heavy chain J1
424	11	45.8	16	2	PH1346	Ig heavy chain DJ	497	11	45.8	18	2	A32220	T-cell receptor de
425	11	45.8	16	2	S23184	redoxendonuclease	498	11	45.8	18	2	A25941	Ig heavy chain J-H
426	11	45.8	16	2	PH1637	Ig H chain V-D-J r	499	11	45.8	18	2	S29264	ovoheremerythrin - d
427	11	45.8	16	2	PH1638	Ig H chain V-D-J r	500	11	45.8	18	2	S55501	thrombospondin pre
428	11	45.8	16	2	PH1604	Ig H chain V-D-J r	501	11	45.8	18	2	S52125	gamma2-gliadin P25
429	11	45.8	16	2	A48839	T-cell receptor al	502	11	45.8	18	2	C56211	progesterone recep
430	11	45.8	16	2	PH0748	T-cell receptor be	503	11	45.8	18	2	S46418	Nr1L protein - cur
431	11	45.8	16	2	D49037	TCR delta chain V-	504	11	45.8	18	2	I40062	shikimate 5-dehydr
432	11	45.8	16	2	A46236	transforming prote	505	11	45.8	18	2	S21669	1H-4-oxoquinoline
433	11	45.8	16	2	S33589	beta-crystallin A4	506	11	45.8	18	2	T03799	leader peptide trp
434	11	45.8	16	2	B44820	7K protein - Esche	507	11	45.8	18	2	S19914	choline O-acetyltr
435	11	45.8	16	2	PC1299	subtilisin (EC 3.4	508	11	45.8	18	2	I52623	hypothetical prote
436	11	45.8	16	2	A24099	crystal protein, 2	509	11	45.8	18	2	PT0239	Ig heavy chain CDR
437	11	45.8	16	2	T44936	calmodulin kinase	510	11	45.8	18	2	PT0286	Ig heavy chain CDR
438	11	45.8	16	2	A20190	hypoermin B - ear	511	11	45.8	18	2	PH1349	Ig heavy chain DJ
439	11	45.8	16	2	A48630	bothrojaracin - ja	512	11	45.8	18	2	PH1350	Ig heavy chain DJ
440	11	45.8	16	2	I37452	protein kinase - h	513	11	45.8	18	2	S43958	Ig mu chain V regi
441	11	45.8	16	2	S13898	alkaline phosphata	514	11	45.8	18	2	A40256	interleukin-7 rece
442	11	45.8	16	2	B23692	transcription fact	515	11	45.8	18	2	I35141	T-cell receptor de
443	11	45.8	16	2	E37290	homeotic protein G	516	11	45.8	18	2	C49254	TCR C gamma 1 chai
444	11	45.8	16	2	S05703	homeotic protein c	517	11	45.8	18	2	G49037	TCR delta chain V-
445	11	45.8	16	4	I79565	hypothetical TCL3/	518	11	45.8	18	2	A61577	24k serine protein
446	11	45.8	17	1	GMSH	gastrin - sheep	519	11	45.8	18	2	S20322	gluten - wheat
447	11	45.8	17	2	S66198	alcohol dehydrogen	520	11	45.8	18	2	JU0124	polyphemusin I - A
448	11	45.8	17	2	A60071	gastrin - rhesus m	521	11	45.8	18	2	JU0125	polyphemusin II -
449	11	45.8	17	2	S24570	Ig heavy chain J r	522	11	45.8	18	2	A35678	hypothetical prote
450	11	45.8	17	2	H49048	T-cell receptor be	523	11	45.8	18	2	S27141	hypothetical prote
451	11	45.8	17	2	I49048	T-cell receptor be	524	11	45.8	18	2	A24749	neuropeptide A - b
452	11	45.8	17	2	S03531	Ig heavy chain J5	525	11	45.8	19	1	EWSMAN	ancovenin - Strept
453	11	45.8	17	2	S26747	Ig heavy chain J r	526	11	45.8	19	2	A28702	cytochrome P450-C-
454	11	45.8	17	2	S26744	Ig heavy chain J r	527	11	45.8	19	2	I49422	L-lactate dehydrog
455	11	45.8	17	2	B44873	caldesmon - rabbit	528	11	45.8	19	2	S71871	glutathione transf
456	11	45.8	17	2	I57941	beta 3-adrenergic	529	11	45.8	19	2	I45957	protein kinase (EC
457	11	45.8	17	2	I51910	SP-A2 - human (fra	530	11	45.8	19	2	PC1251	testin II - rat (f
458	11	45.8	17	2	A41053	glutamate receptor	531	11	45.8	19	2	S60633	H+-transporting tw
459	11	45.8	17	2	E40442	integrase homolog	532	11	45.8	19	2	PH1304	Ig heavy chain DJ
460	11	45.8	17	2	S18534	hypothetical prote	533	11	45.8	19	2	PT0244	Ig heavy chain CDR
461	11	45.8	17	2	B44923	carboxypeptidase 3	534	11	45.8	19	2	G49048	T-cell receptor be
462	11	45.8	17	2	S19614	globin - polychaet	535	11	45.8	19	2	PH1307	Ig heavy chain DJ
463	11	45.8	17	2	S03533	Ig heavy chain J r	536	11	45.8	19	2	S43960	Ig mu chain V regi
464	11	45.8	17	2	PT0234	Ig heavy chain CRD	537	11	45.8	19	2	A28814	Ig kappa chain V r
465	11	45.8	17	2	PT0235	Ig heavy chain CRD	538	11	45.8	19	2	I53673	amyloid protein -
466	11	45.8	17	2	PH1367	Ig heavy chain DJ	539	11	45.8	19	2	B61409	genome polyprotein
467	11	45.8	17	2	PH1331	Ig heavy chain DJ	540	11	45.8	19	2	PX0062	beta-galactoside-b

541	11	45.8	19	2	S02269	glycogen(starch) s
542	11	45.8	19	2	B56613	virion morphogenes
543	11	45.8	19	2	S63489	dissimilatory sulf
544	11	45.8	19	2	T50329	wd-repeat protein
545	11	45.8	19	2	S60110	hypothetical prote
546	11	45.8	19	2	PH1352	Ig heavy chain DJ
547	11	45.8	19	2	PH1353	Ig heavy chain DJ
548	11	45.8	19	2	PH1339	Ig heavy chain DJ
549	11	45.8	19	2	PH1315	Ig heavy chain DJ
550	11	45.8	19	2	PH1330	Ig heavy chain DJ
551	11	45.8	19	2	S57515	T cell receptor be
552	11	45.8	19	2	S57516	T cell receptor be
553	11	45.8	19	2	S03519	T-cell receptor ga
554	11	45.8	19	2	I46654	T-cell receptor de
555	11	45.8	19	2	PH1624	Ig H chain V-D-J r
556	11	45.8	19	2	PH0793	T-cell receptor al
557	11	45.8	19	2	I49037	TcR delta chain V-
558	11	45.8	19	2	B46592	lactase-phlorizin
559	11	45.8	19	2	A48354	nonstructural prot
560	11	45.8	19	2	I40063	shikimate 5-dehydr
561	11	45.8	19	2	A44854	L-2,4-diaminobuty
562	11	45.8	19	2	S29212	protein C - oat (f
563	11	45.8	19	2	S19532	globin - polychaet
564	11	45.8	19	2	S19613	globin - polychaet
565	11	45.8	19	2	JX0124	tachyplesin I prec
566	11	45.8	19	2	I52721	gene hMLH1 protein
567	11	45.8	19	2	S12268	Qa-2 antigen - mou
568	11	45.8	19	2	A60505	hemoglobin Cl beta
569	11	45.8	19	2	A58700	actagardine [valid
570	11	45.8	19	4	I54264	rhodopsin single b
571	11	45.8	20	2	A23739	cytochrome P450 MU
572	11	45.8	20	2	S21176	testosterone 6beta
573	11	45.8	20	2	A60728	cytochrome P450 3A
574	11	45.8	20	2	B61080	5-carboxymethyl-2-
575	11	45.8	20	2	B37520	glutathione transf
576	11	45.8	20	2	S29099	glutathione transf
577	11	45.8	20	2	S29100	glutathione transf
578	11	45.8	20	2	S71869	glutathione transf
579	11	45.8	20	2	S30381	glutathione transf
580	11	45.8	20	2	PQ0751	self-incompatibili
581	11	45.8	20	2	PH0111	style glycoprotein
582	11	45.8	20	2	PH0110	style glycoprotein
583	11	45.8	20	2	PC2347	base nonspecific a
584	11	45.8	20	2	S33787	pancreatic elastas
585	11	45.8	20	2	A56900	chymotrypsin I (EC
586	11	45.8	20	2	B61333	chymotrypsin (EC 3
587	11	45.8	20	2	I49423	cytotoxic T-lympho
588	11	45.8	20	2	S46205	comosain (EC 3.4.2
589	11	45.8	20	2	S46204	anana (EC 3.4.22
590	11	45.8	20	2	C54052	phosphoribosyl-AMP
591	11	45.8	20	2	A37111	ribulose-bisphosph
592	11	45.8	20	2	C49164	chromogranin-B - r
593	11	45.8	20	2	PT0248	Ig heavy chain CDR
594	11	45.8	20	2	F49048	T-cell receptor be
595	11	45.8	20	2	A49048	T-cell receptor be
596	11	45.8	20	2	PL0192	Ig lambda 2 chain
597	11	45.8	20	2	S39049	cytotoxin-binding
598	11	45.8	20	2	B33761	actin - Acanthamo
599	11	45.8	20	2	A05313	apolipoprotein A-I
600	11	45.8	20	2	A36045	thrombospondin hom
601	11	45.8	20	2	S03335	photosystem II pho
602	11	45.8	20	2	PW0003	chlorophyll a/b-bi
603	11	45.8	20	2	S04988	gag core shell pro
604	11	45.8	20	2	A44773	pollen allergen I
605	11	45.8	20	2	A60372	pollen allergen Po
606	11	45.8	20	2	D37396	pollen allergen Fe
607	11	45.8	20	2	I64036	hypothetical prote
608	11	45.8	20	2	T46626	hypothetical prote
609	11	45.8	20	2	SL6202	pyrrolidine-5-carbox
610	11	45.8	20	2	D25507	proteinase inhibit
611	11	45.8	20	2	PC1152	equinotoxin 1D - s
612	11	45.8	20	2	S10876	hypothetical prote
613	11	45.8	20	2	S58382	hypothetical prote

614	11	45.8	20	2	PH1358	Ig heavy chain DJ
615	11	45.8	20	2	PH1341	Ig heavy chain DJ
616	11	45.8	20	2	PH1326	Ig heavy chain DJ
617	11	45.8	20	2	PC2248	lambda 112 protein
618	11	45.8	20	2	S60350	kallikrein, pankre
619	11	45.8	20	2	S15861	estrogen receptor
620	11	45.8	20	2	A38689	1-phosphatidylinos
621	11	45.8	20	2	PQ0071	T-cell receptor be
622	11	45.8	20	2	S56756	link protein - rat
623	11	45.8	20	2	S68341	procathepsin L - g
624	11	45.8	20	2	S66222	defensin AMP2 - Da
625	11	45.8	20	2	C56894	intracrystalline c
626	11	45.8	20	2	D84716	hypothetical prote
627	11	45.8	20	2	T44453	acetyl-CoA synthet
628	11	45.8	20	2	A44927	major outer membra
629	11	45.8	20	2	S45637	oxidoreductase - P
630	11	45.8	20	2	S63490	dissimilatory sulf
631	11	45.8	20	2	A40451	dormancy-related p
632	11	45.8	20	2	S29636	jacalin beta-I cha
633	11	45.8	20	2	S29635	jacalin beta chain
634	11	45.8	20	2	S03987	agglutinin beta-2
635	11	45.8	20	2	S35460	alliin lyase (EC 4
636	11	45.8	20	2	PC2084	serine proteinase
637	11	45.8	20	2	S38763	S-adenosyl-L-methi
638	11	45.8	20	2	A34817	collagenolytic pro
639	11	45.8	20	2	A56899	serum heterodimer,
640	11	45.8	20	2	A47105	dystroglycan - chi
641	11	45.8	20	2	A61506	alpha-1-antitrypsi
642	11	45.8	20	2	A56894	intracrystalline c
643	11	45.8	20	2	B56894	intracrystalline c
644	11	45.8	20	2	A85659	hypothetical prote
645	11	45.8	20	2	AE0120	insertion element
646	11	45.8	20	2	AC0269	probable trp opero
647	11	45.8	20	2	B60505	hemoglobin A1-2 be
648	11	45.8	20	2	S08605	hypothetical prote
649	11	45.8	20	2	S27142	hypothetical prote
650	11	45.8	20	2	DIRT	dental fluid tra
651	8	33.3	12	2	A28856	fructose-bisphosph
652	7	29.2	15	2	E41383	23K variable hight
653	7	29.2	20	2	I70108	microsomal triglyc
654	6	25.0	3	3	S68328	blood cell protein
655	6	25.0	4	1	ECXAA	antho-Ramide neur
656	6	25.0	4	2	D41654	hypothetical prote
657	6	25.0	4	2	S53508	starvation-induced
658	6	25.0	4	2	A25844	autho-RF amide neu
659	6	25.0	4	2	S39390	myosin-light-chain
660	6	25.0	4	2	JQ1273	neuropeptide Antho
661	6	25.0	4	2	A35779	neuropeptide Antho
662	6	25.0	4	2	A60418	FMRFamide - polych
663	6	25.0	4	2	A32480	achatin-I - giant
664	6	25.0	4	2	ECNK	cardioexcitatory n
665	6	25.0	5	2	A44955	alkanal monooxygen
666	6	25.0	5	2	S70615	endo-1,4-beta-xyla
667	6	25.0	5	2	P50324	ribulose-bisphosph
668	6	25.0	5	2	B45525	actin I - malaria
669	6	25.0	5	2	B61445	Leu-enkephalin - b
670	6	25.0	5	2	A61445	Met-enkephalin - b
671	6	25.0	5	2	B61168	cocoonase (EC 3.4.
672	6	25.0	5	2	PT0278	Ig heavy chain CRD
673	6	25.0	5	2	A44692	fulicin - giant Af
674	6	25.0	5	2	JS0319	subesophageal gang
675	6	25.0	5	2	PT0644	T-cell receptor be
676	6	25.0	5	4	A58728	serrawettin W2 - S
677	6	25.0	6	2	A61049	halo-toxin - Pseud
678	6	25.0	6	2	A60986	N-formyl oligopept
679	6	25.0	6	2	S11024	hydrogensulfite re
680	6	25.0	6	2	I51317	bHLH transcription
681	6	25.0	6	2	I37263	Y protein - human
682	6	25.0	6	2	I59142	platelet-derived g
683	6	25.0	6	2	A41946	T-cell receptor ga
684	6	25.0	6	2	A27696	contraction-inhibi
685	6	25.0	6	2	B27696	contraction-inhibi
686	6	25.0	6	2	A43129	neuropeptide GNFR

687	6	25.0	7	1	NYPG7	hypothalamic hepta	760	6	25.0	9	2	S36850	Ig heavy chain V r
688	6	25.0	7	1	A61324	dermorphin - Rohde	761	6	25.0	9	2	G41946	T-cell receptor ga
689	6	25.0	7	2	A60224	Met-enkephalin-Arg	762	6	25.0	9	2	A42266	peptidylglycine mo
690	6	25.0	7	2	S36662	dermorphin (Lys-7)	763	6	25.0	9	2	I52974	seminal vesicle pr
691	6	25.0	7	2	PH1408	Ig heavy chain V r	764	6	25.0	9	2	S39767	cardioactive pepti
692	6	25.0	7	2	B39127	phosphotransferase	765	6	25.0	9	2	S39040	lysine-conopressin
693	6	25.0	7	2	I40504	hypothetical prote	766	6	25.0	9	2	G58502	kidney and bladder
694	6	25.0	7	2	H33098	180K exoantigen -	767	6	25.0	9	2	S19523	orf AB protein - S
695	6	25.0	7	2	S68004	hucolin, 75K chain	768	6	25.0	9	2	A31576	xylose isomerase (
696	6	25.0	7	2	E33932	Ig mu chain D regi	769	6	25.0	9	2	S13333	alpha/beta-gliadin
697	6	25.0	7	2	PT0665	T-cell receptor be	770	6	25.0	9	2	PC2021	oxytocin-related p
698	6	25.0	7	2	A59489	protein kinase C i	771	6	25.0	9	2	A26363	cardioactive pepti
699	6	25.0	7	2	B35890	RNA-directed DNA p	772	6	25.0	9	2	A61620	locustamyotropin I
700	6	25.0	7	2	A25269	sex pheromone CAM3	773	6	25.0	9	2	S27233	cardioactive pepti
701	6	25.0	7	2	A30812	sex pheromone cCF1	774	6	25.0	9	2	A41978	calliFMRFamide 1 -
702	6	25.0	7	2	S17976	glucose isomerase	775	6	25.0	9	2	A44787	calliFMRFamide 10
703	6	25.0	7	2	PC2132	FMRFamide-related	776	6	25.0	9	2	D44787	calliFMRFamide 13
704	6	25.0	7	2	B44787	calliFMRFamide 11	777	6	25.0	9	2	B41978	calliFMRFamide 2 -
705	6	25.0	7	2	S08606	hypothetical prote	778	6	25.0	9	2	C41978	calliFMRFamide 3 -
706	6	25.0	8	2	A32523	peptidyl-dipeptida	779	6	25.0	9	2	D41978	calliFMRFamide 4 -
707	6	25.0	8	2	PH1407	Ig heavy chain V r	780	6	25.0	9	2	E41978	calliFMRFamide 5 -
708	6	25.0	8	2	PL0184	capsid protein VP-	781	6	25.0	9	2	F41978	calliFMRFamide 6 -
709	6	25.0	8	2	PA0032	protein QA300040 -	782	6	25.0	9	2	G41978	calliFMRFamide 7 -
710	6	25.0	8	2	S13661	polygalacturonase	783	6	25.0	9	2	S10920	venom protein HR-3
711	6	25.0	8	2	B33099	158K exoantigen -	784	6	25.0	9	2	JN0027	[Phe-6]-mosact - s
712	6	25.0	8	2	A39892	P element, P cytot	785	6	25.0	9	2	B20569	serum amyloid P-co
713	6	25.0	8	2	B45800	serum albumin - do	786	6	25.0	9	2	S77984	cytochrome-c oxida
714	6	25.0	8	2	A42057	fibroblast growth	787	6	25.0	9	2	PT0080	60K Ca binding pro
715	6	25.0	8	2	PC4372	T-cell receptor al	788	6	25.0	9	2	A61386	macrophage inhibit
716	6	25.0	8	2	S66296	telomeric and tetr	789	6	25.0	9	2	B39504	octamer-binding pr
717	6	25.0	8	2	S66296	Na+-transporting A	790	6	25.0	9	2	S66635	alpha-2-macroglobu
718	6	25.0	8	2	S37141	rpsA protein - Erw	791	6	25.0	9	2	S10784	enamelin i - bovin
719	6	25.0	8	2	S21273	cellulase (EC 3.2.	792	6	25.0	9	2	A28924	fructose-bisphosph
720	6	25.0	8	2	A37521	R-phycocerythrin ga	793	6	25.0	9	2	PD0443	3-oxoacid CoA-tran
721	6	25.0	8	2	S11078	glucose-6-phosphat	794	6	25.0	9	2	PC7074	translation elonga
722	6	25.0	8	2	PT0030	inulinase (EC 3.2.	795	6	25.0	9	2	A43065	hydroxyproline-3-b
723	6	25.0	8	2	A46306	spasmogenic toxin	796	6	25.0	9	2	PD0027	pev-tachykinin - p
724	6	25.0	8	2	A23967	leucopyrokinin - M	797	6	25.0	9	2	G85802	hypothetical prote
725	6	25.0	8	2	S66646	cardioacceleratory	798	6	25.0	9	2	S15850	vitamin D3 26-mono
726	6	25.0	8	2	B27867	homeotic protein U	799	6	25.0	9	2	A26744	bradykinin-like pe
727	6	25.0	8	2	H41978	calliFMRFamide 8 -	800	6	25.0	9	2	A61057	Thr-6 bradykinin -
728	6	25.0	8	2	D47393	neuropeptide calla	801	6	25.0	9	2	A60579	bradykinin-like pe
729	6	25.0	8	2	E47393	neuropeptide calla	802	6	25.0	9	2	S19329	sperm-activating p
730	6	25.0	8	2	S71919	alcohol dehydrogen	803	6	25.0	9	2	B60246	ornitho-kinin - ch
731	6	25.0	8	2	A14683	aspartate transami	804	6	25.0	9	2	A61363	bradykinin - commo
732	6	25.0	8	2	A61328	trypsin (EC 3.4.21	805	6	25.0	9	2	A61358	bradykinin-like pe
733	6	25.0	8	2	A28719	thymic humoral fac	806	6	25.0	10	1	ECLQ1M	tachykinin I - mig
734	6	25.0	8	2	S65381	cytochrome-c oxida	807	6	25.0	10	1	ECLQ3M	tachykinin III - m
735	6	25.0	8	2	PC4373	telomeric and tetr	808	6	25.0	10	1	ECLQ4M	tachykinin IV - mi
736	6	25.0	8	2	A59028	MHC class I histoc	809	6	25.0	10	1	SPPGNK	neuromedin K - pig
737	6	25.0	8	2	S20162	leghemoglobin III	810	6	25.0	10	1	GMROL2	leucosulfakinin-II
738	6	25.0	8	2	F60588	sperm-activating p	811	6	25.0	10	2	S28055	cytochrome b559 co
739	6	25.0	8	2	B24749	neuropeptide B - b	812	6	25.0	10	2	S15118	dihydrofolate redu
740	6	25.0	8	2	E60588	sperm-activating p	813	6	25.0	10	2	S39392	calpain (EC 3.4.22
741	6	25.0	8	2	G60588	sperm-activating p	814	6	25.0	10	2	A60624	angiotensin I - Ja
742	6	25.0	8	2	S43972	tumor-associated a	815	6	25.0	10	2	A60410	beta-neoendorphin
743	6	25.0	8	2	S43971	tumor-associated a	816	6	25.0	10	2	JN0024	neurokinin A - chi
744	6	25.0	9	2	A28495	conopressin G - co	817	6	25.0	10	2	S39374	mannose receptor -
745	6	25.0	9	2	A61230	calsequestrin, car	818	6	25.0	10	2	A61617	ecdysteroid UDPglu
746	6	25.0	9	2	D24180	fibrinogen beta ch	819	6	25.0	10	2	S66458	ferredoxin - Rhizo
747	6	25.0	9	2	C24180	fibrinogen beta ch	820	6	25.0	10	2	S70721	heat shock protein
748	6	25.0	9	2	E28854	fibrinopeptide B -	821	6	25.0	10	2	S48182	bacterioferritin -
749	6	25.0	9	2	F28854	fibrinopeptide B -	822	6	25.0	10	2	H28027	protein P11 - curl
750	6	25.0	9	2	D28854	fibrinopeptide B -	823	6	25.0	10	2	C61440	polygalacturonase
751	6	25.0	9	2	D58503	translation elonga	824	6	25.0	10	2	S65432	angiotensin I - ho
752	6	25.0	9	2	S66607	quinoline 2-oxidor	825	6	25.0	10	2	PT0230	Ig heavy chain CDR
753	6	25.0	9	2	S63491	dissimilatory sulf	826	6	25.0	10	2	PT0251	Ig heavy chain CRD
754	6	25.0	9	2	S36898	ribosomal protein	827	6	25.0	10	2	PT0284	Ig heavy chain CRD
755	6	25.0	9	2	T31612	hypothetical prote	828	6	25.0	10	2	B45482	platelet activatin
756	6	25.0	9	2	S39766	cardioactive pepti	829	6	25.0	10	2	S23371	T-cell receptor al
757	6	25.0	9	2	S65433	bradykinin - horn	830	6	25.0	10	2	S66214	cartilage oligomer
758	6	25.0	9	2	PT0225	Ig heavy chain CDR	831	6	25.0	10	2	S71948	matrix metalloprot
759	6	25.0	9	2	PT0315	Ig heavy chain CRD	832	6	25.0	10	2	C39398	Pc mu (IgM) recept

833	6	25.0	10	2	A37268	Ig heavy chain C r
834	6	25.0	10	2	S36849	Ig heavy chain V r
835	6	25.0	10	2	PH0807	T-cell receptor al
836	6	25.0	10	2	PT0215	T-cell receptor be
837	6	25.0	10	2	S65385	cytochrome-c oxida
838	6	25.0	10	2	S68033	cytochrome P450 1A
839	6	25.0	10	2	D37397	hypothetical prote
840	6	25.0	10	2	B46453	e antigen p20e pre
841	6	25.0	10	2	G58501	48K bile/gallblad
842	6	25.0	10	2	I39702	nopaline synthase
843	6	25.0	10	2	S06964	hypothetical prote
844	6	25.0	10	2	S18396	probable glucose-6
845	6	25.0	10	2	S70251	nitrogenase (EC 1.
846	6	25.0	10	2	I40032	trpE protein - Bac
847	6	25.0	10	2	A60476	S-layer protein -
848	6	25.0	10	2	I44644	neurotoxin-associa
849	6	25.0	10	2	A39745	endo-glucosylceram
850	6	25.0	10	2	PC2044	beta-Kirilowin - M
851	6	25.0	10	2	B59272	peptide-N4- (N-acet
852	6	25.0	10	2	S38304	lectin GNL1 alpha
853	6	25.0	10	2	S38305	lectin GNL2 alpha
854	6	25.0	10	2	D28027	protein P7 - curle
855	6	25.0	10	2	B61440	polygalacturonase
856	6	25.0	10	2	D61440	polygalacturonase
857	6	25.0	10	2	PN0165	triase-phosphate i
858	6	25.0	10	2	A58365	neuropeptide FFRfa
859	6	25.0	10	2	B60656	leucosulfakinin II
860	6	25.0	10	2	A43977	FMRFamide-like pro
861	6	25.0	10	2	C44787	calliFMRFamide 12
862	6	25.0	10	2	A56633	neomysuppressin -
863	6	25.0	10	2	D46285	formaldehyde dehyd
864	6	25.0	10	2	A30823	bothropstoxin - ja
865	6	25.0	10	2	A90917	angiotensin precur
866	6	25.0	10	2	A90345	angiotensin precur
867	6	25.0	10	2	S65387	cytochrome-c oxida
868	6	25.0	10	2	TL3838	cytochrome-c oxida
869	6	25.0	10	2	A44871	monodehydroascorba
870	6	25.0	10	2	S74147	glycerinaldehyde-3-p
871	6	25.0	10	2	B33710	ornithine decarbox
872	6	25.0	10	2	A60527	sperm-activating p
873	6	25.0	10	2	B49581	sialokinin II - ye
874	6	25.0	10	2	A49581	sialokinin I - yel
875	6	25.0	10	2	H60787	sperm-activating p
876	6	25.0	10	2	G60787	sperm-activating p
877	6	25.0	10	2	F60787	sperm-activating p
878	6	25.0	10	2	E60787	sperm-activating p
879	6	25.0	10	2	C60787	sperm-activating p
880	6	25.0	10	2	A60787	sperm-activating p
881	6	25.0	10	2	D60787	sperm-activating p
882	6	25.0	10	2	B60787	sperm-activating p
883	6	25.0	10	2	D60588	sperm-activating p
884	6	25.0	10	2	B60588	sperm-activating p
885	6	25.0	10	2	C60588	sperm-activating p
886	6	25.0	10	2	I60527	sperm-activating p
887	6	25.0	10	2	A60588	sperm-activating p
888	6	25.0	10	2	A60788	sperm-activating p
889	6	25.0	10	2	D60527	sperm-activating p
890	6	25.0	10	2	C39572	sperm-activating p
891	6	25.0	10	2	F60527	sperm-activating p
892	6	25.0	10	2	C60527	sperm-activating p
893	6	25.0	10	2	E60527	sperm-activating p
894	6	25.0	10	2	G60527	sperm-activating p
895	6	25.0	10	2	E39572	sperm-activating p
896	6	25.0	10	2	D60788	sperm-activating p
897	6	25.0	10	2	E60788	sperm-activating p
898	6	25.0	10	2	C60788	sperm-activating p
899	6	25.0	10	2	A24867	scyllorhizin I - s
900	6	25.0	10	2	S23307	neurokinin A - ral
901	6	25.0	10	2	S23186	neurokinin A - Atl
902	6	25.0	10	2	S07202	phyllomedulin - tw
903	6	25.0	10	2	F60589	sperm-activating p
904	6	25.0	10	2	C60589	sperm-activating p
905	6	25.0	10	2	D60589	sperm-activating p

906	6	25.0	10	2	I60588	sperm-activating p
907	6	25.0	10	2	B60589	sperm-activating p
908	6	25.0	10	2	C61033	ranatachykinin C -
909	6	25.0	10	2	B61033	ranatachykinin B -
910	6	25.0	10	2	S27178	neurokinin A-relat
911	6	25.0	10	2	A32543	cardioexcitatory n
912	6	25.0	10	4	S14943	UGA3 leader peptid
913	6	25.0	11	1	EC1Q2M	tachykinin II - mi
914	6	25.0	11	1	A60654	substance P - guin
915	6	25.0	11	1	EOOC	eledoisin - musky
916	6	25.0	11	1	EOOC	eledoisin - curled
917	6	25.0	11	1	SPHO	substance P - hors
918	6	25.0	11	1	GMROL	leucosulfakinin -
919	6	25.0	11	2	G42762	proteasome endopep
920	6	25.0	11	2	A33917	dihydroorotase (EC
921	6	25.0	11	2	JN0023	substance P - chic
922	6	25.0	11	2	A38841	rhodopsin homolog
923	6	25.0	11	2	D58502	27K bile and gallb
924	6	25.0	11	2	A58502	38K kidney stone p
925	6	25.0	11	2	S33782	acetolactate synth
926	6	25.0	11	2	E60691	phycobilisome 8K l
927	6	25.0	11	2	D60691	phycobilisome 9K l
928	6	25.0	11	2	PC2372	58K heat shock pro
929	6	25.0	11	2	B41835	translation elonga
930	6	25.0	11	2	S19301	endo-1,4-beta-xyla
931	6	25.0	11	2	PA0028	protein QA300042 -
932	6	25.0	11	2	T06383	hypothetical prote
933	6	25.0	11	2	PU0029	33K protein 3218 -
934	6	25.0	11	2	S78026	ribosomal protein
935	6	25.0	11	2	I33098	173K exoantigen -
936	6	25.0	11	2	B60769	Ig H2 chain - Paci
937	6	25.0	11	2	I52980	glucocerebrosidase
938	6	25.0	11	2	PT0250	Ig heavy chain CRD
939	6	25.0	11	2	PT0287	Ig heavy chain CRD
940	6	25.0	11	2	S57575	T cell receptor V-
941	6	25.0	11	2	S23364	T-cell receptor al
942	6	25.0	11	2	S23373	T-cell receptor al
943	6	25.0	11	2	S51732	T-cell receptor al
944	6	25.0	11	2	A54348	N-acetylglucosamin
945	6	25.0	11	2	PD0442	NIPSNAP2 protein -
946	6	25.0	11	2	PH1376	T antigen variant
947	6	25.0	11	2	PT0214	T-cell receptor be
948	6	25.0	11	2	I60434	68kDa neurofilamen
949	6	25.0	11	2	S53436	beta-D-galactosida
950	6	25.0	11	2	PH0906	T-cell receptor be
951	6	25.0	11	2	C58501	42K bile stone pro
952	6	25.0	11	2	S58244	pyrroloquinoline q
953	6	25.0	11	2	S35490	type II site-speci
954	6	25.0	11	2	B39853	LuxC protein - Pho
955	6	25.0	11	2	PC2330	cycloinulooligosac
956	6	25.0	11	2	A44755	20alpha-hydroxyste
957	6	25.0	11	2	A35594	buccalin - Califor
958	6	25.0	11	2	S69349	neuropeptide FFami
959	6	25.0	11	2	A60656	perisulfakinin - A
960	6	25.0	11	2	I41978	calliFMRFamide 9 -
961	6	25.0	11	2	S33300	probable substance
962	6	25.0	11	2	D42965	talin - chicken (f
963	6	25.0	11	2	E57789	gallbladder stone
964	6	25.0	11	2	S13279	ile-Ser-bradykinin
965	6	25.0	11	2	A32428	amine oxidase (cop
966	6	25.0	11	2	PN0042	stathmin - mouse (
967	6	25.0	11	2	A48973	glucoamylase A1 (E
968	6	25.0	11	2	S09074	cytochrome P450-4b
969	6	25.0	11	2	A57458	gene Gax protein -
970	6	25.0	11	2	S07203	uperolein - frog (
971	6	25.0	11	2	B26744	megascoliakinin -
972	6	25.0	11	2	C60409	kassinin-like pept
973	6	25.0	11	2	E60409	substance P-like p
974	6	25.0	11	2	B60409	kassinin-like pept
975	6	25.0	11	2	F60409	substance P-like p
976	6	25.0	11	2	D60409	kassinin-like pept
977	6	25.0	11	2	YHHU	morphogenetic neur
978	6	25.0	11	2	YHBO	morphogenetic neur



979 6 25.0 11 2 YHJFHY morphogenetic neur  
980 6 25.0 11 2 YHXAE morphogenetic neur  
981 6 25.0 11 2 S23308 substance P - rain  
982 6 25.0 11 2 S23306 substance P - Atla  
983 6 25.0 11 2 S07207 Crinia-angiotensin  
984 6 25.0 11 2 S07201 physalaemin - frog  
985 6 25.0 11 2 A61365 phyllokinin - Rohd  
986 6 25.0 11 2 A61033 ranatachykinin A -  
987 6 25.0 11 2 D61033 ranatachykinin D -  
988 6 25.0 11 2 YHRT morphogenetic neur  
989 6 25.0 11 4 S41909 hypothetical prote  
990 6 25.0 11 4 PC2124 aminotransferase c  
991 6 25.0 11 4 S52252 hypothetical prote  
992 6 25.0 12 1 A43975 locustamyotropin -  
993 6 25.0 12 1 LFECPF pyrE leader peptid  
994 6 25.0 12 2 S17869 glutathione transf  
995 6 25.0 12 2 C36201 l-aminocyclopropan  
996 6 25.0 12 2 A61309 glycoprotein hormo  
997 6 25.0 12 2 S26552 T-cell receptor be  
998 6 25.0 12 2 S26549 T-cell receptor be  
999 6 25.0 12 2 S26544 Ig heavy chain - m  
1000 6 25.0 12 2 S25056

ALIGNMENTS

RESULT 1  
A24244  
adipokinetic hormone - bollworm  
N;Alternate names: Hez-AKH  
C;Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)  
C;Date: 31-Mar-1988 #sequence\_revision 23-Mar-1995 #text\_change 09-Jul-2004  
C;Accession: A24244  
R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway  
Biochem. Biophys. Res. Commun. 135, 622-628, 1986  
A;Title: Isolation and primary structure of a peptide from the corpora cardiaca of Helic  
A;Reference number: A24244; MUID:86186794; PMID:3964263  
A;Accession: A24244  
A;Molecule type: protein  
A;Residues: 1-9 <JAF>  
A;Cross-references: UNIPROT:P08901  
A;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 70.8%; Score 17; DB 2; Length 9;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
| |  
Db 4 FTSSW 8

RESULT 2  
A28004  
adipokinetic hormone G - two-spotted cricket  
N;Alternate names: AKH-G  
C;Species: Gryllus bimaculatus (two-spotted cricket)  
C;Date: 30-Jun-1989 #sequence\_revision 24-Oct-1997 #text\_change 09-Jul-2004  
C;Accession: A28004  
R;Gaede, G.; Rinehart, K.L.  
Biochem. Biophys. Res. Commun. 149, 908-914, 1987  
A;Title: Primary sequence analysis by fast atom bombardment mass spectrometry of a pepti  
A;Reference number: A28004; MUID:88106553; PMID:3426616  
A;Accession: A28004  
A;Molecule type: protein  
A;Residues: 1-8 <GAE>  
A;Cross-references: UNIPROT:P14086  
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Modified site: amidated carboxyl end (Trp) #status experimental  
Query Match 66.7%; Score 16; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 FXXXW 6  
| |  
Db 4 FSTGW 8

RESULT 3  
A31571  
hypertrehalosemic/adipokinetic hormone - bollworm  
N;Alternate names: Hez-HrTH  
C;Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)  
C;Date: 30-Jun-1989 #sequence\_revision 23-Mar-1995 #text\_change 09-Jul-2004  
C;Accession: A31571  
R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Bird, T.G.; Tseng, C.M.; Zhang, Y.S.  
Biochem. Biophys. Res. Commun. 155, 344-350, 1988  
A;Title: Isolation and primary structure of a neuropeptide hormone from Heliothis zea wit  
A;Reference number: A31571; MUID:88326324; PMID:3415690  
A;Accession: A31571  
A;Molecule type: protein  
A;Residues: 1-10 <JAF>  
A;Cross-references: UNIPROT:P16353  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;10/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 66.7%; Score 16; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 6.3e+02;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
| |  
Db 4 FSSGW 8

RESULT 4  
S10596  
adipokinetic hormone - pond skimmer  
C;Species: Libellula auripennis  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C;Accession: S10596  
R;Gaede, G.  
Biol. Chem. Hoppe-Seyler 371, 475-483, 1990  
A;Title: The putative ancestral peptide of the adipokinetic/red-pigment-concentrating hor  
A;Reference number: S10596; MUID:90359055; PMID:2390213  
A;Accession: S10596  
A;Molecule type: protein  
A;Residues: 1-8 <BIO>  
A;Cross-references: UNIPROT:P25418  
C;Comment: This peptide has both adipokinetic and hypertrehalosemic activities.  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 62.5%; Score 15; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
| |  
Db 4 FTPSW 8

RESULT 5  
D57444



neuropeptide Grb-AST B4 - two-spotted cricket  
C;Species: Gryllus bimaculatus (two-spotted cricket)  
C;Date: 26-Jan-1996 #sequence\_revision 26-Jan-1996 #text\_change 09-Jul-2004  
C;Accession: D57444  
R;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.  
J. Biol. Chem. 270, 21103-21108, 1995  
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cricket  
A;Reference number: A57444; MUID:95403341; PMID:7673141  
A;Accession: D57444  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-9 <LOR>  
A;Cross-references: UNIPROT:Q7M3N6

Query Match 62.5%; Score 15; DB 2; Length 9;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |  
Db 5 FHGSW 9

## RESULT 6

T17063  
cytochrome-c oxidase (EC 1.9.3.1) chain I - Hoplocercus spinosus mitochondrion (fragment)  
C;Species: mitochondrion Hoplocercus spinosus  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T17063  
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.  
J. Mol. Evol. 44, 660-674, 1997  
A;Title: Evolutionary shifts in three major structural features of the mitochondrial gene  
A;Reference number: Z18674; MUID:97315309; PMID:9169559  
A;Accession: T17063  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-10 <MAC>  
A;Cross-references: UNIPROT:Q79897; EMBL:U82683; NID:g3603124; PID:g3603127; PIDN:AAC622  
C;Genetics:  
A;Genome: mitochondrion  
A;Note: COI  
C;Keywords: mitochondrion; oxidoreductase

Query Match 62.5%; Score 15; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 1.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |  
Db 2 FISRW 6

## RESULT 7

T12325  
cytochrome-c oxidase (EC 1.9.3.1) chain I - Leiocephalus carinatus mitochondrion (fragment)  
C;Species: mitochondrion Leiocephalus carinatus  
C;Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 09-Jul-2004  
C;Accession: T12325  
R;Schulte, J.A.; Macey, J.R.; Larson, A.; Papenfuss, T.J.  
Mol. Phylogenet. Evol. 10, 367-376, 1998  
A;Title: Molecular tests of phylogenetic taxonomies: A general procedure and example using  
A;Reference number: Z17488; MUID:99162288; PMID:10051389  
A;Accession: T12325  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-10 <SCH>  
A;Cross-references: UNIPROT:Q9ZYT2; EMBL:AF049864; NID:g4105754; PID:g4105757; PIDN:AAD0  
C;Genetics:  
A;Genome: mitochondrion  
A;Note: COI  
C;Keywords: mitochondrion; oxidoreductase

Query Match 62.5%; Score 15; DB 2; Length 10;

Best Local Similarity 40.0%; Pred. No. 1.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 FXXXW 6  
| |  
Db 2 FITRW 6  
RESULT 8  
S53789  
neuropeptide Pec-HrTH - Platypus capensis  
C;Species: Platypus capensis  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C;Accession: S53789  
R;Gaede, G.; Janssens, M.P.E.  
Biol. Chem. Hoppe-Seyler 375, 803-809, 1994  
A;Title: Cicadas contain novel members of the AKH/RPCH family peptides with hypertrehalose  
A;Reference number: S53789; MUID:95225985; PMID:7710694  
A;Accession: S53789  
A;Molecule type: protein  
A;Residues: 1-10 <GAE>  
A;Cross-references: UNIPROT:Q7M465  
C;Keywords: blocked amino end; blocked carboxyl end

Query Match 62.5%; Score 15; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 1.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |  
Db 4 FSPSW 8

## RESULT 9

PH1613  
Ig H chain V-D-J region (clone B-less 17) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C;Accession: PH1613  
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
A;Reference number: PH1580; MUID:93301609; PMID:8315387  
A;Accession: PH1613  
A;Molecule type: DNA  
A;Residues: 1-15 <LEV>  
A;Experimental source: bone marrow pre-B lymphocyte  
C;Keywords: immunoglobulin

Query Match 62.5%; Score 15; DB 2; Length 15;  
Best Local Similarity 40.0%; Pred. No. 1.5e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |  
Db 10 FTMLW 14

## RESULT 10

A34704  
protein-tyrosine kinase (EC 2.7.1.112) 1, neuron-specific - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 06-Jul-1990 #sequence\_revision 06-Jul-1990 #text\_change 09-Jul-2004  
C;Accession: A34704  
R;Pyper, J.M.; Bolen, J.B.  
Mol. Cell. Biol. 10, 2035-2040, 1990  
A;Title: Identification of a novel neuronal C-SRC exon expressed in human brain.  
A;Reference number: A34704; MUID:90220588; PMID:1691439  
A;Accession: A34704  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-17 <PYP>  
A;Cross-references: UNIPROT:Q14925

C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

Query Match 62.5%; Score 15; DB 2; Length 17;  
Best Local Similarity 40.0%; Pred. No. 1.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6  
| |  
Db 10 FTRW 14

## RESULT 11

S77981

cytochrome-c oxidase (EC 1.9.3.1) chain Va.1 - bigeye tuna (fragment)

C;Species: Thunnus obesus (bigeye tuna)

C;Date: 17-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004

C;Accession: S77981

R;Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.

submitted to the Protein Sequence Database, June 1997

A;Reference number: S77980

A;Accession: S77981

A;Molecule type: protein

A;Residues: 1-20 <ARN>

A;Cross-references: UNIPROT:P80972

A;Experimental source: heart; liver

C;Genetics:

A;Genome: nuclear

C;Function:

A;Pathway: oxidative phosphorylation; respiratory chain

C;Superfamily: mammalian cytochrome-c oxidase chain Va

C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 62.5%; Score 15; DB 2; Length 20;  
Best Local Similarity 40.0%; Pred. No. 1.9e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6  
| |  
Db 11 FDRW 15

## RESULT 12

PN0171

peptidylprolyl isomerase (EC 5.2.1.8) b, cytosolic - fungus (Fusarium sporotrichioides)

N;Contains: cyclophilin

C;Species: Fusarium sporotrichioides

C;Date: 05-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 02-Sep-2000

C;Accession: PN0171

R;Fukaya, N.; Chow, L.P.; Sugiyura, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.

submitted to JIPID, May 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi

A;Reference number: PN0160

A;Accession: PN0171

A;Molecule type: protein

A;Residues: 1-20 <FUK>

A;Experimental source: strain M-1-1

C;Superfamily: peptidylprolyl isomerase; cyclophilin homology

C;Keywords: cis-trans-isomerase; cyclosporin A binding; cytosol

Query Match 62.5%; Score 15; DB 2; Length 20;  
Best Local Similarity 40.0%; Pred. No. 1.9e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6  
| |  
Db 6 FDIW 10

## RESULT 13

PH1380

alpha-amylase (EC 3.2.1.1) (Haim sensitive) - Bacillus sp. (fragment)

C;Species: Bacillus sp.

C;Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 09-Jul-2004

C;Accession: PH1380

R;Kawaguchi, T.; Nagae, H.; Murao, S.; Arai, M.

Biosci. Biotechnol. Biochem. 56, 1792-1796, 1992

A;Title: Purification and some properties of a Haim-sensitive alpha-amylase from newly is

A;Reference number: PH1380; MUID:93113087; PMID:1369074

A;Accession: PH1380

A;Molecule type: protein

A;Residues: 1-20 <KAW>

A;Cross-references: UNIPROT:Q9R5E8

A;Experimental source: strain NO.195

C;Comment: This enzyme has an optimum pH of 7.0.

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 62.5%; Score 15; DB 2; Length 20;  
Best Local Similarity 40.0%; Pred. No. 1.9e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6  
| |  
Db 13 FSWT 17

## RESULT 14

A33995

adipokinetic hormone - black horse fly

C;Species: Tabanus atratus (black horse fly)

C;Date: 23-Mar-1990 #sequence\_revision 23-Mar-1990 #text\_change 09-Jul-2004

C;Accession: A33995

R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang, Y.

Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989

A;Title: Primary structure of two neuro peptide hormones with adipokinetic and hypotrehal

A;Reference number: A33995; MUID:90046758; PMID:2813385

A;Accession: A33995

A;Molecule type: protein

A;Residues: 1-8 <JAF>

A;Cross-references: UNIPROT:PI4595

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted

F;8/Modified site: amidated carboxyl end (Trp) #status predicted

Query Match 58.3%; Score 14; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6  
| |  
Db 4 FTPG 8

## RESULT 15

A44960

neuropeptide Led-CC-I - Colorado potato beetle

C;Species: Leptinotarsa decemlineata (Colorado potato beetle)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004

C;Accession: A44960

R;Gaede, G.; Kellner, R.

Peptides 10, 1287-1289, 1989

A;Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle and

A;Reference number: A44960; MUID:90160053; PMID:2576128

A;Accession: A44960

A;Molecule type: protein

A;Residues: 1-8 <GAE>

A;Cross-references: UNIPROT:P04548

C;Superfamily: adipokinetic hormone

C;Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 8;

Best Local Similarity 40.0%; Pred. No. 2.8e+05; Mismatches 3; Indels 0; Gaps 0;  
Matches 2; Conservative 0;

QY 2 FXXXW 6  
|  
Db 4 FSPNW 8

RESULT 16  
B44960  
neuropeptide Led-CC-II - Colorado potato beetle  
C;Species: Leptinotarsa decemlineata (Colorado potato beetle)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C;Accession: B44960  
R;Gaede, G.; Kellner, R.  
Peptides 10, 1287-1289, 1989  
A;Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle and  
A;Reference number: A44960; MUID:90160053; PMID:2576128  
A;Accession: B44960  
A;Molecule type: protein  
A;Residues: 1-8 <GAE>  
A;Cross-references: UNIPROT:P04549  
C;Superfamily: adipokinetic hormone  
C;Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 4 FTPNW 8

RESULT 17  
A58620  
adipokinetic hormone - damselfly (Ischnura senegalensis)  
C;Species: Ischnura senegalensis  
C;Date: 28-Oct-1997 #sequence\_revision 31-Oct-1997 #text\_change 09-Jul-2004  
C;Accession: A58620  
R;Janssens, M.P.E.; Kellner, R.; Gaede, G.  
Biochem. J. 302, 539-543, 1994  
A;Title: A novel adipokinetic octapeptide found in the damselflies Pseudagrion inconspic  
A;Reference number: S55310; MUID:94379987; PMID:8093008  
A;Accession: A58620  
A;Molecule type: protein  
A;Residues: 1-8 <JAN>  
A;Cross-references: UNIPROT:Q7M4H6  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 4 FTPGW 8

RESULT 18  
S11545  
adipokinetic hormone - nestling-sucking blowfly  
C;Species: Protophormia terraenovae (nestling-sucking blowfly)  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
C;Accession: S11545  
R;Gaede, G.; Wilps, H.; Kellner, R.  
Biochem. J. 269, 309-313, 1990  
A;Title: Isolation and structure of a novel charged member of the red-pigment-concentrat

erraenovae (Diptera).  
A;Reference number: S11545; MUID:90351345; PMID:2386478  
A;Accession: S11545  
A;Molecule type: protein  
A;Residues: 1-8 <GAE>  
A;Cross-references: UNIPROT:P61856  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 4 FSPDW 8

RESULT 19  
S55310  
adipokinetic hormone - damselfly (Pseudagrion inconspicuum)  
N;Alternate names: Psi-AKH  
C;Species: Pseudagrion inconspicuum  
C;Date: 19-Mar-1997 #sequence\_revision 31-Oct-1997 #text\_change 09-Jul-2004  
C;Accession: S55310  
R;Janssens, M.P.E.; Kellner, R.; Gaede, G.  
Biochem. J. 302, 539-543, 1994  
A;Title: A novel adipokinetic octapeptide found in the damselflies Pseudagrion inconspic  
A;Reference number: S55310; MUID:94379987; PMID:8093008  
A;Accession: S55310  
A;Molecule type: protein  
A;Residues: 1-8 <JAN>  
A;Cross-references: UNIPROT:Q7M4H7  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 4 FTPGW 8

RESULT 20  
A61348  
red pigment-concentrating hormone - northern shrimp  
N;Alternate names: blanching hormone  
C;Species: Pandalus borealis (northern shrimp)  
C;Date: 02-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 09-Jul-2004  
C;Accession: A61348; S07139  
R;Fernelund, P.; Josefsson, L.  
Science 177, 173-175, 1972  
A;Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.  
A;Reference number: A61348; MUID:72228738; PMID:5041363  
A;Accession: A61348  
A;Molecule type: protein  
A;Residues: 1-8 <FER1>  
A;Cross-references: UNIPROT:P08939  
R;Fernelund, P.  
Biochim. Biophys. Acta 371, 304-311, 1974  
A;Title: Structure of the red-pigment-concentrating hormone of the shrimp, Pandalus bore  
A;Reference number: S07139; MUID:75054965; PMID:4433569  
A;Accession: S07139  
A;Molecule type: protein  
A;Residues: 'E', 2-8 <FER2>  
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
C;Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in pi

zed pigment-containing cells.  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |  
Db 4 FSPGW 8

RESULT 21  
S08995  
hypertrehalosemic hormone I - oriental cockroach  
N;Alternate names: Pea-CAH-I  
C;Species: Blatta orientalis (oriental cockroach)  
C;Date: 30-Jun-1992 #sequence\_revision 24-Oct-1997 #text\_change 09-Jul-2004  
C;Accession: S08995  
R;Gaede, G.; Rinehart, K.L.  
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990  
A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora  
entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment  
A;Reference number: S08995; MUID:90253659; PMID:2340112  
A;Accession: S08995  
A;Molecule type: protein  
A;Residues: 1-8 <GAE>  
A;Cross-references: UNIPROT:P04548  
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |  
Db 4 FSPNW 8

RESULT 22  
S08996  
hypertrehalosemic hormone II - oriental cockroach  
N;Alternate names: Pea-CAH-II  
C;Species: Blatta orientalis (oriental cockroach)  
C;Date: 30-Jun-1992 #sequence\_revision 24-Oct-1997 #text\_change 09-Jul-2004  
C;Accession: S08996  
R;Gaede, G.; Rinehart, K.L.  
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990  
A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora  
entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment  
A;Reference number: S08995; MUID:90253659; PMID:2340112  
A;Accession: S08996  
A;Molecule type: protein  
A;Residues: 1-8 <GAE>  
A;Cross-references: UNIPROT:P04549  
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |  
Db 4 FSPNW 8

Db 4 FTPNW 8

RESULT 23  
A49823  
adipokinetic hormone I - American cockroach  
N;Alternate names: periplanetin CC-1  
C;Species: Periplaneta americana (American cockroach)  
C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 09-Jul-2004  
C;Accession: A49823  
R;Scarborough, R.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller, C.F.  
Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984  
A;Title: Isolation and primary structure of two peptides with cardioacceleratory and hypotensive  
A;Reference number: A49823; MUID:84298179; PMID:6591205  
A;Accession: A49823  
A;Molecule type: protein  
A;Residues: 1-8 <SCA>  
A;Cross-references: UNIPROT:P04548  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |  
Db 4 FSPNW 8

RESULT 24  
B49823  
adipokinetic hormone II - American cockroach  
N;Alternate names: neuropeptide M-II; periplanetin CC-1  
C;Species: Periplaneta americana (American cockroach)  
C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 09-Jul-2004  
C;Accession: B49823; A05170  
R;Scarborough, R.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller, C.F.  
Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984  
A;Title: Isolation and primary structure of two peptides with cardioacceleratory and hypotensive  
A;Reference number: A49823; MUID:84298179; PMID:6591205  
A;Accession: B49823  
A;Molecule type: protein  
A;Residues: 1-8 <SCA>  
A;Cross-references: UNIPROT:P04549  
R;Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.L.  
Biochem. Biophys. Res. Commun. 124, 350-358, 1984  
A;Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mass  
A;Reference number: A90118; MUID:85046530; PMID:6548628  
A;Accession: A05170  
A;Molecule type: protein  
A;Residues: 'E', 2-8 <WIT>  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |  
Db 4 FTPNW 8

RESULT 25  
A43976  
hypertrehalosemic hormone - yellow mealworm  
C;Species: Tenebrio molitor (yellow mealworm)

C;Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 09-Jul-2004  
C;Accession: A43976  
R;Gaede, G.; Rosinski, G.  
Peptides 11, 455-459, 1990  
A;Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid beetle  
A;Reference number: A43976; MUID:90341081; PMID:2381871  
A;Accession: A43976  
A;Molecule type: protein  
A;Residues: 1-8 <GAE>  
A;Cross-references: UNIPROT:P25419  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
|  
Db 4 FSPNW 8

RESULT 26  
B43976  
hypertrehalosemic hormone - beetle (Zophobas rugipes)  
C;Species: Zophobas rugipes  
C;Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 09-Jul-2004  
C;Accession: B43976  
R;Gaede, G.; Rosinski, G.  
Peptides 11, 455-459, 1990  
A;Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid beetle  
A;Reference number: A43976; MUID:90341081; PMID:2381871  
A;Accession: B43976  
A;Molecule type: protein  
A;Residues: 1-8 <GAE>  
A;Cross-references: UNIPROT:P25419  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
|  
Db 4 FSPNW 8

RESULT 27  
A05169  
neuropeptide M-I - American cockroach  
C;Species: Periplaneta americana (American cockroach)  
C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 09-Jul-2004  
C;Accession: A05169  
R;Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.L.  
Biochem. Biophys. Res. Commun. 124, 350-358, 1984  
A;Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mass spectrometry  
A;Reference number: A90118; MUID:85046530; PMID:6548628  
A;Accession: A05169  
A;Molecule type: protein  
A;Residues: 1-8 <WIT>  
A;Cross-references: UNIPROT:P04548  
C;Keywords: neuropeptide

Query Match 58.3%; Score 14; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
|  
Db 4 FSPNW 8

Db 4 FSPNW 8

RESULT 28  
B33995  
hypertrehalosemic hormone - black horse fly  
C;Species: Tabanus atratus (black horse fly)  
C;Date: 23-Mar-1990 #sequence\_revision 23-Mar-1990 #text\_change 09-Jul-2004  
C;Accession: B33995  
R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang, Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989  
A;Title: Primary structure of two neuropeptide hormones with adipokinetic and hypotrehalosemic activities  
A;Reference number: A33995; MUID:90046758; PMID:2813385  
A;Accession: B33995  
A;Molecule type: protein  
A;Residues: 1-10 <JAF>  
A;Cross-references: UNIPROT:P14596  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted  
F;10/Modified site: amidated carboxyl end (Tyr) #status predicted

Query Match 58.3%; Score 14; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
|  
Db 4 FTPGW 8

RESULT 29  
S08997  
hypertrehalosemic neuropeptide Bld-HrTH - cockroach (Gromphadorina portentosa)  
C;Species: Gromphadorina portentosa  
C;Date: 30-Jun-1992 #sequence\_revision 14-Sep-1994 #text\_change 09-Jul-2004  
C;Accession: S08997  
R;Gaede, G.; Rinehart, K.L.  
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990  
A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry  
A;Reference number: S08995; MUID:90253659; PMID:2340112  
A;Accession: S08997  
A;Molecule type: protein  
A;Residues: 1-10 <GAE>  
A;Cross-references: UNIPROT:P10939  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
|  
Db 4 FSPGW 8

RESULT 30  
A60421  
hypertrehalosemic hormone - German cockroach  
N;Alternate names: Bld-HrTH  
C;Species: Blattella germanica (German cockroach)  
C;Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 09-Jul-2004  
C;Accession: A60421; S09137  
R;Veenstra, J.A.; Camps, F.  
Neuropeptides 15, 107-109, 1990  
A;Title: Structure of the hypertrehalosemic neuropeptide of the German cockroach, Blattella germanica  
A;Reference number: A60421; MUID:91179584; PMID:2080017  
A;Accession: A60421

A;Molecule type: protein  
A;Residues: 1-10 <VEE>  
A;Cross-references: UNIPROT:P10939  
R;Gaede, G.; Rinehart, K.L.  
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990  
A;Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corpora allata and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry  
A;Reference number: S08995; MUID:90253659; PMID:2340112  
A;Accession: S09137  
A;Molecule type: protein  
A;Residues: 1-10 <GAE>  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
| |  
Db 4 FSPGW 8

RESULT 31  
S08998  
hypertrehalosemic neuropeptide Bld-HrTH - Madeira cockroach  
C;Species: Leucophaea maderae (Madeira cockroach)  
C;Date: 30-Jun-1992 #sequence\_revision 14-Sep-1994 #text\_change 09-Jul-2004  
C;Accession: S08998  
R;Gaede, G.; Rinehart, K.L.  
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990  
A;Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corpora allata and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry  
A;Reference number: S08995; MUID:90253659; PMID:2340112  
A;Accession: S08998  
A;Molecule type: protein  
A;Residues: 1-10 <GAE>  
C;Cross-references: UNIPROT:P10939  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
| |  
Db 4 FSPGW 8

RESULT 32  
A26381  
hypertrehalosemic hormone - gray cockroach  
C;Species: Nauphoeta cinerea (gray cockroach)  
C;Date: 31-Mar-1988 #sequence\_revision 24-Oct-1997 #text\_change 09-Jul-2004  
C;Accession: A26381  
R;Gaede, G.; Rinehart Jr., K.L.  
Biochem. Biophys. Res. Commun. 141, 774-781, 1986  
A;Title: Amino acid sequence of a hypertrehalosaemic neuropeptide from the corpora allata and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry  
A;Reference number: A26381; MUID:87100208; PMID:3801028  
A;Accession: A26381  
A;Molecule type: protein  
A;Residues: 1-10 <GAD>  
C;Cross-references: UNIPROT:P10939  
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have assigned the sequence as GAD-  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
| |  
Db 4 FSPGW 8

RESULT 33  
JC1416  
hypertrehalosemic hormone I - stick insect (Carausius morosus)  
N;Alternate names: neuropeptide Cam-HrTH-I  
N;Contains: hypertrehalosemic factor II  
C;Species: Carausius morosus  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C;Accession: JC1416; S07157  
R;Gaede, G.; Kellner, R.; Rinehart, K.L.; Proefke, M.L.  
Biochem. Biophys. Res. Commun. 189, 1303-1309, 1992  
A;Title: A tryptophan-substituted member of the AKH/RPCH family isolated from a stick insect  
A;Reference number: JC1416; MUID:93129188; PMID:1482345  
A;Accession: JC1416  
A;Molecule type: protein  
A;Residues: 1-10 <GAE1>  
A;Cross-references: UNIPROT:P11385  
R;Gaede, G.; Rinehart Jr., K.L.  
Biol. Chem. Hoppe-Seyler 368, 67-75, 1987  
A;Title: Primary structure of the hypertrehalosaemic factor II from the corpus cardiacum  
A;Reference number: S07157; MUID:87157103; PMID:3828078  
A;Accession: S07157  
A;Molecule type: protein  
A;Residues: 'Z', 2-10 <GAE2>  
C;Comment: Hypertrehalosemic factor II lacks the tryptophan modification.  
C;Comment: This peptide raises hemolymph levels of trehalose in the cockroach Periplaneta americana  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; glycoprotein; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Binding site: carboxylate (Trp) (covalent) #status experimental  
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
| |  
Db 4 FTPNW 8

RESULT 34  
S09138  
hypertrehalosemic hormone II - stick insect (Extatosoma tiaratum)  
N;Alternate names: Cam-HrTH-II  
C;Species: Extatosoma tiaratum  
C;Date: 30-Jun-1992 #sequence\_revision 24-Oct-1997 #text\_change 09-Jul-2004  
C;Accession: S09138  
R;Gaede, G.; Rinehart, K.L.  
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990  
A;Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corpora allata and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry  
A;Reference number: S08995; MUID:90253659; PMID:2340112  
A;Accession: S09138  
A;Molecule type: protein  
A;Residues: 1-10 <GAE>  
A;Cross-references: UNIPROT:P11385  
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have assigned the sequence as GAE-  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 58.3%; Score 14; DB 2; Length 10;



Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 4 FFPNW 8

RESULT 35  
C39191  
hypothetical protein 1 (Tetx 5' region) - Bacteroides fragilis  
C:Species: Bacteroides fragilis  
C:Date: 08-Nov-1991 #sequence\_revision 08-Nov-1991 #text\_change 30-Sep-1993  
C:Accession: C39191  
R:Speer, B.S.; Bedzyk, L.; Salyers, A.A.  
J. Bacteriol. 173, 176-183, 1991  
A:Title: Evidence that a novel tetracycline resistance gene found on two Bacteroides tra  
A:Reference number: A39191; MUID:91100280; PMID:1846135  
A:Accession: C39191  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-10 <SPE>  
A:Cross-references: GB:M37699

Query Match 58.3%; Score 14; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 3 FSRPW 7

RESULT 36  
PT0322  
Ig heavy chain CRD3 region (clone J2-106A) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PT0322  
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j  
A:Reference number: PT0222; MUID:91108337; PMID:1899102  
A:Accession: PT0322  
A:Molecule type: DNA  
A:Residues: 1-10 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match 58.3%; Score 14; DB 2; Length 10;  
Best Local Similarity 20.0%; Pred. No. 2e+03;  
Matches 1; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
:  
Db 3 YSSSW 7

RESULT 37  
T17066  
cytochrome-c oxidase (EC 1.9.3.1) chain I - Oplurus cuvieri mitochondrion (fragment)  
C:Species: mitochondrion Oplurus cuvieri  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T17066  
R:Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.  
J. Mol. Evol. 44, 660-674, 1997  
A:Title: Evolutionary shifts in three major structural features of the mitochondrial gen  
A:Reference number: Z18674; MUID:97315309; PMID:9169559  
A:Accession: T17066  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-10 <MAC>  
A:Cross-references: UNIPROT:O79903; EMBL:U82685; NID:g3603136; PID:g3603139; PIDN:AAC622

C:Genetics:  
A:Genome: mitochondrion  
A>Note: COI  
C:Keywords: mitochondrion; oxidoreductase

Query Match 58.3%; Score 14; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 2 FINRW 6

RESULT 38  
T17069  
cytochrome-c oxidase (EC 1.9.3.1) chain I - Phrynosoma douglassii mitochondrion (fragmen  
C:Species: mitochondrion Phrynosoma douglassii  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T17069  
R:Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.  
J. Mol. Evol. 44, 660-674, 1997  
A:Title: Evolutionary shifts in three major structural features of the mitochondrial gen  
A:Reference number: Z18674; MUID:97315309; PMID:9169559  
A:Accession: T17069  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-10 <MAC>  
A:Cross-references: UNIPROT:O79906; EMBL:U82686; NID:g3603144; PID:g3603147; PIDN:AAC622  
C:Genetics:  
A:Genome: mitochondrion  
A>Note: COI  
C:Keywords: mitochondrion; oxidoreductase

Query Match 58.3%; Score 14; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 2 FINRW 6

RESULT 39  
T12329  
cytochrome-c oxidase (EC 1.9.3.1) chain I - Stenocercus crasicaudatus mitochondrion (fra  
C:Species: mitochondrion Stenocercus crasicaudatus  
C:Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 09-Jul-2004  
C:Accession: T12329  
R:Schulte, J.A.; Macey, J.R.; Larson, A.; Papenfuss, T.J.  
Mol. Phylogenet. Evol. 10, 367-376, 1998  
A:Title: Molecular tests of phylogenetic taxonomies: A general procedure and example usi  
A:Reference number: Z17488; MUID:99162288; PMID:10051389  
A:Accession: T12329  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-10 <SCH>  
A:Cross-references: UNIPROT:Q9ZYS6; EMBL:AF049866; NID:g4105762; PID:g4105765; PIDN:AADO  
C:Genetics:  
A:Genome: mitochondrion  
A>Note: COI  
C:Keywords: mitochondrion; oxidoreductase

Query Match 58.3%; Score 14; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 2 FINRW 6

RESULT 40



PT0274  
Ig heavy chain CRD3 region (clone 3-109B) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C;Accession: PT0274  
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j  
A;Reference number: PT0222; MUID:91108337; PMID:1899102  
A;Accession: PT0274  
A;Molecule type: DNA  
A;Residues: 1-12 <YAM>  
A;Experimental source: B lymphocyte  
C;Keywords: heterotetramer; immunoglobulin

Query Match 58.3%; Score 14; DB 2; Length 12;  
Best Local Similarity 20.0%; Pred. No. 2.3e+03;  
Matches 1; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
Db 3 YSSSW 7

Search completed: October 18, 2005, 15:59:23  
Job time : 26.3529 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:32:19 ; Search time 117.529 Seconds  
(without alignments)  
39.213 Million cell updates/sec

Title: US-09-214-371-11  
Perfect score: 24  
Sequence: 1 XFXXXWXXX 9

Scoring table: BLOSUM62  
Gapop 10.0 ; Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 12050

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : UniProt.03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	17	70.8	9	1	AKH_HELZE	P67787 heliothis z
2	17	70.8	13	2	Q9XLI2	Q9xli2 bemisia tab
3	16	66.7	8	1	AKHG_GRYBI	P67785 gryllus bim
4	16	66.7	8	1	AKH_ROMMI	P67786 romalea mic
5	16	66.7	10	1	HTF_HELZE	P16353 heliothis z
6	16	66.7	11	2	Q6E5N4	Q6esn4 mantheyus p
7	16	66.7	11	2	Q9G649	Q9g649 otocryptis
8	16	66.7	17	2	O15276	O15276 homo sapien
9	16	66.7	17	2	Q7Y1X8	Q7y1x8 lilium long
10	16	66.7	19	2	O91329	O91329 human immun
11	16	66.7	19	2	Q9WJB1	Q9wjb1 human immun
12	16	66.7	20	2	Q6LD18	Q6ld18 mus musculu
13	15	62.5	8	1	AKH_LIBAU	P25418 libellula a
14	15	62.5	9	2	Q7M3N6	Q7m3n6 gryllus bim
15	15	62.5	9	2	Q8WGE6	Q8wge6 procambarus
16	15	62.5	10	1	AKHX_LOCFI	P81626 locusta mig
17	15	62.5	10	2	Q7M465	Q7m465 platypleura
18	15	62.5	10	2	Q70F01	Q70f01 sus scrofa
19	15	62.5	10	2	Q79897	Q79897 hoplocercus
20	15	62.5	10	2	P92707	P92707 platysaurus
21	15	62.5	10	2	Q6UJL5	Q6ujl5 strophurus
22	15	62.5	10	2	Q6WBU4	Q6wbu4 sceloporu
23	15	62.5	10	2	Q6XOE7	Q6xoe7 anolis marc
24	15	62.5	10	2	Q71DW3	Q71dw3 polychrus m
25	15	62.5	10	2	Q71DW6	Q71dw6 polychrus a
26	15	62.5	10	2	Q71DW9	Q71dw9 anisolepis
27	15	62.5	10	2	Q71E17	Q71e17 morunasauru
28	15	62.5	10	2	Q71E20	Q71e20 enyalioides
29	15	62.5	10	2	Q9ZYT2	Q9zyt2 leiocephalu
30	15	62.5	11	2	Q8WES0	Q8wes0 ceratophora
31	15	62.5	11	2	Q9G365	Q9g365 calotes emm

32	15	62.5	11	2	Q9G368	Q9g368 draco blanf
33	15	62.5	11	2	Q9G5Y9	Q9g5y9 pseudocalot
34	15	62.5	11	2	Q9G5Z2	Q9g5z2 pseudocalot
35	15	62.5	11	2	Q9G601	Q9g601 bronchocela
36	15	62.5	11	2	Q9G625	Q9g625 calotes ver
37	15	62.5	11	2	Q9G628	Q9g628 calotes mys
38	15	62.5	11	2	Q9G631	Q9g631 calotes nig
39	15	62.5	11	2	Q9G634	Q9g634 calotes lio
40	15	62.5	11	2	Q9G640	Q9g640 calotes cey
41	15	62.5	11	2	Q9G643	Q9g643 calotes cal
42	15	62.5	11	2	Q9G646	Q9g646 sitana pont
43	15	62.5	12	2	Q6WR31	Q6wr31 mycteria am
44	15	62.5	12	2	Q6WR52	Q6wr52 asio otus (
45	15	62.5	12	2	Q6WR67	Q6wr67 neomorphus
46	15	62.5	12	2	Q6WR73	Q6wr73 coccyzus er
47	15	62.5	12	2	Q6WR79	Q6wr79 cuculus can
48	15	62.5	14	2	Q71H30	Q71h30 andrena bra
49	15	62.5	16	2	Q760I9	Q760i9 aspergillus
50	15	62.5	19	2	Q7S645	Q7s645 neurospora
51	15	62.5	20	1	COXA_THUOB	P80972 thunnus obe
52	15	62.5	20	2	Q95MK5	Q95mk5 varecia var
53	15	62.5	20	2	Q673D5	Q673d5 dehalococco
54	15	62.5	20	2	Q9R5E8	Q9r5e8 bacillus sp
55	14	58.3	8	1	AKH_PROTE	P61856 protophormi
56	14	58.3	8	1	AKH_TABAT	P14595 tabanus atr
57	14	58.3	8	1	HTF1_PERAM	P04548 periplaneta
58	14	58.3	8	1	HTF2_PERAM	P04549 periplaneta
59	14	58.3	8	1	HTF_TENMO	P67789 tenebrio mo
60	14	58.3	8	1	HTF_ZOPRU	P67790 zophobas ru
61	14	58.3	8	1	RPCH_PANBO	P08939 pandalus bo
62	14	58.3	8	2	Q7M4H6	Q7m4h6 ischnura se
63	14	58.3	8	2	Q7M4H7	Q7m4h7 pseudagrion
64	14	58.3	10	1	HTF1_ROMMI	P18110 romalea mic
65	14	58.3	10	1	HTF2_CARMO	P62542 carausius m
66	14	58.3	10	1	HTF2_EXTTI	P62543 extatosoma
67	14	58.3	10	1	HTF_BLAG	P84220 blattella g
68	14	58.3	10	1	HTF_GROPO	P84221 gromphadori
69	14	58.3	10	1	HTF_LEUMA	P84219 leucophaea
70	14	58.3	10	1	HTF_NAUCI	P84218 nauphoeta c
71	14	58.3	10	1	HTF_TABAT	P14596 tabanus atr
72	14	58.3	10	2	Q79885	Q79885 anolis pate
73	14	58.3	10	2	Q79903	Q79903 oplurus cuv
74	14	58.3	10	2	Q79906	Q79906 phrynosoma
75	14	58.3	10	2	Q8W7U4	Q8w7u4 anolis nite
76	14	58.3	10	2	Q8W8Q2	Q8w8q2 anolis punc
77	14	58.3	10	2	Q8W8Q3	Q8w8q3 anolis nite
78	14	58.3	10	2	Q8W8Q4	Q8w8q4 anolis punc
79	14	58.3	10	2	Q8W969	Q8w969 anolis orto
80	14	58.3	10	2	Q8W970	Q8w970 anolis nite
81	14	58.3	10	2	Q8W971	Q8w971 anolis fusc
82	14	58.3	10	2	Q8WDG6	Q8wdg6 anolis trac
83	14	58.3	10	2	Q8WDH0	Q8wdh0 anolis limi
84	14	58.3	10	2	Q8WDH2	Q8wdh2 anolis lemu
85	14	58.3	10	2	Q8WDH4	Q8wdh4 anolis carp
86	14	58.3	10	2	Q8WDH6	Q8wdh6 anolis wood
87	14	58.3	10	2	Q8WDH8	Q8wdh8 anolis mest
88	14	58.3	10	2	Q8WDI8	Q8wdi8 anolis tran
89	14	58.3	10	2	Q6WBN7	Q6wbn7 sceloporu
90	14	58.3	10	2	Q6WBR1	Q6wbr1 sceloporu
91	14	58.3	10	2	Q6WBR4	Q6wbr4 sceloporu
92	14	58.3	10	2	Q6WBS3	Q6wbs3 sceloporu
93	14	58.3	10	2	Q6WBT8	Q6wbt8 sceloporu
94	14	58.3	10	2	Q6WBU1	Q6wbu1 sceloporu
95	14	58.3	10	2	Q6WBW2	Q6wbw2 phrynosoma
96	14	58.3	10	2	Q6WBW5	Q6wbw5 phrynosoma
97	14	58.3	10	2	Q6WBW8	Q6wbw8 phrynosoma
98	14	58.3	10	2	Q6WBX1	Q6wbx1 phrynosoma
99	14	58.3	10	2	Q6WBX4	Q6wbx4 phrynosoma
100	14	58.3	10	2	Q6WZN6	Q6wzn6 anolis cybo
101	14	58.3	10	2	Q6X061	Q6x061 anolis haet
102	14	58.3	10	2	Q6X071	Q6x071 anolis shre
103	14	58.3	10	2	Q6X0C3	Q6x0c3 anolis whit
104	14	58.3	10	2	Q6X0D2	Q6x0d2 anolis armo

105	14	58.3	10	2	Q6X0D8	Q6x0d8 anolis long	178	14	58.3	19	2	Q44506	Q44506 anabaena va
106	14	58.3	10	2	Q71DR5	Q71dr5 leiocephalu	179	14	58.3	19	2	Q6QLM2	Q6qlm2 influenza a
107	14	58.3	10	2	Q71DR8	Q71dr8 leiocephalu	180	14	58.3	20	1	CRTC_SPIOL	P30806 spinacia oi
108	14	58.3	10	2	Q71DS4	Q71ds4 tropidurus	181	14	58.3	20	1	GBB4_RAT	Q35353 rattus norv
109	14	58.3	10	2	Q71DS7	Q71ds7 tropidurus	182	14	58.3	20	2	Q95MJ7	Q95mj7 tarsius syr
110	14	58.3	10	2	Q71DT0	Q71dt0 uranoscodon	183	14	58.3	20	2	Q95MJ8	Q95mj8 galago moho
111	14	58.3	10	2	Q71DT3	Q71dt3 tropidurus	184	14	58.3	20	2	Q95MJ9	Q95mj9 pan troglod
112	14	58.3	10	2	Q71DT6	Q71dt6 uracentron	185	14	58.3	20	2	Q95MK0	Q95mk0 pongo pygma
113	14	58.3	10	2	Q71DT9	Q71dt9 stenocercus	186	14	58.3	20	2	Q95MK1	Q95mk1 colobus ang
114	14	58.3	10	2	Q71DU2	Q71du2 stenocercus	187	14	58.3	20	2	Q95MK2	Q95mk2 papio cynoc
115	14	58.3	10	2	Q71DU5	Q71du5 stenocercus	188	14	58.3	20	2	Q95MK3	Q95mk3 ateles belz
116	14	58.3	10	2	Q71DU8	Q71du8 sceloporos	189	14	58.3	20	2	Q95MK4	Q95mk4 cheirogaleu
117	14	58.3	10	2	Q71DW0	Q71dw0 phrynosoma	190	14	58.3	20	2	Q95MK6	Q95mk6 eulemur cor
118	14	58.3	10	2	Q71DX5	Q71dx5 urostrophus	191	14	58.3	20	2	Q9TRA4	Q9tra4 sus scrofa
119	14	58.3	10	2	Q71DX8	Q71dx8 enyalius le	192	14	58.3	20	2	Q66548	Q66548 human herpe
120	14	58.3	10	2	Q71DY1	Q71dy1 pristidactyl	193	13	54.2	6	1	EI01_LITRU	P82096 litoria rub
121	14	58.3	10	2	Q71DY4	Q71dy4 leiosaurus	194	13	54.2	9	2	Q28121	Q28121 bos taurus
122	14	58.3	10	2	Q71DY7	Q71dy7 leiosaurus	195	13	54.2	15	2	Q6JQC4	Q6jcg4 tetraleurod
123	14	58.3	10	2	Q71DZ0	Q71dz0 diplolaemus	196	13	54.2	15	2	Q6JCS2	Q6jcs2 aleurolatu
124	14	58.3	10	2	Q71DZ3	Q71dz3 diplolaemus	197	13	54.2	16	2	Q697F2	Q697f2 bemisia sp.
125	14	58.3	10	2	Q71E08	Q71e08 anolis cybo	198	13	54.2	16	2	Q9XNP6	Q9xnp6 boophilus m
126	14	58.3	10	2	Q71E11	Q71e11 chalarodon	199	13	54.2	18	2	Q7S173	Q7s173 neurospora
127	14	58.3	10	2	Q71E23	Q71e23 corytophane	200	13	54.2	18	2	Q8RU82	Q8ru82 zea mays (m
128	14	58.3	10	2	Q71E35	Q71e35 basiliscus	201	13	54.2	19	2	Q9TU41	Q9tu41 loxodonta a
129	14	58.3	10	2	Q71ESD0	Q71sd0 liolaemus w	202	13	54.2	19	2	Q9TU42	Q9tu42 mammothus p
130	14	58.3	10	2	Q9T8U8	Q9t8u8 liolaemus p	203	13	54.2	19	2	Q99722	Q99722 lamprotorni
131	14	58.3	10	2	Q9T8X1	Q9t8x1 liolaemus a	204	13	54.2	20	2	Q90X92	Q90x92 gallus gall
132	14	58.3	10	2	Q9ZYS6	Q9zys6 stenocercus	205	12	50.0	8	2	Q7GEM6	Q7gem6 branchiosto
133	14	58.3	12	2	Q6WR34	Q6wr34 phoenicopte	206	12	50.0	10	1	GON1_PETMA	P04378 petromyzon
134	14	58.3	12	2	Q6WR37	Q6wr37 buteo jamai	207	12	50.0	10	2	Q6UJL2	Q6ujl2 strophurus
135	14	58.3	12	2	Q6WR43	Q6wr43 scolopax mi	208	12	50.0	11	1	CA31_LITCI	P82089 litoria cit
136	14	58.3	12	2	Q6WR55	Q6wr55 crinifer pi	209	12	50.0	11	1	CA32_LITCI	P82090 litoria cit
137	14	58.3	12	2	Q6WR58	Q6wr58 musophaga v	211	12	50.0	11	1	CORZ_PERAM	P11496 periplaneta
138	14	58.3	12	2	Q6WR82	Q6wr82 urocolius m	212	12	50.0	11	2	Q6E5M8	Q6e5m8 ptyctolaemu
139	14	58.3	12	2	Q6WR88	Q6wr88 coracias sp	213	12	50.0	11	2	Q9G359	Q9g359 japalura fl
140	14	58.3	12	2	Q6WR91	Q6wr91 trogon curu	214	12	50.0	12	2	Q9G607	Q9g607 aphaniotis
141	14	58.3	12	2	Q6WR94	Q6wr94 tockus eryt	215	12	50.0	16	2	P92680	P92680 trimeresuru
142	14	58.3	12	2	Q6WR97	Q6wr97 anseranas s	216	12	50.0	17	2	Q8MJ33	Q8mj33 sus scrofa
143	14	58.3	12	2	Q6WRA0	Q6wra0 chauna torq	217	12	50.0	17	2	Q9TR22	Q9tr22 bos taurus
144	14	58.3	12	2	Q6WRA3	Q6wra3 megapodius	218	12	50.0	18	2	Q9QW51	Q9qw51 mus sp. . a
145	14	58.3	12	2	Q6WRA6	Q6wra6 alectura la	219	12	50.0	19	2	Q7REE1	Q7ree1 plasmodium
146	14	58.3	12	2	Q6WRA9	Q6wra9 crax rubra	220	11	45.8	2	1	GWA_SEPOF	P83570 sepia offic
147	14	58.3	12	2	Q8HN63	Q8hn63 sayornis ph	221	11	45.8	4	1	OCP3_OCTMI	P58649 octopus min
148	14	58.3	12	2	Q8HN66	Q8hn66 acryllium v	222	11	45.8	5	1	BPP7_BOTIN	P30425 bothrops in
149	14	58.3	12	2	Q53579	Q53579 rhodobacter	223	11	45.8	5	1	UF01_MOUSE	P38639 mus musculu
150	14	58.3	13	1	BML2_BOMVA	P84211 bombina var	224	11	45.8	6	1	LOK1_LOCOMI	P41491 locusta mig
151	14	58.3	13	1	YPNP_PHOLU	P41122 photorhabdu	225	11	45.8	7	1	BRHP_CONIM	P58803 conus imper
152	14	58.3	13	2	Q7M1F5	Q7mf5 freesia ref	226	11	45.8	7	1	TPFY_PACDA	P83455 pachymedusa
153	14	58.3	13	2	Q66NE7	Q66ne7 borrelia bu	227	11	45.8	7	1	TY51_LITRU	P82065 litoria rub
154	14	58.3	13	2	Q718T2	Q718t2 newcastle d	228	11	45.8	7	1	WWA1_ACHFU	P35919 achatina fu
155	14	58.3	15	2	Q6LCZ7	Q6lcz7 homo sapien	229	11	45.8	7	1	WWA2_ACHFU	P35920 achatina fu
156	14	58.3	15	2	Q9UC22	Q9uc22 homo sapien	230	11	45.8	7	1	Q9BR4	P35921 achatina fu
157	14	58.3	15	2	Q53580	Q53580 rhodobacter	231	11	45.8	7	2	Q95945	Q95945 saccharomyc
158	14	58.3	15	2	Q9R5D6	Q9r5d6 chromatium	232	11	45.8	7	2	O49223	O49223 glycine max
159	14	58.3	16	2	Q79B06	Q79b06 helicobacte	233	11	45.8	7	2	Q8KMS9	Q8kms9 enterobacte
160	14	58.3	16	2	Q9R4F2	Q9r4f2 streptomyce	234	11	45.8	7	2	Q8GL00	Q8gl00 borrelia bu
161	14	58.3	16	2	Q9QW76	Q9qw76 mus sp. hom	235	11	45.8	7	2	Q8GL04	Q8gl04 borrelia bu
162	14	58.3	16	2	Q8QGA1	Q8qgai brachydanio	236	11	45.8	7	2	Q8JE81	Q8je81 human immun
163	14	58.3	17	2	Q8MIG9	Q8mig9 cynopterus	237	11	45.8	8	1	ACI_THUAL	P18691 thunnus alb
164	14	58.3	17	2	Q9QUJ4	Q9quj4 mus sp. mep	238	11	45.8	8	1	AKI_GEOST	P84241 geotrupees s
165	14	58.3	17	2	Q6QLL7	Q6ql17 influenza a	239	11	45.8	8	1	AKH_MELML	P84240 melolontha
166	14	58.3	17	2	Q6QLL9	Q6ql19 influenza a	240	11	45.8	8	1	AKH_PACMA	P84242 pachnoda ma
167	14	58.3	17	2	Q6QLM0	Q6qlm0 influenza a	241	11	45.8	8	1	AKH_PACMA	P83661 cyphononyx
168	14	58.3	17	2	Q6QLM1	Q6qlm1 influenza a	242	11	45.8	8	1	C125_CYPDO	P68125 dasyurus vi
169	14	58.3	18	2	Q8N0X8	Q8n0x8 homo sapien	243	11	45.8	8	1	CCKN_DASVI	P68126 macropus eu
170	14	58.3	18	2	Q71U72	Q71u72 homo sapien	244	11	45.8	8	1	CCKN_MACEU	P58785 conus purpu
171	14	58.3	18	2	Q9ZYW4	Q9zyw4 habrobracon	245	11	45.8	8	1	COW2_CONPU	P21140 leucophaea
172	14	58.3	18	2	Q9ZYX7	Q9zyx7 perga conde	246	11	45.8	8	1	LCK1_LEUMA	P21141 leucophaea
173	14	58.3	19	2	P83003	P83003 entamoeba h	247	11	45.8	8	1	LCK2_LEUMA	P21142 leucophaea
174	14	58.3	19	2	Q9N1W2	Q9n1w2 equus cabal	248	11	45.8	8	1	LCK3_LEUMA	P21143 leucophaea
175	14	58.3	19	2	Q9T2V5	Q9t2v5 crithidia f	249	11	45.8	8	1	LCK4_LEUMA	P19987 leucophaea
176	14	58.3	19	2	Q9ZYW7	Q9zyw7 aphidius ro	250	11	45.8	8	1	LCK5_LEUMA	
177	14	58.3	19	2	Q9ZYW8	Q9zyw8 ichneutes b							

251	11	45.8	8	1	LCK6_LEUMA	P19988 leucophaea	324	11	45.8	9	1	LITR_PHYRO	P08946 phyllomedus
252	11	45.8	8	1	LCK7_LEUMA	P19989 leucophaea	325	11	45.8	9	1	LMIP_LOCFMI	P31799 locusta mig
253	11	45.8	8	1	LCK8_LEUMA	P19990 leucophaea	326	11	45.8	9	1	NEF_HV1Z8	P12481 human immun
254	11	45.8	8	1	NGIF_RAT	P82598 rattus norv	327	11	45.8	9	1	PTSP_BOMMO	P82003 bombyx mori
255	11	45.8	8	1	PK1_PERAM	P82685 periplaneta	328	11	45.8	9	2	O95953	O95953 homo sapien
256	11	45.8	8	1	PK2_PERAM	P82686 periplaneta	329	11	45.8	9	2	O16386	O16386 homo sapien
257	11	45.8	8	1	PK3_PERAM	P82687 periplaneta	330	11	45.8	9	2	O61DB5	O61DB5 homo sapien
258	11	45.8	8	1	PK4_PERAM	P82688 periplaneta	331	11	45.8	9	2	O6QF45	O6QF45 homo sapien
259	11	45.8	8	1	PK5_PERAM	P82689 periplaneta	332	11	45.8	9	2	O71EB9	O71EB9 homo sapien
260	11	45.8	8	1	PLP_BRANA	P81707 brassica na	333	11	45.8	9	2	O7M4S2	O7M4S2 homo sapien
261	11	45.8	8	1	RT34_BOVIN	P82929 bos taurus	334	11	45.8	9	2	O9H326	O9H326 homo sapien
262	11	45.8	8	1	VAM6_MOUSE	P83853 mus musculu	335	11	45.8	9	2	O9H3Y3	O9H3Y3 homo sapien
263	11	45.8	8	2	Q15888	Q15888 homo sapien	336	11	45.8	9	2	O9UC36	O9UC36 homo sapien
264	11	45.8	8	2	Q15890	Q15890 homo sapien	337	11	45.8	9	2	O9UCQ9	O9UCQ9 homo sapien
265	11	45.8	8	2	Q81VK3	Q81VK3 homo sapien	338	11	45.8	9	2	O9UK44	O9UK44 homo sapien
266	11	45.8	8	2	Q86SL0	Q86SL0 homo sapien	339	11	45.8	9	2	O9UUA0	O9UUA0 homo sapien
267	11	45.8	8	2	Q7M3S2	Q7M3S2 trypanosoma	340	11	45.8	9	2	O9UMF3	O9UMF3 homo sapien
268	11	45.8	8	2	Q7M3S3	Q7M3S3 trypanosoma	341	11	45.8	9	2	O9UQW0	O9UQW0 homo sapien
269	11	45.8	8	2	Q02831	Q02831 oryctolagus	342	11	45.8	9	2	O7M3N7	O7M3N7 gryllus bim
270	11	45.8	8	2	Q95M23	Q95M23 sus scrofa	343	11	45.8	9	2	O7M3N8	O7M3N8 gryllus bim
271	11	45.8	8	2	Q9TRY3	Q9TRY3 sus sp. ins	344	11	45.8	9	2	O7M3N9	O7M3N9 gryllus bim
272	11	45.8	8	2	Q8W8G2	Q8W8G2 diadema sav	345	11	45.8	9	2	O7M4D5	O7M4D5 diadema set
273	11	45.8	8	2	Q8W8G3	Q8W8G3 diadema pau	346	11	45.8	9	2	O9MW43	O9MW43 homo sapien
274	11	45.8	8	2	Q8W8G4	Q8W8G4 diadema mex	347	11	45.8	9	2	O8SHF0	O8SHF0 chamaeleo n
275	11	45.8	8	2	Q8W8G5	Q8W8G5 diadema ant	348	11	45.8	9	2	O8W8W5	O8W8W5 diadema set
276	11	45.8	8	2	Q8W8G6	Q8W8G6 diadema mex	349	11	45.8	9	2	O8W8W6	O8W8W6 diadema ant
277	11	45.8	8	2	Q8WGD7	Q8WGD7 lomix hirta	350	11	45.8	9	2	O8W8X4	O8W8X4 diadema mex
278	11	45.8	8	2	Q94PX5	Q94PX5 felis silve	351	11	45.8	9	2	O8WFS4	O8WFS4 diadema mex
279	11	45.8	8	2	Q94PX6	Q94PX6 felis libyc	352	11	45.8	9	2	O94NA9	O94NA9 daubentonia
280	11	45.8	8	2	Q94PX7	Q94PX7 felis silve	353	11	45.8	9	2	O94NB0	O94NB0 microcebus
281	11	45.8	8	2	Q94V82	Q94V82 varanus yuw	354	11	45.8	9	2	O94NB1	O94NB1 microcebus
282	11	45.8	8	2	Q94V88	Q94V88 varanus tri	355	11	45.8	9	2	O94NB2	O94NB2 microcebus
283	11	45.8	8	2	Q94V91	Q94V91 varanus tim	356	11	45.8	9	2	O94VC6	O94VC6 varanus pil
284	11	45.8	8	2	Q94VA7	Q94VA7 varanus sal	357	11	45.8	9	2	O94VD8	O94VD8 varanus nil
285	11	45.8	8	2	Q94VB2	Q94VB2 varanus sal	358	11	45.8	9	2	O94VE1	O94VE1 varanus mer
286	11	45.8	8	2	Q94VB5	Q94VB5 varanus sal	359	11	45.8	9	2	O94VG2	O94VG2 varanus ind
287	11	45.8	8	2	Q94VC1	Q94VC1 varanus rud	360	11	45.8	9	2	O94VH4	O94VH4 varanus gla
288	11	45.8	8	2	Q94VE4	Q94VE4 varanus mel	361	11	45.8	9	2	O94VI0	O94VI0 varanus gig
289	11	45.8	8	2	Q94VF6	Q94VF6 varanus job	362	11	45.8	9	2	O94VI8	O94VI8 varanus ere
290	11	45.8	8	2	Q94VF9	Q94VF9 varanus ind	363	11	45.8	9	2	O94VJ1	O94VJ1 varanus dor
291	11	45.8	8	2	Q94VJ4	Q94VJ4 varanus ben	364	11	45.8	9	2	O94XE6	O94XE6 tectocoris
292	11	45.8	8	2	Q70Y57	Q70Y57 fuerstia af	365	11	45.8	9	2	O691D6	O691D6 anolis sagr
293	11	45.8	8	2	Q70Y84	Q70Y84 plectranthu	366	11	45.8	9	2	O71DX2	O71DX2 urostrophus
294	11	45.8	8	2	Q715L5	Q715L5 varanus dum	367	11	45.8	9	2	O85DB0	O85DB0 lepitemur s
295	11	45.8	8	2	Q9T4Y2	Q9T4Y2 asterina pe	368	11	45.8	9	2	O85DB8	O85DB8 lepitemur e
296	11	45.8	8	2	Q9TD02	Q9TD02 terranatos	369	11	45.8	9	2	O9T688	O9T688 gekko gekko
297	11	45.8	8	2	Q6ZZ01	Q6ZZ01 silene conl	370	11	45.8	9	2	O38366	O38366 bacterioph
298	11	45.8	8	2	Q6ZZ02	Q6ZZ02 lychnis cor	371	11	45.8	9	2	O6A1H7	O6A1H7 hordeum vul
299	11	45.8	8	2	O85406	O85406 coxiella bu	372	11	45.8	9	2	O6ZZ00	O6ZZ00 silene rotu
300	11	45.8	8	2	O6LDP8	O6LDP8 pseudomonas	373	11	45.8	9	2	O47410	O47410 escherichia
301	11	45.8	8	2	O7M0L0	O7M0L0 clostridium	374	11	45.8	9	2	O6VCX0	O6VCX0 streptomyce
302	11	45.8	8	2	O7M124	O7M124 kluyvera ci	375	11	45.8	9	2	O8GL26	O8GL26 borrelia bu
303	11	45.8	8	2	O8G940	O8G940 borrelia bu	376	11	45.8	9	2	O8GL31	O8GL31 borrelia bu
304	11	45.8	8	2	O8GL21	O8GL21 borrelia bu	377	11	45.8	9	2	O9R5M1	O9R5M1 staphylococ
305	11	45.8	8	2	O35835	O35835 rattus sp.	378	11	45.8	9	2	O9R635	O9R635 chlamydia t
306	11	45.8	8	2	P70243	P70243 mus musculu	379	11	45.8	9	2	O9R9C4	O9R9C4 borrelia bu
307	11	45.8	8	2	Q99MN0	Q99MN0 mus musculu	380	11	45.8	9	2	O6LAQ1	O6LAQ1 rattus norv
308	11	45.8	8	2	Q62721	Q62721 rattus norv	381	11	45.8	9	2	O7M078	O7M078 rattus norv
309	11	45.8	8	2	Q9ET16	Q9ET16 mesocricetu	382	11	45.8	9	2	O80X07	O80X07 mus.sp. thr
310	11	45.8	8	2	Q9ET17	Q9ET17 mus caroli	383	11	45.8	9	2	O90350	O90350 gb virus c/
311	11	45.8	8	2	Q9ET18	Q9ET18 mus spretus	384	11	45.8	9	2	O65711	O65711 berne virus
312	11	45.8	8	2	Q64971	Q64971 alfalfa mos	385	11	45.8	9	2	O69100	O69100 human herpe
313	11	45.8	8	2	P79940	P79940 xenopus lae	386	11	45.8	9	2	O89491	O89491 murine minu
314	11	45.8	8	2	Q98TU5	Q98TU5 xenopus lae	387	11	45.8	9	2	O673W5	O673W5 tyrannus me
315	11	45.8	8	2	Q68LF1	Q68LF1 myrmotherul	388	11	45.8	9	2	O673W6	O673W6 terpsiphone
316	11	45.8	8	2	Q68LG3	Q68LG3 sakesphorus	389	11	45.8	9	2	O673W7	O673W7 telophorus
317	11	45.8	8	2	Q6R7U6	Q6R7U6 gnypetoscin	390	11	45.8	9	2	O673W8	O673W8 tchagra sen
318	11	45.8	8	2	O7L227	O7L227 naja oxiana	391	11	45.8	9	2	O673W9	O673W9 tchagra aus
319	11	45.8	9	1	CAER_PHYSA	Q71ZC4 phyllomedus	392	11	45.8	9	2	O673X0	O673X0 rhodophoneu
320	11	45.8	9	1	COW_CONVE	P83047 conus ventr	393	11	45.8	9	2	O673X1	O673X1 rhipidura a
321	11	45.8	9	1	D1_NEPNO	P24816 nephrops no	394	11	45.8	9	2	O673X2	O673X2 pseudobias
322	11	45.8	9	1	DSIP_RABIT	P01158 oryctolagus	395	11	45.8	9	2	O673X3	O673X3 prionops sc
323	11	45.8	9	1	LITO_LITAU	P08945 litoria aur	396	11	45.8	9	2	O673X4	O673X4 prionops re

397	11	45.8	9	2	Q673X5	Q673x5 platysteira
398	11	45.8	9	2	Q673X6	Q673x6 oriolus xan
399	11	45.8	9	2	Q673X7	Q673x7 nilaus afer
400	11	45.8	9	2	Q673X8	Q673x8 bias flammu
401	11	45.8	9	2	Q673X9	Q673x9 malacotus
402	11	45.8	9	2	Q673Y0	Q673y0 lanius coll
403	11	45.8	9	2	Q673Y1	Q673y1 lanioturdus
404	11	45.8	9	2	Q673Y2	Q673y2 laniarius i
405	11	45.8	9	2	Q673Y3	Q673y3 laniarius f
406	11	45.8	9	2	Q673Y4	Q673y4 laniarius b
407	11	45.8	9	2	Q673Y5	Q673y5 laniarius a
408	11	45.8	9	2	Q673Y6	Q673y6 platysteira
409	11	45.8	9	2	Q673Y7	Q673y7 dryoscopus
410	11	45.8	9	2	Q673Y8	Q673y8 dryoscopus
411	11	45.8	9	2	Q673Y9	Q673y9 dicrurus pa
412	11	45.8	9	2	Q673Z0	Q673z0 cyanolanius
413	11	45.8	9	2	Q673Z1	Q673z1 corvus coro
414	11	45.8	9	2	Q673Z2	Q673z2 coracina me
415	11	45.8	9	2	Q673Z3	Q673z3 telophorus
416	11	45.8	9	2	Q673Z4	Q673z4 telophorus
417	11	45.8	9	2	Q673Z5	Q673z5 telophorus
418	11	45.8	9	2	Q673Z6	Q673z6 campehaga
419	11	45.8	9	2	Q673Z7	Q673z7 tchagra min
420	11	45.8	9	2	Q673Z8	Q673z8 bias musicu
421	11	45.8	9	2	Q673Z9	Q673z9 batis poens
422	11	45.8	9	2	Q78DU2	Q78du2 gallus gall
423	11	45.8	9	2	Q7LZ66	Q7Lz66 meleagris g
424	11	45.8	9	2	Q801K0	Q801k0 ilicura mil
425	11	45.8	9	2	Q801K1	Q801k1 chiroxiphia
426	11	45.8	9	2	Q801K2	Q801k2 antilophia
427	11	45.8	9	2	Q9PRJ4	Q9prj4 lepisosteus
428	11	45.8	9	2	Q85723	Q85723 simian sarc
429	11	45.8	10	1	AEGL_AGRAE	P83465 agrocybe ae
430	11	45.8	10	1	APE_CAPGI	P80474 capnocytoph
431	11	45.8	10	1	BPP2_BOTIN	P30422 bothrops in
432	11	45.8	10	1	BPP2_BOTJA	P01022 bothrops ja
433	11	45.8	10	1	BPP8_BOTIN	P30426 bothrops in
434	11	45.8	10	1	BPP_VIPAS	P31351 vipera aspi
435	11	45.8	10	1	BRK_ONCMY	Q9prz1 oncorhynchu
436	11	45.8	10	1	CAL2_LITCI	P62540 litoria cit
437	11	45.8	10	1	CAL2_LITSP	P62541 litoria spl
438	11	45.8	10	1	CAER_LITXA	P56264 litoria xan
439	11	45.8	10	1	GON1_ALLMI	P37041 alligator m
440	11	45.8	10	1	GON1_CHEPR	P80677 chelysoma
441	11	45.8	10	1	GON1_CLUPA	P81749 clupea pall
442	11	45.8	10	1	GON2_ALLMI	P68073 alligator m
443	11	45.8	10	1	GON2_CHEPR	P80678 chelysoma
444	11	45.8	10	1	GON2_CHICK	P68072 gallus gall
445	11	45.8	10	1	GON2_CLUPA	P68075 clupea pall
446	11	45.8	10	1	GON2_HYDCO	P68076 hydrolagus
447	11	45.8	10	1	GON2_SQUAC	P68074 squalus aca
448	11	45.8	10	1	GON3_ONCKE	P20367 oncorhynchu
449	11	45.8	10	1	GON3_PETMA	P30948 petromyzon
450	11	45.8	10	1	GONL_SQUAC	P27429 squalus aca
451	11	45.8	10	1	GRP_RANRI	P23260 rana ridibu
452	11	45.8	10	1	LABA_JATMU	P13270 jatropha mu
453	11	45.8	10	1	MP2_MICOC	P81533 microplitis
454	11	45.8	10	1	NO40_TOBAC	P55962 nicotiana t
455	11	45.8	10	1	PNAL_PRUDU	P81899 prunus dulc
456	11	45.8	10	1	TPIS_NICPL	P19118 nicotiana p
457	11	45.8	10	2	Q7M530	Q7m530 pyrococcus
458	11	45.8	10	2	Q7M4X1	Q7m4x1 basidiobolu
459	11	45.8	10	2	Q7SA62	Q7sa62 neurospora
460	11	45.8	10	2	Q15342	Q15342 homo sapien
461	11	45.8	10	2	Q8WTT4	Q8wtt4 homo sapien
462	11	45.8	10	2	Q96QA7	Q96qa7 homo sapien
463	11	45.8	10	2	Q6LA62	Q6la62 homo sapien
464	11	45.8	10	2	Q25355	Q25355 locusta mig
465	11	45.8	10	2	Q25356	Q25356 locusta mig
466	11	45.8	10	2	Q7RRV6	Q7rrv6 plasmodium
467	11	45.8	10	2	Q7M2Z8	Q7m2z8 bos taurus
468	11	45.8	10	2	Q7M3E8	Q7m3e8 sus scrofa
469	11	45.8	10	2	Q9N1X1	Q9n1x1 equus cabal

470	11	45.8	10	2	Q9TR47	Q9tr47 bos taurus
471	11	45.8	10	2	Q9TS43	Q9ts43 sus scrofa
472	11	45.8	10	2	Q9TU33	Q9tu33 canis famil
473	11	45.8	10	2	Q79888	Q79888 basiliscus
474	11	45.8	10	2	Q79891	Q79891 crotophytus
475	11	45.8	10	2	Q79894	Q79894 gambelia wi
476	11	45.8	10	2	Q79900	Q79900 liolaemus p
477	11	45.8	10	2	Q79909	Q79909 sauromalus
478	11	45.8	10	2	Q79912	Q79912 chamaeleo f
479	11	45.8	10	2	Q79915	Q79915 leirolepis b
480	11	45.8	10	2	Q79924	Q79924 elgaria pan
481	11	45.8	10	2	Q79924	P92616 aspidosceli
482	11	45.8	10	2	P92632	P92632 eremias gra
483	11	45.8	10	2	P92648	P92648 lialis jica
484	11	45.8	10	2	P92654	P92654 euprepis au
485	11	45.8	10	2	P92733	P92733 fejervarya
486	11	45.8	10	2	P92758	P92758 teratoscinc
487	11	45.8	10	2	P92762	P92762 uromastyx a
488	11	45.8	10	2	P92766	P92766 varanus gri
489	11	45.8	10	2	P92771	P92771 xenosaurus
490	11	45.8	10	2	P92774	P92774 xantusia vi
491	11	45.8	10	2	Q8SH83	Q8sh83 brookesia t
492	11	45.8	10	2	Q8SH85	Q8sh85 brookesia t
493	11	45.8	10	2	Q8SH88	Q8sh88 brookesia t
494	11	45.8	10	2	Q8SH90	Q8sh90 brookesia s
495	11	45.8	10	2	Q8SH93	Q8sh93 brookesia p
496	11	45.8	10	2	Q8SH96	Q8sh96 brookesia p
497	11	45.8	10	2	Q8SH99	Q8sh99 brookesia n
498	11	45.8	10	2	Q8SHA2	Q8sha2 brookesia b
499	11	45.8	10	2	Q8SHA5	Q8sha5 brookesia a
500	11	45.8	10	2	Q8SHA8	Q8sha8 rhampholeon
501	11	45.8	10	2	Q8SHB1	Q8shb1 rhampholeon
502	11	45.8	10	2	Q8SHB4	Q8shb4 furcifer ve
503	11	45.8	10	2	Q8SHB7	Q8shb7 furcifer ou
504	11	45.8	10	2	Q8SHC0	Q8shc0 furcifer la
505	11	45.8	10	2	Q8SHC3	Q8shc3 furcifer la
506	11	45.8	10	2	Q8SHC6	Q8shc6 furcifer be
507	11	45.8	10	2	Q8SHC9	Q8shc9 furcifer ba
508	11	45.8	10	2	Q8SHD2	Q8shd2 chamaeleo w
509	11	45.8	10	2	Q8SHD5	Q8shd5 chamaeleo s
510	11	45.8	10	2	Q8SHD8	Q8shd8 chamaeleo r
511	11	45.8	10	2	Q8SHE1	Q8she1 chamaeleo q
512	11	45.8	10	2	Q8SHE4	Q8she4 chamaeleo q
513	11	45.8	10	2	Q8SHE7	Q8she7 chamaeleo p
514	11	45.8	10	2	Q8SHF3	Q8shf3 chamaeleo m
515	11	45.8	10	2	Q8SHF6	Q8shf6 chamaeleo m
516	11	45.8	10	2	Q8SHF9	Q8shf9 chamaeleo j
517	11	45.8	10	2	Q8SHG2	Q8shg2 chamaeleo j
518	11	45.8	10	2	Q8SHG5	Q8shg5 chamaeleo h
519	11	45.8	10	2	Q8SHG8	Q8shg8 chamaeleo g
520	11	45.8	10	2	Q8SHH1	Q8shh1 chamaeleo f
521	11	45.8	10	2	Q8SHH4	Q8shh4 chamaeleo f
522	11	45.8	10	2	Q8SHH7	Q8shh7 chamaeleo e
523	11	45.8	10	2	Q8SHI0	Q8shi0 chamaeleo d
524	11	45.8	10	2	Q8SHI3	Q8shi3 chamaeleo c
525	11	45.8	10	2	Q8SHI6	Q8shi6 chamaeleo c
526	11	45.8	10	2	Q8SHI9	Q8shi9 chamaeleo c
527	11	45.8	10	2	Q8SHJ2	Q8shj2 chamaeleo a
528	11	45.8	10	2	Q8SHJ5	Q8shj5 calumma par
529	11	45.8	10	2	Q8SHJ8	Q8shj8 calumma osh
530	11	45.8	10	2	Q8SHK1	Q8shk1 calumma nas
531	11	45.8	10	2	Q8SHK4	Q8shk4 calumma hil
532	11	45.8	10	2	Q8SHK7	Q8shk7 calumma glo
533	11	45.8	10	2	Q8SHL0	Q8shl0 calumma gas
534	11	45.8	10	2	Q8SHL3	Q8shl3 calumma fur
535	11	45.8	10	2	Q8SHL6	Q8shl6 calumma cuc
536	11	45.8	10	2	Q8SHL9	Q8shl9 calumma bre
537	11	45.8	10	2	Q8SHM2	Q8shm2 calumma boe
538	11	45.8	10	2	Q8SHM5	Q8shm5 bradypodion
539	11	45.8	10	2	Q8SHM8	Q8shm8 bradypodion
540	11	45.8	10	2	Q8SHN1	Q8shn1 bradypodion
541	11	45.8	10	2	Q8SHN4	Q8shn4 bradypodion
542	11	45.8	10	2	Q8SHN7	Q8shn7 bradypodion

543	11	45.8	10	2	Q8SHPO	Q8shp0 bradypodion	616	11	45.8	10	2	Q6WBL6	Q6wbl6 scelopor
544	11	45.8	10	2	Q8SIT8	Q8sit8 xantusia ar	617	11	45.8	10	2	Q6WBL9	Q6wbl9 scelopor
545	11	45.8	10	2	Q8SIU1	Q8siu1 xantusia be	618	11	45.8	10	2	Q6WBM2	Q6wbm2 scelopor
546	11	45.8	10	2	Q8SIU4	Q8siu4 xantusia he	619	11	45.8	10	2	Q6WBM5	Q6wbm5 scelopor
547	11	45.8	10	2	Q8W916	Q8w916 liolaemus m	620	11	45.8	10	2	Q6WBM8	Q6wbm8 scelopor
548	11	45.8	10	2	Q8WDG8	Q8wdg8 anolis line	621	11	45.8	10	2	Q6WBN1	Q6wbn1 scelopor
549	11	45.8	10	2	Q8WDI0	Q8wdi0 anolis sagr	622	11	45.8	10	2	Q6WBN4	Q6wbn4 scelopor
550	11	45.8	10	2	Q8WFT5	Q8wft5 diadema ant	623	11	45.8	10	2	Q6WBP0	Q6wbp0 scelopor
551	11	45.8	10	2	Q8WFT6	Q8wft6 diadema ant	624	11	45.8	10	2	Q6WBP3	Q6wbp3 scelopor
552	11	45.8	10	2	Q94NH4	Q94nh4 rana muscos	625	11	45.8	10	2	Q6WBP6	Q6wbp6 scelopor
553	11	45.8	10	2	Q94PD8	Q94pd8 varanus sca	626	11	45.8	10	2	Q6WBP9	Q6wbp9 scelopor
554	11	45.8	10	2	Q94V85	Q94v85 varanus var	627	11	45.8	10	2	Q6WBQ2	Q6wbq2 scelopor
555	11	45.8	10	2	Q94V97	Q94v97 varanus spe	628	11	45.8	10	2	Q6WBQ5	Q6wbq5 scelopor
556	11	45.8	10	2	Q94VC9	Q94vc9 varanus pan	629	11	45.8	10	2	Q6WBQ8	Q6wbq8 scelopor
557	11	45.8	10	2	Q94VD2	Q94vd2 varanus pan	630	11	45.8	10	2	Q6WBR7	Q6wbr7 scelopor
558	11	45.8	10	2	Q94VD5	Q94vd5 varanus oli	631	11	45.8	10	2	Q6WBS0	Q6wbs0 scelopor
559	11	45.8	10	2	Q94VF0	Q94vf0 varanus kin	632	11	45.8	10	2	Q6WBS6	Q6wbs6 scelopor
560	11	45.8	10	2	Q94VG5	Q94vg5 varanus gri	633	11	45.8	10	2	Q6WBS9	Q6wbs9 scelopor
561	11	45.8	10	2	Q94VH1	Q94vh1 varanus gle	634	11	45.8	10	2	Q6WBT2	Q6wbt2 scelopor
562	11	45.8	10	2	Q958J8	Q958j8 rana muscos	635	11	45.8	10	2	Q6WBT5	Q6wbt5 scelopor
563	11	45.8	10	2	Q958K0	Q958k0 rana cascad	636	11	45.8	10	2	Q6WBU7	Q6wbu7 urosaurus o
564	11	45.8	10	2	Q958K3	Q958k3 rana aurora	637	11	45.8	10	2	Q6WBV0	Q6wbv0 callisaurus
565	11	45.8	10	2	Q958K6	Q958k6 rana pretio	638	11	45.8	10	2	Q6WBV3	Q6wbv3 holbrookia
566	11	45.8	10	2	Q958K9	Q958k9 rana boylli	639	11	45.8	10	2	Q6WBV6	Q6wbv6 holbrookia
567	11	45.8	10	2	Q958L2	Q958l2 rana tempor	640	11	45.8	10	2	Q6WBV9	Q6wbv9 cophosaurus
568	11	45.8	10	2	Q958L5	Q958l5 rana sylvat	641	11	45.8	10	2	Q6X0E4	Q6x0e4 anolis stra
569	11	45.8	10	2	Q958L8	Q958l8 rana cateeb	642	11	45.8	10	2	Q71DS1	Q71ds1 microlophus
570	11	45.8	10	2	Q6UJG7	Q6ujg7 heteronotia	643	11	45.8	10	2	Q71DV1	Q71dv1 scelopor
571	11	45.8	10	2	Q6UJH0	Q6ujh0 gehyra vari	644	11	45.8	10	2	Q71DV4	Q71dv4 scelopor
572	11	45.8	10	2	Q6UJH3	Q6ujh3 lialis jica	645	11	45.8	10	2	Q71DV7	Q71dv7 scelopor
573	11	45.8	10	2	Q6UJH6	Q6ujh6 pseudotheca	646	11	45.8	10	2	Q71E02	Q71e02 anolis dist
574	11	45.8	10	2	Q6UJH9	Q6ujh9 phyllurus c	647	11	45.8	10	2	Q71E05	Q71e05 anolis cris
575	11	45.8	10	2	Q6UJ12	Q6uj12 nephurus m	648	11	45.8	10	2	Q71E14	Q71e14 brachylophu
576	11	45.8	10	2	Q6UJ15	Q6uj15 nephurus w	649	11	45.8	10	2	Q71E26	Q71e26 corytophane
577	11	45.8	10	2	Q6UJ18	Q6uj18 nephurus l	650	11	45.8	10	2	Q71E29	Q71e29 laemanctus
578	11	45.8	10	2	Q6UJ11	Q6uj11 nephurus v	651	11	45.8	10	2	Q71E32	Q71e32 basiliscus
579	11	45.8	10	2	Q6UJ14	Q6uj14 nephurus l	652	11	45.8	10	2	Q71G22	Q71gz2 andrena lim
580	11	45.8	10	2	Q6UJ17	Q6uj17 carphodactyl	653	11	45.8	10	2	Q71SB8	Q71sb8 liolaemus r
581	11	45.8	10	2	Q6UJ10	Q6uj10 crenadactyl	654	11	45.8	10	2	Q71SC1	Q71sc1 liolaemus f
582	11	45.8	10	2	Q6UJ13	Q6uj13 oedura marm	655	11	45.8	10	2	Q71SC4	Q71sc4 liolaemus a
583	11	45.8	10	2	Q6UJ16	Q6uj16 rhynchoedur	656	11	45.8	10	2	Q71SC7	Q71sc7 liolaemus s
584	11	45.8	10	2	Q6UJ19	Q6uj19 diplodactyl	657	11	45.8	10	2	Q71SD6	Q71sd6 liolaemus a
585	11	45.8	10	2	Q6UJ18	Q6uj18 strophurus	658	11	45.8	10	2	Q71SD9	Q71sd9 liolaemus a
586	11	45.8	10	2	Q6UJ11	Q6uj11 strophurus	659	11	45.8	10	2	Q71SE2	Q71se2 phymaturus
587	11	45.8	10	2	Q6UJ14	Q6uj14 diplodactyl	660	11	45.8	10	2	Q71SE5	Q71se5 phymaturus
588	11	45.8	10	2	Q6UJ17	Q6uj17 strophurus	661	11	45.8	10	2	Q71SE8	Q71se8 ctenoblepha
589	11	45.8	10	2	Q6UJ10	Q6uj10 diplodactyl	662	11	45.8	10	2	Q76MK5	Q76mk5 eurypharynx
590	11	45.8	10	2	Q6UJ13	Q6uj13 diplodactyl	663	11	45.8	10	2	Q76ML6	Q76ml6 eurypharynx
591	11	45.8	10	2	Q6UJ16	Q6uj16 diplodactyl	664	11	45.8	10	2	Q76MM1	Q76mm1 eurypharynx
592	11	45.8	10	2	Q6UJ19	Q6uj19 diplodactyl	665	11	45.8	10	2	Q7J5U5	Q7j5u5 ovis aries
593	11	45.8	10	2	Q6UJ12	Q6uj12 diplodactyl	666	11	45.8	10	2	Q85J75	Q85j75 varanus bre
594	11	45.8	10	2	Q6UJ15	Q6uj15 diplodactyl	667	11	45.8	10	2	Q85J75	Q85j75 varanus bre
595	11	45.8	10	2	Q6UJ18	Q6uj18 diplodactyl	668	11	45.8	10	2	Q9B0Z6	Q9b0z6 salamandra
596	11	45.8	10	2	Q6UJ11	Q6uj11 diplodactyl	669	11	45.8	10	2	Q9B1W9	Q9b1w9 mertensiell
597	11	45.8	10	2	Q6UJ14	Q6uj14 strophurus	670	11	45.8	10	2	Q9B1X0	Q9b1x0 mertensiell
598	11	45.8	10	2	Q6UJ17	Q6uj17 strophurus	671	11	45.8	10	2	Q9B4S0	Q9b4s0 mertensiell
599	11	45.8	10	2	Q6UJ10	Q6uj10 strophurus	672	11	45.8	10	2	Q9B4S5	Q9b4s5 mertensiell
600	11	45.8	10	2	Q6WBG8	Q6wbg8 liolaemus c	673	11	45.8	10	2	Q9B4S8	Q9b4s8 mertensiell
601	11	45.8	10	2	Q6WBH1	Q6wbh1 liolaemus x	674	11	45.8	10	2	Q9B4T1	Q9b4t1 mertensiell
602	11	45.8	10	2	Q6WBH4	Q6wbh4 liolaemus r	675	11	45.8	10	2	Q9B4U2	Q9b4u2 mertensiell
603	11	45.8	10	2	Q6WBH7	Q6wbh7 liolaemus h	676	11	45.8	10	2	Q9B4U5	Q9b4u5 mertensiell
604	11	45.8	10	2	Q6WB10	Q6wb10 liolaemus s	677	11	45.8	10	2	Q9B4U8	Q9b4u8 salamandra
605	11	45.8	10	2	Q6WB13	Q6wb13 liolaemus p	678	11	45.8	10	2	Q9B4V5	Q9b4v5 mertensiell
606	11	45.8	10	2	Q6WB16	Q6wb16 liolaemus k	679	11	45.8	10	2	Q9B4V8	Q9b4v8 chioglossa
607	11	45.8	10	2	Q6WB19	Q6wb19 liolaemus h	680	11	45.8	10	2	Q9B4W1	Q9b4w1 triturus vu
608	11	45.8	10	2	Q6WB12	Q6wb12 liolaemus p	681	11	45.8	10	2	Q9B4W4	Q9b4w4 pachytriton
609	11	45.8	10	2	Q6WB15	Q6wb15 liolaemus g	682	11	45.8	10	2	Q9B4W7	Q9b4w7 tylototrito
610	11	45.8	10	2	Q6WB18	Q6wb18 liolaemus n	683	11	45.8	10	2	Q9B4X0	Q9b4x0 notophthalm
611	11	45.8	10	2	Q6WBK1	Q6wbk1 scelopor	684	11	45.8	10	2	Q9G362	Q9g362 acanthosaur
612	11	45.8	10	2	Q6WBK4	Q6wbk4 scelopor	685	11	45.8	10	2	Q9G697	Q9g697 chamaeleo d
613	11	45.8	10	2	Q6WBK7	Q6wbk7 scelopor	686	11	45.8	10	2	Q9MJQ5	Q9mjq5 podospora c
614	11	45.8	10	2	Q6WBL0	Q6wbl0 scelopor	687	11	45.8	10	2	Q9T4P9	Q9t4p9 liolaemus d
615	11	45.8	10	2	Q6WBL3	Q6wbl3 scelopor	688	11	45.8	10	2	Q9T8F5	Q9t8f5 liolaemus b

689	11	45.8	10	2	Q9T8G0	Q9t8g0	liolaemus l	762	11	45.8	10	2	Q9TG74	Q9tg74	wetmorena h
690	11	45.8	10	2	Q9T8G5	Q9t8g5	liolaemus o	763	11	45.8	10	2	Q9TG77	Q9tg77	sauresia ag
691	11	45.8	10	2	Q9T8G8	Q9t8g8	liolaemus c	764	11	45.8	10	2	Q9TG80	Q9tg80	ophiodes st
692	11	45.8	10	2	Q9T8H1	Q9t8h1	liolaemus u	765	11	45.8	10	2	Q9TG83	Q9tg83	diploglossu
693	11	45.8	10	2	Q9T8H4	Q9t8h4	liolaemus i	766	11	45.8	10	2	Q9TG86	Q9tg86	diploglossu
694	11	45.8	10	2	Q9T8H7	Q9t8h7	liolaemus a	767	11	45.8	10	2	Q9TG89	Q9tg89	celestus en
695	11	45.8	10	2	Q9T8I0	Q9t8i0	liolaemus o	768	11	45.8	10	2	Q9TG92	Q9tg92	anniella pu
696	11	45.8	10	2	Q9T8I3	Q9t8i3	liolaemus q	769	11	45.8	10	2	Q9TG95	Q9tg95	anniella ge
697	11	45.8	10	2	Q9T8I6	Q9t8i6	liolaemus k	770	11	45.8	10	2	Q9TG98	Q9tg98	shinisaurus
698	11	45.8	10	2	Q9T8I9	Q9t8i9	liolaemus a	771	11	45.8	10	2	Q9TGA1	Q9tga1	heloderma s
699	11	45.8	10	2	Q9T8J2	Q9t8j2	liolaemus r	772	11	45.8	10	2	Q9XMB4	Q9xmb4	aegilops ta
700	11	45.8	10	2	Q9T8J5	Q9t8j5	liolaemus m	773	11	45.8	10	2	Q9ZYS9	Q9zys9	phymaturus
701	11	45.8	10	2	Q9T8J8	Q9t8j8	liolaemus w	774	11	45.8	10	2	Q9ZYT5	Q9zyt5	uta stansbu
702	11	45.8	10	2	Q9T8K1	Q9t8k1	liolaemus s	775	11	45.8	10	2	Q9ZYT8	Q9zyt8	urosaurus g
703	11	45.8	10	2	Q9T8K4	Q9t8k4	liolaemus s	776	11	45.8	10	2	Q9ZYU1	Q9zyu1	uma scopari
704	11	45.8	10	2	Q9T8K7	Q9t8k7	liolaemus m	777	11	45.8	10	2	Q9ZYU4	Q9zyu4	sceloporus
705	11	45.8	10	2	Q9T8L0	Q9t8l0	liolaemus o	778	11	45.8	10	2	Q9ZYU7	Q9zyu7	sator angus
706	11	45.8	10	2	Q9T8L3	Q9t8l3	liolaemus l	779	11	45.8	10	2	Q9ZVV0	Q9zyv0	petrosaurus
707	11	45.8	10	2	Q9T8L6	Q9t8l6	liolaemus p	780	11	45.8	10	2	Q9ZVV3	Q9zyv3	dipsosaurus
708	11	45.8	10	2	Q9T8L9	Q9t8l9	liolaemus f	781	11	45.8	10	2	P82443	P82443	nicotiana t
709	11	45.8	10	2	Q9T8M2	Q9t8m2	liolaemus c	782	11	45.8	10	2	Q99213	Q99213	aegilops ta
710	11	45.8	10	2	Q9T8M5	Q9t8m5	liolaemus a	783	11	45.8	10	2	P6TS30	P6ts30	lycopersico
711	11	45.8	10	2	Q9T8M8	Q9t8m8	liolaemus m	784	11	45.8	10	2	Q8GZC8	Q8gzc8	hordeum vul
712	11	45.8	10	2	Q9T8N1	Q9t8n1	liolaemus p	785	11	45.8	10	2	Q8KHN9	Q8khn9	clostridium
713	11	45.8	10	2	Q9T8N4	Q9t8n4	liolaemus d	786	11	45.8	10	2	Q93LX4	Q93lx4	vibrio chol
714	11	45.8	10	2	Q9T8N7	Q9t8n7	liolaemus o	787	11	45.8	10	2	Q93T35	Q93t35	acinetobact
715	11	45.8	10	2	Q9T8P0	Q9t8p0	liolaemus f	788	11	45.8	10	2	Q47561	Q47561	escherichia
716	11	45.8	10	2	Q9T8P3	Q9t8p3	liolaemus a	789	11	45.8	10	2	Q6JL97	Q6jl97	neisseria g
717	11	45.8	10	2	Q9T8P6	Q9t8p6	liolaemus r	790	11	45.8	10	2	Q6RI01	Q6ri01	clostridium
718	11	45.8	10	2	Q9T8P9	Q9t8p9	liolaemus m	791	11	45.8	10	2	Q79AV7	Q79av7	klebsiella
719	11	45.8	10	2	Q9T8Q2	Q9t8q2	liolaemus s	792	11	45.8	10	2	Q8G8W5	Q8g8w5	borrelia bu
720	11	45.8	10	2	Q9T8Q5	Q9t8q5	liolaemus l	793	11	45.8	10	2	Q9F9H5	Q9f9h5	helicobacte
721	11	45.8	10	2	Q9T8Q8	Q9t8q8	liolaemus e	794	11	45.8	10	2	Q9R5N2	Q9r5n2	clostridium
722	11	45.8	10	2	Q9T8R1	Q9t8r1	liolaemus a	795	11	45.8	10	2	O70580	O70580	mus musculu
723	11	45.8	10	2	Q9T8R4	Q9t8r4	liolaemus p	796	11	45.8	10	2	Q6LBT3	Q6lbt3	mus musculu
724	11	45.8	10	2	Q9T8R7	Q9t8r7	liolaemus c	797	11	45.8	10	2	Q8CJE0	Q8cje0	rattus norv
725	11	45.8	10	2	Q9T8R9	Q9t8r9	liolaemus b	798	11	45.8	10	2	Q9ESU5	Q9esu5	mus musculu
726	11	45.8	10	2	Q9T8S1	Q9t8s1	liolaemus l	799	11	45.8	10	2	O42355	O42355	brachydanio
727	11	45.8	10	2	Q9T8S4	Q9t8s4	liolaemus c	800	11	45.8	10	2	Q8JFE7	Q8jfe7	ficedula al
728	11	45.8	10	2	Q9T8S7	Q9t8s7	liolaemus n	801	11	45.8	10	2	Q8JJ33	Q8jj33	ficedula hy
729	11	45.8	10	2	Q9T8T0	Q9t8t0	liolaemus f	802	11	45.8	10	2	Q7LZC5	Q7lzc5	kassina mac
730	11	45.8	10	2	Q9T8T3	Q9t8t3	liolaemus n	803	11	45.8	10	2	Q9PRU9	Q9pru9	sparus aura
731	11	45.8	10	2	Q9T8T6	Q9t8t6	liolaemus m	804	11	45.8	10	2	Q8UT83	Q8ut83	human immun
732	11	45.8	10	2	Q9T8T9	Q9t8t9	liolaemus l	805	11	45.8	10	1	CEP1_ACHFU	P22790	achatina fu
733	11	45.8	10	2	Q9T8U2	Q9t8u2	liolaemus t	806	11	45.8	11	1	CX5A_CONAL	P58848	conus aulic
734	11	45.8	10	2	Q9T8U5	Q9t8u5	liolaemus z	807	11	45.8	11	1	CX5B_CONAL	P58849	conus aulic
735	11	45.8	10	2	Q9T8V0	Q9t8v0	liolaemus c	808	11	45.8	11	1	LPW_THETH	P05624	thermyz the
736	11	45.8	10	2	Q9T8V3	Q9t8v3	liolaemus c	809	11	45.8	11	1	MLG_THETH	P41989	theromyzon
737	11	45.8	10	2	Q9T8V6	Q9t8v6	liolaemus b	810	11	45.8	11	1	OAIF_SARBU	P83518	sarcophaga
738	11	45.8	10	2	Q9T8V9	Q9t8v9	liolaemus g	811	11	45.8	11	1	RANC_RANPI	P08951	rana pipien
739	11	45.8	10	2	Q9T8W2	Q9t8w2	liolaemus b	812	11	45.8	11	1	RR2_CONAM	P42341	conopholis
740	11	45.8	10	2	Q9T8W5	Q9t8w5	liolaemus r	813	11	45.8	11	2	Q9CIR7	Q9c1r7	saccharomyc
741	11	45.8	10	2	Q9T8W8	Q9t8w8	liolaemus b	814	11	45.8	11	2	Q8TDA8	Q8tda8	homo sapien
742	11	45.8	10	2	Q9T8X4	Q9t8x4	liolaemus c	815	11	45.8	11	2	Q9UCR1	Q9ucr1	homo sapien
743	11	45.8	10	2	Q9T8X7	Q9t8x7	phymaturus	816	11	45.8	11	2	Q9UE69	Q9ue69	homo sapien
744	11	45.8	10	2	Q9TFU6	Q9tfu6	teratoscinc	817	11	45.8	11	2	Q9UEL0	Q9uel0	homo sapien
745	11	45.8	10	2	Q9TFU9	Q9tfu9	teratoscinc	818	11	45.8	11	2	Q6UZ55	Q6uz55	littorina s
746	11	45.8	10	2	Q9TFV2	Q9tfv2	teratoscinc	819	11	45.8	11	2	Q7RH63	Q7rh63	plasmodium
747	11	45.8	10	2	Q9TFV5	Q9tfv5	eublepharus	820	11	45.8	11	2	Q6DW13	Q6dw13	bos taurus
748	11	45.8	10	2	Q9TG32	Q9tg32	ophisaurus	821	11	45.8	11	2	Q9GL48	Q9gl48	sus scrofa
749	11	45.8	10	2	Q9TG35	Q9tg35	ophisaurus	822	11	45.8	11	2	O77884	O77884	oreochromis
750	11	45.8	10	2	Q9TG38	Q9tg38	ophisaurus	823	11	45.8	11	2	O77885	O77885	oreochromis
751	11	45.8	10	2	Q9TG41	Q9tg41	ophisaurus	824	11	45.8	11	2	O77892	O77892	oreochromis
752	11	45.8	10	2	Q9TG44	Q9tg44	anguis frag	825	11	45.8	11	2	O77893	O77893	oreochromis
753	11	45.8	10	2	Q9TG47	Q9tg47	ophisaurus	826	11	45.8	11	2	O77894	O77894	oreochromis
754	11	45.8	10	2	Q9TG50	Q9tg50	elgaria mul	827	11	45.8	11	2	O77895	O77895	oreochromis
755	11	45.8	10	2	Q9TG53	Q9tg53	elgaria pau	828	11	45.8	11	2	O77896	O77896	oreochromis
756	11	45.8	10	2	Q9TG56	Q9tg56	elgaria kin	829	11	45.8	11	2	O77898	O77898	oreochromis
757	11	45.8	10	2	Q9TG59	Q9tg59	elgaria coe	830	11	45.8	11	2	O77906	O77906	oreochromis
758	11	45.8	10	2	Q9TG62	Q9tg62	mesaspis mo	831	11	45.8	11	2	O77908	O77908	oreochromis
759	11	45.8	10	2	Q9TG65	Q9tg65	abronia oax	832	11	45.8	11	2	O77913	O77913	oreochromis
760	11	45.8	10	2	Q9TG68	Q9tg68	gerrhonotus	833	11	45.8	11	2	O77914	O77914	oreochromis
761	11	45.8	10	2	Q9TG71	Q9tg71	barisia imb	834	11	45.8	11	2	O77918	O77918	pseudotroph



835	11	45.8	11	2	078118	078118 oreochromis
836	11	45.8	11	2	078120	078120 oreochromis
837	11	45.8	11	2	09UEX7	09uex7 homo sapien
838	11	45.8	11	2	079636	079636 laudakia hi
839	11	45.8	11	2	079639	079639 laudakia le
840	11	45.8	11	2	079642	079642 laudakia mi
841	11	45.8	11	2	079918	079918 physignathu
842	11	45.8	11	2	079921	079921 phrynoceph
843	11	45.8	11	2	079985	079985 laudakia ca
844	11	45.8	11	2	079986	079986 laudakia er
845	11	45.8	11	2	08MAZ1	08mazi maripa pani
846	11	45.8	11	2	08MAZ3	08mazi maripa repe
847	11	45.8	11	2	08MB39	08mb39 wilsonia hu
848	11	45.8	11	2	08MB58	08mb58 seddera hir
849	11	45.8	11	2	08MB77	08mb77 odonellia h
850	11	45.8	11	2	08MB79	08mb79 aniseia arg
851	11	45.8	11	2	08MB97	08mb97 merremia pe
852	11	45.8	11	2	08MBE1	08mbel ipomoea alb
853	11	45.8	11	2	08SKN0	08skn0 ctenophorus
854	11	45.8	11	2	08SKN3	08skn3 ctenophorus
855	11	45.8	11	2	08SKN6	08skn6 ctenophorus
856	11	45.8	11	2	08SKN9	08skn9 ctenophorus
857	11	45.8	11	2	08SKP2	08skp2 ctenophorus
858	11	45.8	11	2	08SKP5	08skp5 ctenophorus
859	11	45.8	11	2	08SKP8	08skp8 ctenophorus
860	11	45.8	11	2	08SKQ1	08skq1 ctenophorus
861	11	45.8	11	2	08SKQ4	08skq4 ctenophorus
862	11	45.8	11	2	08SKQ7	08skq7 ctenophorus
863	11	45.8	11	2	08SKR0	08skr0 rankinia di
864	11	45.8	11	2	08WC29	08wc29 ctenophorus
865	11	45.8	11	2	08WD02	08wd02 ctenophorus
866	11	45.8	11	2	08WD05	08wd05 ctenophorus
867	11	45.8	11	2	08WD08	08wd08 ctenophorus
868	11	45.8	11	2	08WD11	08wd11 ctenophorus
869	11	45.8	11	2	08WD14	08wd14 ctenophorus
870	11	45.8	11	2	08WD17	08wd17 ctenophorus
871	11	45.8	11	2	08WD20	08wd20 ctenophorus
872	11	45.8	11	2	08WD23	08wd23 ctenophorus
873	11	45.8	11	2	08WD26	08wd26 ctenophorus
874	11	45.8	11	2	08WD29	08wd29 ctenophorus
875	11	45.8	11	2	08WD50	08wd50 ceratophora
876	11	45.8	11	2	08WER4	08wer4 ceratophora
877	11	45.8	11	2	08WER7	08wer7 ceratophora
878	11	45.8	11	2	094V74	094v74 lanthanotus
879	11	45.8	11	2	094V77	094v77 heloderma s
880	11	45.8	11	2	094V94	094v94 varanus sto
881	11	45.8	11	2	094VB8	094vb8 varanus sal
882	11	45.8	11	2	094VE7	094ve7 varanus kom
883	11	45.8	11	2	094VG8	094vg8 varanus gou
884	11	45.8	11	2	094VH7	094vh7 varanus gil
885	11	45.8	11	2	094V15	094vi5 varanus exa
886	11	45.8	11	2	094VK1	094vk1 varanus aca
887	11	45.8	11	2	06E5N1	06esn1 ptyctolaemu
888	11	45.8	11	2	06WR61	06wr61 nandayus ne
889	11	45.8	11	2	06WR64	06wr64 neophema el
890	11	45.8	11	2	07M2E6	07m2e6 solanum tub
891	11	45.8	11	2	07M2F2	07m2f2 lycopersico
892	11	45.8	11	2	07Y9B6	07y9b6 amphiboluru
893	11	45.8	11	2	07Y9B9	07y9b9 tympanocryp
894	11	45.8	11	2	07Y9C2	07y9c2 tympanocryp
895	11	45.8	11	2	07Y9C5	07y9c5 tympanocryp
896	11	45.8	11	2	07Y9C8	07y9c8 tympanocryp
897	11	45.8	11	2	07Y9D1	07y9d1 tympanocryp
898	11	45.8	11	2	07Y9D7	07y9d7 pogona vitt
899	11	45.8	11	2	07Y9E0	07y9e0 pogona null
900	11	45.8	11	2	07Y9E3	07y9e3 pogona mitc
901	11	45.8	11	2	07Y9E6	07y9e6 pogona mino
902	11	45.8	11	2	07Y9E9	07y9e9 pogona mini
903	11	45.8	11	2	07Y9F2	07y9f2 pogona henn
904	11	45.8	11	2	07Y9F5	07y9f5 pogona brev
905	11	45.8	11	2	07Y9F8	07y9f8 lophognathu
906	11	45.8	11	2	07Y9G1	07y9g1 hypsilurus
907	11	45.8	11	2		

908	11	45.8	11	2	07Y9G4	07y9g4 hypsilurus
909	11	45.8	11	2	07Y9G7	07y9g7 hypsilurus
910	11	45.8	11	2	07Y9H0	07y9h0 hypsilurus
911	11	45.8	11	2	07Y9H3	07y9h3 hypsilurus
912	11	45.8	11	2	07Y9H6	07y9h6 hypsilurus
913	11	45.8	11	2	07Y9H9	07y9h9 diporiphora
914	11	45.8	11	2	07Y9I2	07y9i2 diporiphora
915	11	45.8	11	2	07Y9I5	07y9i5 diporiphora
916	11	45.8	11	2	07Y9I8	07y9i8 diporiphora
917	11	45.8	11	2	07Y9J1	07y9j1 diporiphora
918	11	45.8	11	2	07Y9J4	07y9j4 diporiphora
919	11	45.8	11	2	07Y9J7	07y9j7 diporiphora
920	11	45.8	11	2	07Y9K0	07y9k0 diporiphora
921	11	45.8	11	2	07Y9K3	07y9k3 diporiphora
922	11	45.8	11	2	07Y9K6	07y9k6 diporiphora
923	11	45.8	11	2	07Y9K9	07y9k9 amphiboluru
924	11	45.8	11	2	07Y9L3	07y9l3 amphiboluru
925	11	45.8	11	2	07Y9L5	07y9l5 amphiboluru
926	11	45.8	11	2	09G2N4	09g2n4 chlamydosau
927	11	45.8	11	2	09G350	09g350 laudakia sa
928	11	45.8	11	2	09G353	09g353 trapelus sa
929	11	45.8	11	2	09G356	09g356 agama atra
930	11	45.8	11	2	09G371	09g371 pogona barb
931	11	45.8	11	2	09G374	09g374 moloch horr
932	11	45.8	11	2	09G5V0	09g5v0 laudakia st
933	11	45.8	11	2	09G5V3	09g5v3 phrynoceph
934	11	45.8	11	2	09G5V6	09g5v6 phrynoceph
935	11	45.8	11	2	09G5V9	09g5v9 laudakia st
936	11	45.8	11	2	09G5W2	09g5w2 laudakia tu
937	11	45.8	11	2	09G5W5	09g5w5 laudakia nu
938	11	45.8	11	2	09G5W8	09g5w8 trapelus sa
939	11	45.8	11	2	09G5X1	09g5x1 trapelus pe
940	11	45.8	11	2	09G5X4	09g5x4 trapelus ag
941	11	45.8	11	2	09G5X7	09g5x7 trapelus ru
942	11	45.8	11	2	09G5Y0	09g5y0 pseudotrape
943	11	45.8	11	2	09G5Y3	09g5y3 agama impal
944	11	45.8	11	2	09G5Y6	09g5y6 agama agama
945	11	45.8	11	2	09G5Z5	09g5z5 japalura sp
946	11	45.8	11	2	09G5Z8	09g5z8 acanthosaur
947	11	45.8	11	2	09G604	09g604 gonocephalu
948	11	45.8	11	2	09G610	09g610 lyriocephal
949	11	45.8	11	2	09G613	09g613 cophotis ce
950	11	45.8	11	2	09G616	09g616 ceratophora
951	11	45.8	11	2	09G619	09g619 ceratophora
952	11	45.8	11	2	09G622	09g622 salea horsf
953	11	45.8	11	2	09G637	09g637 calotes lio
954	11	45.8	11	2	09G652	09g652 japalura va
955	11	45.8	11	2	09G655	09g655 japalura tr
956	11	45.8	11	2	09G658	09g658 hydrosaurus
957	11	45.8	11	2	09G661	09g661 tympanocryp
958	11	45.8	11	2	09G664	09g664 diporiphora
959	11	45.8	11	2	09G667	09g667 caimanops a
960	11	45.8	11	2	09G670	09g670 rankinia ad
961	11	45.8	11	2	09G673	09g673 ctenophorus
962	11	45.8	11	2	09G676	09g676 amphiboluru
963	11	45.8	11	2	09G679	09g679 hypsilurus
964	11	45.8	11	2	09G682	09g682 chelosania
965	11	45.8	11	2	09G685	09g685 arua modest
966	11	45.8	11	2	09G688	09g688 physignathu
967	11	45.8	11	2	09G691	09g691 lophognathu
968	11	45.8	11	2	09G694	09g694 elaeis guin
969	11	45.8	11	2	094IR5	094ir5 pinus radia
970	11	45.8	11	2	06T302	06t302 chlamydomon
971	11	45.8	11	2	07M1U2	07m1u2 oryza sativ
972	11	45.8	11	2	07M1W2	07m1w2 canavalia e
973	11	45.8	11	2	047602	047602 escherichia e
974	11	45.8	11	2	056413	056413 escherichia
975	11	45.8	11	2	0700S6	0700s6 mycoplasma
976	11	45.8	11	2	0798K4	0798k4 bacillus su
977	11	45.8	11	2	08GL19	08gl19 borrelia bu
978	11	45.8	11	2	08GL24	08gl24 borrelia bu
979	11	45.8	11	2	08K432	08k432 spalax juda
980	11	45.8	11	2	08K433	08k433 spalax gali

981	11	45.8	11	2	Q99JJC3	Q99jc3 rattus sp.
982	11	45.8	11	2	Q6LD68	Q6ld68 mus sp. acu
983	11	45.8	11	2	Q80W11	Q80w11 mus sp. nt-
984	11	45.8	11	2	Q8CGW6	Q8cgw6 rattus norv
985	11	45.8	11	2	Q9QVH3	Q9qvh3 rattus sp.
986	11	45.8	11	2	Q80GP0	Q80gp0 tomato leaf
987	11	45.8	11	2	Q65CG7	Q65cg7 sinaloa tom
988	11	45.8	11	2	Q90735	Q90735 gallus gall
989	11	45.8	11	2	Q7LZ10	Q7lzi0 gadus sp. a
990	11	45.8	11	2	Q83410	Q83410 mouse mamma
991	11	45.8	11	2	Q8ADI8	Q8adi8 human immun
992	11	45.8	11	2	Q9DZ32	Q9dz32 human immun
993	11	45.8	12	1	LICA_BACSU	P83878 bacillus su
994	11	45.8	12	1	NO40_LOTJA	O22426 lotus japon
995	11	45.8	12	1	NO40_SEGRO	O24369 sesbania ro
996	11	45.8	12	1	NO40_SOYBN	P55960 glycine max
997	11	45.8	12	1	RF1_CONSP	P58805 conus spuri
998	11	45.8	12	1	UP01_CAEEL	P55954 caenorhabdi
999	11	45.8	12	1	UR2A_CATCO	P04558 catostomus
1000	11	45.8	12	2	Q90XU4	Q90xu4 phalacrocor

ALIGNMENTS

RESULT 1  
AKH\_HELZE  
ID AKH\_HELZE STANDARD; PRT; 9 AA.  
AC P67787; P08901;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 25-OCT-2004 (Rel. 45, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Adipokinetic hormone (Hez-AKH)  
OS Heliothis zea (Corn earworm) (Bollworm).  
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;  
OC Noctuidae; Heliothinae; Helicoverpa.  
OX NCBI\_TaxID=7113;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=86186794; PubMed=3964263;  
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Holman G.M.,  
RA Wagner R.M., Ridgway R.L., Hayes D.K.  
RT "Isolation and primary structure of a peptide from the corpora  
cardiaca of Heliothis zea with adipokinetic activity."  
RL Biochem. Biophys. Res. Commun. 135:622-628(1986).  
CC -!- FUNCTION: This hormone, released from cells in the corpora  
cardiaca after the beginning of flight, causes release of  
diglycerides from the fat body and then stimulates the flight  
muscles to use these diglycerides as an energy source.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.  
DR PIR; A24244; A24244.  
DR InterPro; IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
KW Pyroliadone carboxylic acid.  
FT MOD\_RES 1 1 Pyroliadone carboxylic acid.  
FT MOD\_RES 9 9 Glycine amide.  
SQ SEQUENCE 9 AA; 1026 MW; 403665A5A1A9D1A7 CRC64;

Query Match 70.8%; Score 17; DB 1; Length 9;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	2	FXXW 6
Db	4	FTSSW 8

RESULT 2  
Q9XLI2  
ID Q9XLI2 PRELIMINARY; PRT; 13 AA.

AC	Q9XLI2;	Q99JJC3
DT	01-NOV-1999 (TrEMBLrel. 12, Created)	Q6LD68
DT	01-NOV-1999 (TrEMBLrel. 12, Last sequence update)	Q80W11
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)	Q8CGW6
DE	Cytochrome oxidase I (Fragment).	Q9QVH3
OS	Bemisia tabaci (Sweetpotato whitefly).	Q80GP0
OG	Mitochondrion.	Q65CG7
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	Q90735
OC	Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aleyrodiformes;	Q7LZ10
OC	Aleyrodidae; Aleyrodinae; Bemisia.	Q83410
OX	NCBI_TaxID=7038;	Q8ADI8
RN	[1]	Q9DZ32
RP	SEQUENCE FROM N.A.	LICA_BACSU
RX	PubMed=10583831;	NO40_LOTJA
RA	Frohlich D.R., Torres-Jerez I., Bedford I.D., Markham P.G.,	NO40_SEGRO
RA	Brown J.K.;	NO40_SOYBN
RT	"A phylogeographical analysis of the Bemisia tabaci species complex based on mitochondrial DNA markers.";	RF1_CONSP
RL	Mol. Ecol. 8:1683-1691(1999).	UP01_CAEEL
DR	EMBL; AF110703; AAD28415.1; -.	UR2A_CATCO
DR	GO; GO:0005739; C:mitochondrion; IEA.	
KW	Mitochondrion.	
FT	NON_TER 1 1	
SQ	SEQUENCE 13 AA; 1639 MW; 8DD68729F5744365 CRC64;	

Query Match 70.8%; Score 17; DB 2; Length 13;  
Best Local Similarity 40.0%; Pred. No. 2.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	2	FXXW 6
Db	3	FTSSW 7

RESULT 3  
AKHG-GRYBI  
ID AKHG-GRYBI STANDARD; PRT; 8 AA.  
AC P67785; P14086;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Adipokinetic hormone G (AKH-G).  
OS Gryllus bimaculatus (Two-spotted cricket).  
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;  
OC Gryllus.  
OX NCBI\_TaxID=6999;  
RN [1]  
RP SEQUENCE.  
RX TISSUE=Corpora cardiaca;  
RX MEDLINE=88106553; PubMed=3426616;  
RA Gaede G., Rinehart K.L. Jr.;  
RT "Primary sequence analysis by fast atom bombardment mass spectrometry  
of a peptide with adipokinetic activity from the corpora cardiaca of  
the cricket Gryllus bimaculatus."  
RL Biochem. Biophys. Res. Commun. 149:908-914(1987).  
CC -!- FUNCTION: This hormone, released from cells in the corpora  
cardiaca after the beginning of flight, causes release of  
diglycerides from the fat body and then stimulates the flight  
muscles to use these diglycerides as an energy source.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.  
DR PIR; A28004; A28004.  
DR InterPro; IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
KW Pyroliadone carboxylic acid.  
FT MOD\_RES 1 1 Pyroliadone carboxylic acid.  
FT MOD\_RES 8 8 Tryptophan amide.  
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 66.7%; Score 16; DB 1; Length 8;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 4 FSTGW 8

## RESULT 4

AKH\_ROMMI STANDARD; PRT; 8 AA.  
AC P67786; P14086;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Adipokinetic hormone (AKH) (RO II).  
OS Romalea microptera (lubber grasshopper).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Romaleidae; Romalea.  
OX NCBI\_TaxID=7007;  
RN [1]  
RP SEQUENCE.

RC TISSUE=Corpora cardiaca;  
RX MEDLINE=89145002; PubMed=3226948; DOI=10.1016/0196-9781(88)90107-6;  
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;  
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from  
RL the lubber grasshopper, Romalea microptera.";  
RL Peptides 9:681-688(1988).

CC -!- FUNCTION: This hormone, released from cells in the corpora  
CC cardiaca after the beginning of flight, causes release of  
CC diglycerides from the fat body and then stimulates the flight  
CC muscles to use these diglycerides as an energy source.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.

DR InterPro: IPR002047; AKH.

DR PROSITE; PS00256; AKH; 1.

KW Amidation; Direct protein sequencing; Flight; Neuropeptide;

KW Pyrrolidone carboxylic acid.

FT MOD\_RES 1 1 Pyrrolidone carboxylic acid.

FT MOD\_RES 8 8 Tryptophan amide.

SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 66.7%; Score 16; DB 1; Length 8;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 4 FSTGW 8

## RESULT 5

HTF\_HELZE STANDARD; PRT; 10 AA.  
AC P16353;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Hypertrehalosaemic hormone (HeZ-HRTH).  
OS Heliothis zea (Corn earworm) (Bollworm).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;  
OC Noctuidae; Heliothinae; Helicoverpa.  
OX NCBI\_TaxID=7113;  
RN [1]  
RP SEQUENCE.

RC TISSUE=Corpora cardiaca;  
RX MEDLINE=88326324; PubMed=3415690;  
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Bird T.G., Tseng C.M.,  
RA Zhang Y.S., Hayes D.K.;  
RT "Isolation and primary structure of a neuropeptide hormone from  
RT Heliothis zea with hypertrehalosemic and adipokinetic activities.";  
RL Biochem. Biophys. Res. Commun. 155:344-350(1988).

CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that  
CC elevate the level of trehalose in the hemolymph (trehalose is the  
CC major carbohydrate in the hemolymph of insects).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.

DR PIR; A31571; A31571.

DR InterPro: IPR002047; AKH.

DR PROSITE; PS00256; AKH; 1.

KW Amidation; Direct protein sequencing; Neuropeptide;

KW Pyrrolidone carboxylic acid.

FT MOD\_RES 1 1 Pyrrolidone carboxylic acid.

FT MOD\_RES 10 10 Asparagine amide.

SQ SEQUENCE 10 AA; 1096 MW; 8E70367865A5B9D1 CRC64;

Query Match 66.7%; Score 16; DB 1; Length 10;  
Best Local Similarity 40.0%; Pred. No. 3.8e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 4 FSSGW 8

## RESULT 6

Q6E5N4 PRELIMINARY; PRT; 11 AA.

ID Q6E5N4 PRELIMINARY; PRT; 11 AA.

AC Q6E5N4; 25-OCT-2004 (TReMBLrel. 28, Created)

DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)

DE Cytochrome c oxidase subunit I (Fragment).

GN Name=COI;

OS Mantheyus phuwanensis.

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;

OC Mantheyus.

OX NCBI\_TaxID=282162;

RN [1]

RP SEQUENCE FROM N.A.

RA Schulte J.A. II, Vindum J.V., Win H., Thin T., Lwin K.S., Shein A.K.,

RA Tun H.;

RT "Phylogenetic relationships of the genus Ptyctolaemus (Squamata:  
RT Agamidae), with a description of a new species from the Chin Hills of  
RT Western Myanmar.";

RL Proceedings Calif. Acad. Sci. 55:222-247(2004).

DR EMBL; AY555836; AAT74867.1; -.

DR GO; GO:0005739; C:mitochondrion; IEA.

KW Mitochondrion.

FT NON\_TER 11 11

SQ SEQUENCE 11 AA; 1343 MW; 932D371E336411B1 CRC64;

Query Match 66.7%; Score 16; DB 2; Length 11;  
Best Local Similarity 40.0%; Pred. No. 4.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 3 FTTRW 7

## RESULT 7

Q9G649 PRELIMINARY; PRT; 11 AA.

ID Q9G649 PRELIMINARY; PRT; 11 AA.

AC Q9G649; 01-MAR-2001 (TReMBLrel. 16, Created)

DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)

DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)

DE Cytochrome c oxidase subunit I (Fragment).

GN Name=COI;

OS Otopharyngus wiegmanni.

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;  
OC Otophysa;  
OX NCBI\_TaxID=118220;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;  
RA Macey J.R., Schulte J.A. II, Larson A.;  
RT "Evolution and phylogenetic information content of mitochondrial  
genomic structural features illustrated with acrodont lizards.";  
RL Syst. Biol. 49:257-277(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;  
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
RA Pathiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
RT "Evaluating trans-tethys migration: an example using acrodont lizard  
phylogenetics.";  
RL Syst. Biol. 49:233-256(2000).  
DR EMBL; AF128480; AAC00677.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 11  
SQ SEQUENCE 11 AA; 1347 MW; 932D3710D3640DC1 CRC64;  
  
Query Match 66.7%; Score 16; DB 2; Length 11;  
Best Local Similarity 40.0%; Pred. No. 4.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXXW 6  
Db 3 FTARW 7  
  
RESULT 8  
O15276 PRELIMINARY; PRT; 17 AA.  
AC O15276;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Mitochondrial translation elongation factor EF-Tu (Fragment).  
GN Name=EF-Tu;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Jacobs H.T., Smurthwaite L., Koshy R.;  
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Y11797; CAA72493.1; -.  
DR GO; GO:0003746; F:translation elongation factor activity; IEA.  
KW Elongation factor.  
FT NON\_TER 1  
FT NON\_TER 17  
SQ SEQUENCE 17 AA; 2019 MW; BF737D12D2AB0A7E CRC64;  
  
Query Match 66.7%; Score 16; DB 2; Length 17;  
Best Local Similarity 40.0%; Pred. No. 5.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXXW 6  
Db 1 FSLTW 5  
  
RESULT 9  
Q7Y1X8 PRELIMINARY; PRT; 17 AA.  
AC Q7Y1X8;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Male gametic cell-specific (Fragment).  
GN Name=IGC1;  
OS Lilium longiflorum (Trumpet lily).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Lilium.  
OX NCBI\_TaxID=4690;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22615576; PubMed=12729896; DOI=10.1016/S0014-5793(03)00335-1;  
RA Singh M., Bhalla P.L., Xu H., Singh M.B.;  
RT "Isolation and characterization of a flowering plant male gametic  
cell-specific promoter(1).";  
RL FEBS Lett. 542:47-52(2003).  
DR EMBL; AY207012; AAP37155.1; -.  
FT NON\_TER 17  
SQ SEQUENCE 17 AA; 1880 MW; 661B63484969679F CRC64;  
  
Query Match 66.7%; Score 16; DB 2; Length 17;  
Best Local Similarity 40.0%; Pred. No. 5.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXXW 6  
Db 11 FSSVW 15  
  
RESULT 10  
O91329 PRELIMINARY; PRT; 19 AA.  
AC O91329;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN Name=env;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98285741; PubMed=9621043;  
RA Belec L., Si Mohamed A., Muller-Trutwin M.C., Gilquin J., Gutmann L.,  
RA Safar M., Barre-Sinoussi F., Kazatchkine M.D.;  
RT "Genetically related human immunodeficiency virus type 1 in three  
adults of a family with no identified risk factor for intrafamilial  
transmission.";  
RL J. Virol. 72:5831-5839(1998).  
DR EMBL; U87220; AAC32980.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 19 AA; 2324 MW; 379CB14A9E073911 CRC64;  
  
Query Match 66.7%; Score 16; DB 2; Length 19;  
Best Local Similarity 40.0%; Pred. No. 6.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXXW 6  
Db 10 FNSTW 14  
  
RESULT 11  
Q9WJB1 PRELIMINARY; PRT; 19 AA.  
AC Q9WJB1;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

```
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98285741; PubMed=9621043;
RA Belec L., Si Mohamed A., Muller-Trutwin M.C., Gilquin J., Gutmann L.,
RA Safar M., Barre-Sinoussi F., Kazatchkine M.D.;
RT "Genetically related human immunodeficiency virus type 1 in three
RT adults of a family with no identified risk factor for intrafamilial
RT transmission.";
RL J. Virol. 72:5831-5839(1998).
DR EMBL; U87216; AAC32976.1; -.
DR GO; GO:016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
KW NON_TER 1
FT SEQUENCE 19 AA; 2294 MW; 3781714A9E073911 CRC64;
SQ

Query Match 66.7%; Score 16; DB 2; Length 19;
Best Local Similarity 40.0%; Pred. No. 6.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 10 FNSTW 14

RESULT 12
Q6LD18 PRELIMINARY; PRT; 20 AA.
AC Q6LD18;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Interferon alpha/beta receptor (Fragment).
GN Name=IFNAR;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95047447; PubMed=7958966; DOI=10.1016/0378-1119(94)90710-2;
RA Lutfalla G., Uze G.;
RT "Structure of the murine interferon alpha/beta receptor-encoding gene:
RT high-frequency rearrangements in the interferon-resistant L1210 cell
RT line.";
RL Gene 148:343-346(1994).
DR EMBL; U06242; AAA65007.1; -.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
KW Receptor.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2204 MW; 9B9C1DF0C12EBC43 CRC64;

Query Match 66.7%; Score 16; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 2 FSTIW 6
```

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RESULT 13
AKH LIBAU
ID AKH LIBAU STANDARD; PRT; 8 AA.
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Adipokinetic hormone (AKH).
OS Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
OX NCBI_TaxID=6966;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90359055; PubMed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokinetic/red-pigment-
RT concentrating hormone family isolated and sequenced from a
RT dragonfly.";
RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC -!- FUNCTION: This hormone, released from cells in the corpora
CC cardiaca after the beginning of flight, causes release of
CC diglycerides from the fat body and then stimulates the flight
CC muscles to use these diglycerides as an energy source.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; S10596; S10596.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Amidation; Direct protein sequencing; Flight; Neuropeptide;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT MOD_RES 8 8 Tryptophan amide.
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 62.5%; Score 15; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
Db 4 FTSPW 8

RESULT 14
Q7M3N6 PRELIMINARY; PRT; 9 AA.
AC Q7M3N6;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Neuropeptide Grb-AST B4.
OS Gryllus bimaculatus (Two-spotted cricket).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Gryllus.
OX NCBI_TaxID=6999;
RN [1]
RP SEQUENCE.
RX MEDLINE=95403341; PubMed=7673141; DOI=10.1074/jbc.270.36.21103;
RA Lorenz M.W., Kellner R., Hoffmann K.H.;
RT "A family of neuropeptides that inhibit juvenile hormone biosynthesis
RT in the cricket, Gryllus bimaculatus.";
RL J. Biol. Chem. 270:21103-21108(1995).
DR PIR; D57444; D57444.
SQ SEQUENCE 9 AA; 1175 MW; 3860B871E9D40B03 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
```

Db 5 FHGSW 9

RESULT 15

Q8WGE6

ID Q8WGE6 PRELIMINARY; PRT; 9 AA.

AC Q8WGE6;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Cytochrome oxidase subunit 1 (Fragment).

OS Procambrium clarkii (Red swamp crayfish).

OG Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;

OC Astacoidea; Cambaridae; Procambrium.

OX NCBI\_TaxID=6728;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21884466; PubMed=11886621; DOI=10.1098/rspb.2001.1886;

RA Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,

RA Cunningham C.W.;

RT "Mitochondrial gene rearrangements confirm the parallel evolution of the crab-like form."

RL Proc. R. Soc. Lond., B, Biol. Sci. 269:345-350(2002).

DR EMBL; AF436024; AAL31599.1; -.

DR GO; GO:0005739; C:mitochondrion; IEA.

KW Mitochondrion.

FT NON\_TER 1 1

FT NON\_TER 9 9

SQ SEQUENCE 9 AA; 1185 MW; 936BB9C733640321 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 9;

Best Local Similarity 40.0%; Pred. No. 1.6e+06;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6

Db 1 FTKRW 5

RESULT 16

AKHX\_LOCM1

ID AKHX\_LOCM1 STANDARD; PRT; 10 AA.

AC P81626;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Peptide hormone.

OS Locusta migratoria (Migratory locust).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;

OC Acridoidea; Acrididae; Oedipodinae; Locusta.

OX NCBI\_TaxID=7004;

RN [1]

RP SEQUENCE.

RC TISSUE=Corpora cardiaca;

RA Siebert K.J.;

RL Submitted (DEC-1998) to Swiss-Prot.

CC -!- FUNCTION: Probably involved in the regulation of locust intermediary metabolism, behavior and/or development.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.

DR InterPro; IPR002047; AKH.

DR PROSITE; PS00256; AKH; 1.

KW Amidation; Direct protein sequencing; Neuropeptide;

KW Pyroglutamate carboxylic acid.

FT MOD\_RES 1 1 Pyroglutamate carboxylic acid.

FT MOD\_RES 10 10 Proline amide.

SQ SEQUENCE 10 AA; 1222 MW; 81BFF67AB415B9D1 CRC64;

Query Match 62.5%; Score 15; DB 1; Length 10;

Best Local Similarity 40.0%; Pred. No. 6.5e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6

Db 4 FSRDW 8

RESULT 17

Q7M465

ID Q7M465 PRELIMINARY; PRT; 10 AA.

AC Q7M465;

DT 01-MAR-2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Neuropeptide Pec-HrTH.

OS Platypleura capensis.

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Cicadoidea; Cicadidae;

OC Cicadinae; Platypleurini; Platypleura.

OX NCBI\_TaxID=70904;

RN [1]

RP SEQUENCE.

RA Gaede G., Janssens M.P.E.;

RT "Cicadas contain novel members of the AKH/RPCH family peptides with hyperthrehalosaemic activity."

RL Biol. Chem. Hoppe-Seyler 375:803-809(1994).

DR PIR; S53789; S53789.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0005179; F:hormone activity; IEA.

DR InterPro; IPR002047; AKH.

DR PROSITE; PS00256; AKH; 1.

SQ SEQUENCE 10 AA; 1135 MW; 10823665A775B9C4 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 10;

Best Local Similarity 40.0%; Pred. No. 6.5e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6

Db 4 FSPSW 8

RESULT 18

Q70F01

ID Q70F01 PRELIMINARY; PRT; 10 AA.

AC Q70F01;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Calpastatin type 2 (Fragment).

GN Name=CAST;

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI\_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21531263; PubMed=11673859; DOI=10.1006/abbi.2001.2546;

RA Parr T., Sensky P.L., Bardsley R.G., Buttery P.J.;

RT "Calpastatin expression in porcine cardiac and skeletal muscle and partial gene structure."

RL Arch. Biochem. Biophys. 395:1-13(2001).

RN [2]

RP SEQUENCE FROM N.A.

RA Parr T.;

RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ583410; CAE47431.1; -.

FT NON\_TER 10 10

SQ SEQUENCE 10 AA; 1291 MW; CFF912436365BDD9 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 10;

Best Local Similarity 40.0%; Pred. No. 6.5e+03;



Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |  
Db 3 FASW 7

## RESULT 19

079897 PRELIMINARY; PRT; 10 AA.  
AC 079897;

DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).

GN Name=COI;  
OS Hoplocercus spinosus (Club-tail iguana).

OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Iguanidae; Hoplocercinae;

OC Hoplocercus.  
OX NCBI\_TaxID=52193;  
RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=9715309; PubMed=9169559;

RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;

RT "Evolutionary shifts in three major structural features of the  
mitochondrial genome among iguanian lizards.";

RL J. Mol. Evol. 44:660-674(1997).

DR EMBL; U82683; AAC62284.1; -.

DR PIR; T17063; T17063.

DR GO; GO:0005739; C:mitochondrion; IEA.

KW Mitochondrion.

FT NON\_TER 10 10

SQ SEQUENCE 10 AA; 1288 MW; OA3480C7336415B0 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 10;

Best Local Similarity 40.0%; Pred. No. 6.5e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |  
Db 2 FISRW 6

## RESULT 20

P92707 PRELIMINARY; PRT; 10 AA.  
AC P92707;

DT 01-MAY-1997 (TrEMBLrel. 03, Created)

DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Cytochrome c oxidase subunit I (Fragment).

GN Name=COI;

OS Platysaurus capensis.

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;

OC Cordylidae; Platysaurus.

OX NCBI\_TaxID=52175;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97153826; PubMed=9000757;

RA Macey J.R., Larson A., Ananjeva N.B., Fang Z., Papenfuss T.J.;

RT "Two novel gene orders and the role of light-strand replication in

rearrangement of the vertebrate mitochondrial genome.";

RL Mol. Biol. Evol. 14:91-104(1997).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=97153820; PubMed=9000751;

RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;

RT "Replication slippage may cause parallel evolution in the secondary

structures of mitochondrial transfer RNAs.";

RL Mol. Biol. Evol. 14:30-39(1997).

DR EMBL; U71329; AAB48286.1; -.

DR GO; GO:0005739; C:mitochondrion; IEA.

KW Mitochondrion.

FT NON\_TER 10 10

SQ SEQUENCE 10 AA; 1322 MW; OA3480C9D36415B0 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 10;

Best Local Similarity 40.0%; Pred. No. 6.5e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |

Db 2 FISRW 6

## RESULT 21

Q6UJL5 PRELIMINARY; PRT; 10 AA.

AC Q6UJL5;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Cytochrome c oxidase subunit I (Fragment).

GN Name=COI;

OS Strophurus pulcher.

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Gekkota; Gekkonidae; Strophurus.

OX NCBI\_TaxID=255186;

RN [1]

RP SEQUENCE FROM N.A.

RA Melville J., Schulte J.A. II, Larson A.;

RT "A Molecular Study of Phylogenetic Relationships and Evolution of

Antipredator Strategies in Australian Diplodactylus Geckos, Subgenus

Strophurus.";

RL Biol. J. Linn. Soc. Lond. 82:123-138(2004).

DR EMBL; AY369011; AAR18865.1; -.

DR GO; GO:0005739; C:mitochondrion; IEA.

KW Mitochondrion.

FT NON\_TER 10 10

SQ SEQUENCE 10 AA; 1288 MW; OA3480C7336415B0 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 10;

Best Local Similarity 40.0%; Pred. No. 6.5e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |

Db 2 FISRW 6

## RESULT 22

Q6WBU4 PRELIMINARY; PRT; 10 AA.

AC Q6WBU4;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Cytochrome oxidase subunit I (Fragment).

GN Name=COI;

OS Sceloporus siniferus.

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;

OC Sceloporus.

OX NCBI\_TaxID=59719;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22801591; PubMed=12920297; DOI=10.1126/science.1084786;

RA Harmon L.J., Schulte J.A., Larson A., Losos J.B.;

RT "Tempo and mode of evolutionary radiation in iguanian lizards.";

RL Science 301:961-964(2003).



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DR EMBL; AY297494; AAP84453.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 10
SQ SEQUENCE 10 AA; 1303 MW; 933480C733640451 CRC64;

Query Match      62.5%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
| |
Db 2 FTNRW 6

RESULT 23
Q6X0E7 PRELIMINARY; PRT; 10 AA.
AC Q6X0E7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
GN Name=COI;
OS Anolis marmoratus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OC NCBI_TaxID=75264;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22990428; PubMed=14628926;
RA Glor R.E., Kolbe J.J., Powell R., Larson A., Losos J.B.;
RT "Phylogenetic analysis of ecological and morphological diversification
RT in Hispaniolan trunk-ground anoles (Anolis cybotes group).";
RL Evolution 57:2383-2397(2003).
DR EMBL; AY263006; AAP94301.1; -.
DR EMBL; AY263005; AAP94298.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 10
SQ SEQUENCE 10 AA; 1370 MW; C93480C9D36411A9 CRC64;

Query Match      62.5%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
| |
Db 2 FTNRW 6

RESULT 24
Q71DW3 PRELIMINARY; PRT; 10 AA.
AC Q71DW3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Polychrus marmoratus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Polychrus.
OC NCBI_TaxID=38934;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte J.A. II, Valladares J.P., Larson A.;
RT "Phylogenetic relationships within Iguanidae inferred using molecular
RT and morphological data and a phylogenetic taxonomy of iguanian
RT lizards.";
RL Herpetologica 59:399-419(2003).
, RL
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RN [2]
RP SEQUENCE FROM N.A.
RA Schulte J.A., Valladares J.P., Larson A.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF528738; AAQ09176.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 10
SQ SEQUENCE 10 AA; 1302 MW; 0A3480C7336411A0 CRC64;

Query Match      62.5%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
| |
Db 2 FITRW 6

RESULT 25
Q71DW6 PRELIMINARY; PRT; 10 AA.
AC Q71DW6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Polychrus acutirostris (Iguanid lizard).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Polychrus.
OC NCBI_TaxID=161137;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte J.A. II, Valladares J.P., Larson A.;
RT "Phylogenetic relationships within Iguanidae inferred using molecular
RT and morphological data and a phylogenetic taxonomy of iguanian
RT lizards.";
RL Herpetologica 59:399-419(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Schulte J.A., Valladares J.P., Larson A.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF528737; AAQ09173.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 10
SQ SEQUENCE 10 AA; 1302 MW; 0A3480C7336411A0 CRC64;

Query Match      62.5%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6
| |
Db 2 FITRW 6

RESULT 26
Q71DW9 PRELIMINARY; PRT; 10 AA.
AC Q71DW9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Anisolepis longicauda.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anisolepis.
OC NCBI_TaxID=161142;
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RN [1]
RP SEQUENCE FROM N.A.
RA Schulte J.A. II, Valladares J.P., Larson A.;
RT "Phylogenetic relationships within Iguanidae inferred using molecular
and morphological data and a phylogenetic taxonomy of iguanian
lizards.";
RL Herpetologica 59:399-419(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Schulte J.A., Valladares J.P., Larson A.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF528736; AAQ09170.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1288 MW; 0A3480C7336415B0 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
Db 2 FISRW 6

RESULT 27
Q71E17 PRELIMINARY; PRT; 10 AA.
AC Q71E17;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Morunasaurus annularis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Hoplocercinae;
OC Morunasaurus.
OX NCBI_TaxID=211988;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte J.A. II, Valladares J.P., Larson A.;
RT "Phylogenetic relationships within Iguanidae inferred using molecular
and morphological data and a phylogenetic taxonomy of iguanian
lizards.";
RL Herpetologica 59:399-419(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Schulte J.A., Valladares J.P., Larson A.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF528720; AAQ09122.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1288 MW; 0A3480C7336415B0 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
Db 2 FISRW 6

RESULT 28
Q71E20 PRELIMINARY; PRT; 10 AA.
AC Q71E20;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Enyalioides laticeps (Amazon wood lizard).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Hoplocercinae;
OC Enyalioides.
OX NCBI_TaxID=51206;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte J.A. II, Valladares J.P., Larson A.;
RT "Phylogenetic relationships within Iguanidae inferred using molecular
and morphological data and a phylogenetic taxonomy of iguanian
lizards.";
RL Herpetologica 59:399-419(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Schulte J.A., Valladares J.P., Larson A.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF528719; AAQ09119.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1288 MW; 0A3480C7336415B0 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
Db 2 FISRW 6

RESULT 29
Q9ZYT2 PRELIMINARY; PRT; 10 AA.
AC Q9ZYT2;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Leiocephalus carinatus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Tropidurinae;
OC Leiocephalus.
OX NCBI_TaxID=81825;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99162288; PubMed=10051389; DOI=10.1006/mpev.1998.0541;
RA Schulte J.A., Macey J.R., Larson A., Papenfuss T.J.;
RT "Molecular tests of phylogenetic taxonomies: a general procedure and
example using four subfamilies of the lizard family Iguanidae.";
RL Mol. Phylogenet. Evol. 10:367-376(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Schulte J.A. II, Macey J.R., Larson A., Papenfuss T.J.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF049864; AAD02535.1; -.
DR PIR; T12325; T12325.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1302 MW; 0A3480C7336411A0 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6
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Db 2 FITRW 6

RESULT 30

Q8WES0 PRELIMINARY; PRT; 11 AA.

AC Q8WES0; 20, Created

DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)

DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)

DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)

DE Cytochrome c oxidase subunit I (Fragment).

GN Name=COI;

OS Ceratophora karu.

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidodermata; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;

OC Ceratophora.

OX NCBI\_TaxID=118086;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;

RA Macey J.R., Schulte J.A. II, Larson A.;

RT "Evolution and phylogenetic information content of mitochondrial genomic structural features illustrated with acrodont lizards.";

RL Syst. Biol. 49:257-277(2000).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=21655505; PubMed=11796034; DOI=10.1006/mpev.2001.1041;

RA Schulte J.A. II, Macey J.R., Pethiyagoda R., Larson A.;

RT "Rostral horn evolution among agamid lizards of the genus Ceratophora endemic to Sri Lanka.";

RL Mol. Phylogenet. Evol. 22:111-117(2002).

DR EMBL; AF128520; AAL67604.1; -.

DR GO; GO:0005739; C:mitochondrion; IEA.

KW Mitochondrion.

FT NON TER 11

SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 11;

Best Local Similarity 40.0%; Pred. No. 7e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6

Db 3 FLTRW 7

RESULT 31

Q9G365 PRELIMINARY; PRT; 11 AA.

AC Q9G365; 16, Created

DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)

DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)

DE Cytochrome c oxidase subunit I (Fragment).

GN Name=COI;

OS Calotes emma.

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidodermata; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;

OC Calotes.

OX NCBI\_TaxID=52214;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97153820; PubMed=9000751;

RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;

RT "Replication slippage may cause parallel evolution in the secondary structures of mitochondrial transfer RNAs.";

RL Mol. Biol. Evol. 14:30-39(1997).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;

RA Macey J.R., Schulte J.A. II, Larson A.;

RT "Evolution and phylogenetic information content of mitochondrial genomic structural features illustrated with acrodont lizards.";

RL Syst. Biol. 49:257-277(2000).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;

RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.;

RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;

RT "Evaluating trans-tethys migration: an example using acrodont lizard phylogenetics.";

RL Syst. Biol. 49:233-256(2000).

DR EMBL; AF128487; AAG00698.1; -.

DR GO; GO:0005739; C:mitochondrion; IEA.

KW Mitochondrion.

FT NON TER 11

SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 11;

Best Local Similarity 40.0%; Pred. No. 7e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6

Db 3 FLTRW 7

RESULT 32

Q9G368 PRELIMINARY; PRT; 11 AA.

AC Q9G368;

DT 01-MAR-2001 (TReMBLrel. 16, Created)

DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)

DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)

DE Cytochrome c oxidase subunit I (Fragment).

GN Name=COI;

OS Draco blanfordii.

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidodermata; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;

OC Draco.

OX NCBI\_TaxID=89021;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97153820; PubMed=9000751;

RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;

RT "Replication slippage may cause parallel evolution in the secondary structures of mitochondrial transfer RNAs.";

RL Mol. Biol. Evol. 14:30-39(1997).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;

RA Macey J.R., Schulte J.A. II, Larson A.;

RT "Evolution and phylogenetic information content of mitochondrial genomic structural features illustrated with acrodont lizards.";

RL Syst. Biol. 49:257-277(2000).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;

RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.;

RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;

RT "Evaluating trans-tethys migration: an example using acrodont lizard phylogenetics.";

RL Syst. Biol. 49:233-256(2000).

DR EMBL; AF128477; AAG00668.1; -.

DR GO; GO:0005739; C:mitochondrion; IEA.

KW Mitochondrion.

FT NON TER 11

SQ SEQUENCE 11 AA; 1341 MW; 4B2D371E336415B7 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 11;

Best Local Similarity 40.0%; Pred. No. 7e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;



DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN Name=COI;  
OS Calotes versicolor.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;  
OC Calotes.  
OX NCBI\_TaxID=48253;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;  
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
RA "Evolution and phylogenetic information content of mitochondrial  
RT genomic structural features illustrated with acrodont lizards."  
RL Syst. Biol. 49:257-277(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;  
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.,  
RT "Evaluating trans-tethys migration: an example using acrodont lizard  
RT phylogenetics."  
RL Syst. Biol. 49:233-256(2000).  
DR EMBL; AF128489; AAG00704.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 11 11  
SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;  
  
Query Match 62.5%; Score 15; DB 2; Length 11;  
Best Local Similarity 40.0%; Pred. No. 7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXXW 6  
Db 3 FLTRW 7  
  
RESULT 37  
Q9G628  
ID Q9G628 PRELIMINARY; PRT; 11 AA.  
AC Q9G628; 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN Name=COI;  
OS Calotes mystaceus.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;  
OC Calotes.  
OX NCBI\_TaxID=118097;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;  
RA Macey J.R., Schulte J.A. II, Larson A.,  
RA "Evolution and phylogenetic information content of mitochondrial  
RT genomic structural features illustrated with acrodont lizards."  
RL Syst. Biol. 49:257-277(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;  
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.,  
RT "Evaluating trans-tethys migration: an example using acrodont lizard  
RT phylogenetics."  
RL Syst. Biol. 49:233-256(2000).  
DR EMBL; AF128488; AAG00701.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.

FT NON TER 11 11  
SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;  
  
Query Match 62.5%; Score 15; DB 2; Length 11;  
Best Local Similarity 40.0%; Pred. No. 7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXXW 6  
Db 3 FLTRW 7  
  
RESULT 38  
Q9G631  
ID Q9G631 PRELIMINARY; PRT; 11 AA.  
AC Q9G631; 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN Name=COI;  
OS Calotes nigrilabris.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;  
OC Calotes.  
OX NCBI\_TaxID=118098;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;  
RA Macey J.R., Schulte J.A. II, Larson A.,  
RA "Evolution and phylogenetic information content of mitochondrial  
RT genomic structural features illustrated with acrodont lizards."  
RL Syst. Biol. 49:257-277(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;  
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.,  
RT "Evaluating trans-tethys migration: an example using acrodont lizard  
RT phylogenetics."  
RL Syst. Biol. 49:233-256(2000).  
DR EMBL; AF128486; AAG00695.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 11 11  
SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;  
  
Query Match 62.5%; Score 15; DB 2; Length 11;  
Best Local Similarity 40.0%; Pred. No. 7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXXW 6  
Db 3 FLTRW 7  
  
RESULT 39  
Q9G634  
ID Q9G634 PRELIMINARY; PRT; 11 AA.  
AC Q9G634; 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN Name=COI;  
OS Calotes liolepis.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;  
OC Calotes.  
OX NCBI\_TaxID=118096;  
RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;  
RA Macey J.R., Schulte J.A. II, Larson A.;  
RT "Evolution and phylogenetic information content of mitochondrial  
genomic structural features illustrated with acrodont lizards.";  
RL Syst. Biol. 49:257-277(2000).  
RN [2]

RP SEQUENCE FROM N.A.  
RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;  
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
RT "Evaluating trans-tethys migration: an example using acrodont lizard  
phylogenetics.";  
RL Syst. Biol. 49:233-256(2000).  
DR EMBL; AF128485; AAG00692.1; --  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 11 11  
SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 11;  
Best Local Similarity 40.0%; Pred. No. 7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 3 FLTRW 7

RESULT 40  
Q9G640  
ID Q9G640 PRELIMINARY; PRT; 11 AA.  
AC Q9G640;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN Name=COI;  
OS Calotes ceylonensis.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;  
OC Calotes.  
OX NCBI\_TaxID=118094;  
RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;  
RA Macey J.R., Schulte J.A. II, Larson A.;  
RT "Evolution and phylogenetic information content of mitochondrial  
genomic structural features illustrated with acrodont lizards.";  
RL Syst. Biol. 49:257-277(2000).  
RN [2]

RP SEQUENCE FROM N.A.  
RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;  
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
RT "Evaluating trans-tethys migration: an example using acrodont lizard  
phylogenetics.";  
RL Syst. Biol. 49:233-256(2000).  
DR EMBL; AF128483; AAG00686.1; --  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 11 11  
SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match 62.5%; Score 15; DB 2; Length 11;  
Best Local Similarity 40.0%; Pred. No. 7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
|  
Db 3 FLTRW 7

Search completed: October 18, 2005, 15:58:34  
Job time : 118.529 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:19:12 ; Search time 32.2941 Seconds  
(without alignments)  
20.804 Million cell updates/sec

Title: US-09-214-371-11  
Perfect score: 24  
Sequence: 1 XFXXXWXXX 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Issued\_Patents\_AA: \*  
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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	70.8	13	3	US-09-085-072-7
2	17	70.8	15	4	US-09-142-524D-87
3	17	70.8	15	4	US-09-142-524D-88
4	17	70.8	29	4	US-08-469-260A-428
5	17	70.8	29	4	US-08-488-446-428
6	17	70.8	29	4	US-08-467-344A-428
7	17	70.8	29	4	US-08-424-550B-428
8	17	70.8	34	1	US-08-118-270-134
9	17	70.8	34	1	US-08-118-270-172
10	17	70.8	34	5	PCT-US93-08528-134
11	17	70.8	34	5	PCT-US93-08528-172
12	17	70.8	36	3	US-08-467-023-137
13	17	70.8	37	4	US-09-330-914A-10
14	17	70.8	41	3	US-08-467-023-136
15	17	70.8	45	3	US-08-467-023-135
16	17	70.8	45	4	US-09-149-476-475
17	17	70.8	47	4	US-09-369-247-129
18	17	70.8	49	1	US-08-118-270-209
19	17	70.8	49	5	PCT-US93-08528-209
20	17	70.8	54	4	US-09-434-840-73
21	17	70.8	54	4	US-09-733-643B-21
22	17	70.8	56	4	US-09-621-976-6592
23	17	70.8	60	4	US-09-270-767-35869
24	17	70.8	60	4	US-09-270-767-51086
25	17	70.8	61	3	US-09-134-001C-4258
26	17	70.8	62	4	US-09-252-991A-28658
27	17	70.8	62	4	US-09-621-976-5704
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					Sequence 87, Appl
					Sequence 88, Appl
					Sequence 428, App
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					Sequence 172, App
					Sequence 134, App
					Sequence 172, App
					Sequence 137, App
					Sequence 10, Appl
					Sequence 136, App
					Sequence 135, App
					Sequence 475, App
					Sequence 129, App
					Sequence 209, App
					Sequence 73, Appl
					Sequence 21, Appl
					Sequence 6592, Ap
					Sequence 35869, A
					Sequence 51086, A
					Sequence 4258, Ap
					Sequence 28658, A
					Sequence 5704, Ap

28	17	70.8	62	4	US-09-248-796A-26247	Sequence 26247, A
29	17	70.8	63	4	US-09-902-540-11838	Sequence 11838, A
30	17	70.8	69	4	US-09-621-976-6715	Sequence 6715, Ap
31	17	70.8	69	4	US-09-248-796A-24056	Sequence 24056, A
32	17	70.8	80	4	US-09-330-914A-4	Sequence 4, Appli
33	17	70.8	80	4	US-09-270-767-37303	Sequence 37303, A
34	17	70.8	80	4	US-09-270-767-52520	Sequence 52520, A
35	17	70.8	80	4	US-09-248-796A-24759	Sequence 24759, A
36	17	70.8	82	4	US-09-248-796A-19864	Sequence 19864, A
37	17	70.8	84	2	US-08-353-476-78	Sequence 78, Appl
38	17	70.8	84	3	US-08-679-493A-97	Sequence 97, Appl
39	17	70.8	86	4	US-09-583-110-3199	Sequence 3199, Ap
40	17	70.8	89	4	US-09-621-976-6168	Sequence 6168, Ap
41	17	70.8	91	2	US-08-598-873-19	Sequence 19, Appl
42	17	70.8	91	3	US-08-605-430-19	Sequence 19, Appl
43	17	70.8	91	4	US-09-717-054-19	Sequence 19, Appl
44	17	70.8	93	4	US-09-621-976-6449	Sequence 6449, Ap
45	17	70.8	93	4	US-09-248-796A-16647	Sequence 16647, A
46	17	70.8	95	4	US-09-949-016-9308	Sequence 9308, Ap
47	17	70.8	98	4	US-09-252-991A-22311	Sequence 22311, A
48	17	70.8	102	3	US-08-984-295-3	Sequence 3, Appli
49	17	70.8	102	3	US-08-741-411-12	Sequence 12, Appl
50	17	70.8	104	6	5210073-1	Patent No. 5210073
51	17	70.8	104	6	5210073-1	Patent No. 5210073
52	17	70.8	105	2	US-08-826-910-3	Sequence 3, Appli
53	17	70.8	105	2	US-08-826-910-4	Sequence 4, Appli
54	17	70.8	105	4	US-09-601-144-68	Sequence 68, Appl
55	17	70.8	105	4	US-09-513-999C-8037	Sequence 8037, Ap
56	17	70.8	105	4	US-09-107-433-2856	Sequence 2856, Ap
57	17	70.8	109	4	US-09-902-540-13327	Sequence 13327, A
58	17	70.8	114	3	US-09-450-520A-9	Sequence 9, Appli
59	17	70.8	114	3	US-09-450-520A-10	Sequence 10, Appl
60	17	70.8	114	3	US-09-450-520A-11	Sequence 11, Appl
61	17	70.8	114	4	US-09-897-425-41	Sequence 41, Appl
62	17	70.8	116	3	US-09-065-059-9	Sequence 9, Appli
63	17	70.8	116	3	US-08-545-809A-134	Sequence 134, App
64	17	70.8	116	4	US-09-134-000C-6570	Sequence 6570, Ap
65	17	70.8	116	4	US-09-949-016-10735	Sequence 10735, A
66	17	70.8	117	1	US-07-634-278-105	Sequence 105, App
67	17	70.8	117	1	US-08-477-728-105	Sequence 105, App
68	17	70.8	117	1	US-08-474-040-105	Sequence 105, App
69	17	70.8	117	1	US-08-487-200-105	Sequence 105, App
70	17	70.8	117	3	US-08-484-537-105	Sequence 105, App
71	17	70.8	120	3	US-09-065-059-1	Sequence 1, Appli
72	17	70.8	121	4	US-09-107-532A-5275	Sequence 5275, Ap
73	17	70.8	122	3	US-09-540-014-2	Sequence 2, Appli
74	17	70.8	122	4	US-09-538-864-25	Sequence 25, Appl
75	17	70.8	122	4	US-10-091-841A-2	Sequence 2, Appli
76	17	70.8	125	4	US-09-949-016-9663	Sequence 9663, Ap
77	17	70.8	127	3	US-09-540-014-4	Sequence 4, Appli
78	17	70.8	127	4	US-09-252-991A-17639	Sequence 17639, A
79	17	70.8	127	4	US-09-252-991A-24186	Sequence 24186, A
80	17	70.8	127	4	US-10-091-841A-4	Sequence 4, Appli
81	17	70.8	128	3	US-08-467-023-187	Sequence 187, App
82	17	70.8	130	1	US-08-276-852-69	Sequence 69, Appl
83	17	70.8	130	1	US-08-276-852-70	Sequence 70, Appl
84	17	70.8	130	1	US-08-276-852-71	Sequence 71, Appl
85	17	70.8	130	1	US-08-899-575-69	Sequence 69, Appl
86	17	70.8	130	1	US-08-899-575-70	Sequence 70, Appl
87	17	70.8	130	1	US-08-899-575-71	Sequence 71, Appl
88	17	70.8	130	1	US-08-899-575-69	Sequence 69, Appl
89	17	70.8	130	1	US-08-899-575-70	Sequence 70, Appl
90	17	70.8	130	1	US-08-899-575-71	Sequence 71, Appl
91	17	70.8	130	3	US-09-540-014-6	Sequence 6, Appli
92	17	70.8	130	4	US-10-091-841A-6	Sequence 6, Appli
93	17	70.8	130	5	PCT-US95-08743-69	Sequence 69, Appl
94	17	70.8	130	5	PCT-US95-08743-70	Sequence 70, Appl
95	17	70.8	130	5	PCT-US95-08743-71	Sequence 71, Appl
96	17	70.8	131	4	US-09-248-796A-15325	Sequence 15325, A
97	17	70.8	132	4	US-09-386-658A-2	Sequence 2, Appli
98	17	70.8	136	3	US-09-450-520A-4	Sequence 4, Appli
99	17	70.8	136	3	US-09-450-520A-8	Sequence 8, Appli
100	17	70.8	138	4	US-09-252-991A-26095	Sequence 26095, A

ALIGNMENTS

RESULT 1

US-09-085-072-7  
; Sequence 7, Application US/09085072  
; Patent No. 6265150  
; GENERAL INFORMATION:  
; APPLICANT: L. Terstappen et al.  
; TITLE OF INVENTION: PHAGE ANTIBODIES  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hoffmann & Baron, LLP  
; STREET: 350 Jericho Turnpike  
; CITY: Jericho  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 11753  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/085,072  
; FILING DATE: 26-MAY-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Feit, Irving N.  
; REGISTRATION NUMBER: 28,601  
; REFERENCE/DOCKET NUMBER: 890-2 FWC/CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 822-3550  
; TELEFAX: (516) 822-3582  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-085-072-7

Query Match 70.8%; Score 17; DB 3; Length 13;  
Best Local Similarity 40.0%; Pred. No. 1.9e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |  
Db 6 FASSW 10

RESULT 2

US-09-142-524D-87  
; Sequence 87, Application US/09142524D  
; Patent No. 6719976  
; GENERAL INFORMATION:  
; APPLICANT: Sone, Toshio  
; APPLICANT: Kume, Akinori  
; APPLICANT: Dairiki, Kazuo  
; APPLICANT: Iwama, Akiko  
; APPLICANT: Kino, Kohsuke  
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease  
; FILE REFERENCE: SPO-103  
; CURRENT APPLICATION NUMBER: US/09/142,524D  
; CURRENT FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: PCT/JP97/00740  
; PRIOR FILING DATE: 1997-03-10  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 87

; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Cryptomeria japonica  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(15)  
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 4  
US-09-142-524D-87

Query Match 70.8%; Score 17; DB 4; Length 15;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |  
Db 9 FSTAW 13

RESULT 3

US-09-142-524D-88  
; Sequence 88, Application US/09142524D  
; Patent No. 6719976  
; GENERAL INFORMATION:  
; APPLICANT: Sone, Toshio  
; APPLICANT: Kume, Akinori  
; APPLICANT: Dairiki, Kazuo  
; APPLICANT: Iwama, Akiko  
; APPLICANT: Kino, Kohsuke  
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease  
; FILE REFERENCE: SPO-103  
; CURRENT APPLICATION NUMBER: US/09/142,524D  
; CURRENT FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: PCT/JP97/00740  
; PRIOR FILING DATE: 1997-03-10  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 88  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Cryptomeria japonica  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(15)  
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 5  
US-09-142-524D-88

Query Match 70.8%; Score 17; DB 4; Length 15;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |  
Db 4 FSTAW 8

RESULT 4

US-08-469-260A-428  
; Sequence 428, Application US/08469260A  
; Patent No. 6451578  
; GENERAL INFORMATION:  
; APPLICANT: JOHN N. SIMONS  
; APPLICANT: TAMI J. PILOT-MATIAS  
; APPLICANT: GEORGE J. DAWSON  
; APPLICANT: GEORGE G. SCHLAUDER  
; APPLICANT: SURESH M. DESAI  
; APPLICANT: THOMAS P. LEARY  
; APPLICANT: ANTHONY SCOTT MUEHROFF  
; APPLICANT: JAMES C. ERKER  
; APPLICANT: SHERI L. BUIJK  
; APPLICANT: ISA K. MUSHAWAR  
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS REAGENTS AND METHODS FOR THEIR USE  
; NUMBER OF SEQUENCES: 716

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
; STREET: 100 ABBOTT PARK ROAD  
; CITY: ABBOTT PARK  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/469,260A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION NUMBER: US/08/424,550  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: POREMSKI, PRISCILLA E.  
; REGISTRATION NUMBER: 33,207  
; REFERENCE/DOCKET NUMBER: 5527.PC.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 708-937-6365  
; TELEFAX: 708-938-2623  
; INFORMATION FOR SEQ ID NO: 428:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 29 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-469-260A-428

Query Match 70.8%; Score 17; DB 4; Length 29;  
Best Local Similarity 40.0%; Pred. No. 3.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
| |  
Db 12 FASAW 16

RESULT 5  
US-08-488-446-428  
; Sequence 428, Application US/08488446  
; Patent No. 655898  
; GENERAL INFORMATION:  
; APPLICANT: JOHN N. SIMONS  
; APPLICANT: TAMI J. PILOT-MATIAS  
; APPLICANT: GEORGE J. DAWSON  
; APPLICANT: GEORGE G. SCHLAUDER  
; APPLICANT: SURESH M. DESAI  
; APPLICANT: THOMAS P. LEARY  
; APPLICANT: ANTHONY SCOTT MUERHOFF  
; APPLICANT: JAMES C. ERKER  
; APPLICANT: SHERI L. BUIJK  
; APPLICANT: ISA K. MUSHAWAR  
; TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS  
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
; NUMBER OF SEQUENCES: 716  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
; STREET: 100 ABBOTT PARK ROAD  
; CITY: ABBOTT PARK  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,446  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/424,550  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: POREMSKI, PRISCILLA E.  
; REGISTRATION NUMBER: 33,207  
; REFERENCE/DOCKET NUMBER: 5527.PC.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 708-937-6365  
; TELEFAX: 708-938-2623  
; INFORMATION FOR SEQ ID NO: 428:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 29 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-488-446-428

Query Match 70.8%; Score 17; DB 4; Length 29;  
Best Local Similarity 40.0%; Pred. No. 3.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
| |  
Db 12 FASAW 16

RESULT 6  
US-08-467-344A-428  
; Sequence 428, Application US/08467344A  
; Patent No. 6586568  
; GENERAL INFORMATION:  
; APPLICANT: JOHN N. SIMONS  
; APPLICANT: TAMI J. PILOT-MATIAS  
; APPLICANT: GEORGE J. DAWSON  
; APPLICANT: GEORGE G. SCHLAUDER  
; APPLICANT: SURESH M. DESAI  
; APPLICANT: THOMAS P. LEARY  
; APPLICANT: ANTHONY SCOTT MUERHOFF  
; APPLICANT: JAMES C. ERKER  
; APPLICANT: SHERI L. BUIJK  
; APPLICANT: ISA K. MUSHAWAR  
; TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS  
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
; NUMBER OF SEQUENCES: 716  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
; STREET: 100 ABBOTT PARK ROAD  
; CITY: ABBOTT PARK  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,344A  
; FILING DATE: 07-Jun-1995  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/424,550  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: POREMSKI, PRISCILLA E.  
; REGISTRATION NUMBER: 33,207  
; REFERENCE/DOCKET NUMBER: 5527.PC.01  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 428:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 428:  
US-08-467-344A-428

Query Match 70.8%; Score 17; DB 4; Length 29;  
Best Local Similarity 40.0%; Pred. No. 3.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
Db 12 FASAW 16

RESULT 7  
US-08-424-550B-428  
Sequence 428, Application US/08424550B  
Patent No. 6720166  
GENERAL INFORMATION:  
APPLICANT: JOHN N. SIMONS  
APPLICANT: TAMI J. PILOT-MATIAS  
APPLICANT: GEORGE J. DAWSON  
APPLICANT: GEORGE G. SCHLAUDER  
APPLICANT: SURESH M. DESAI  
APPLICANT: THOMAS P. LEARY  
APPLICANT: ANTHONY SCOTT MUERHOFF  
APPLICANT: JAMES C. ERKER  
APPLICANT: SHERI L. BUIJK  
APPLICANT: ISA K. MUSHAWAR  
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
NUMBER OF SEQUENCES: 716  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
STREET: 100 ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: US/08/424,550B  
APPLICANT NUMBER:  
CLASSIFICATION: 435435  
ATTORNEY/AGENT INFORMATION:  
NAME: POREMBSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5527.PC.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 428:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-424-550B-428

Query Match 70.8%; Score 17; DB 4; Length 29;  
Best Local Similarity 40.0%; Pred. No. 3.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
Db 12 FASAW 16

RESULT 8  
US-08-118-270-134  
Sequence 134, Application US/08118270  
Patent No. 5508384  
GENERAL INFORMATION:  
APPLICANT: Murphy, Randall B.  
APPLICANT: Schuster, David I.  
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
NUMBER OF SEQUENCES: 348  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/118,270  
FILING DATE: 09-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/943,236  
FILING DATE: 10-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, Kevin G.  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: MURPHY-2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 134:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-118-270-134

Query Match 70.8%; Score 17; DB 1; Length 34;  
Best Local Similarity 40.0%; Pred. No. 3.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
Db 16 FTSAW 20

RESULT 9  
US-08-118-270-172  
Sequence 172, Application US/08118270  
Patent No. 5508384  
GENERAL INFORMATION:  
APPLICANT: Murphy, Randall B.  
APPLICANT: Schuster, David I.  
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
NUMBER OF SEQUENCES: 348  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington

STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/118,270  
FILING DATE: 09-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/943,236  
FILING DATE: 10-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, Kevin G.  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: MURPHY=2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 172:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-118-270-172

Query Match 70.8%; Score 17; DB 1; Length 34;  
Best Local Similarity 40.0%; Pred. No. 3.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |  
Db 16 FTTAW 20

RESULT 10  
PCT-US93-08528-134  
Sequence 134, Application PC/TUS9308528  
GENERAL INFORMATION:  
APPLICANT: New York University  
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
NUMBER OF SEQUENCES: 348  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/08528  
FILING DATE: 09-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/943,236  
FILING DATE: 10-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, Kevin G.  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528

TELEX: 248633  
INFORMATION FOR SEQ ID NO: 134:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US93-08528-134

Query Match 70.8%; Score 17; DB 5; Length 34;  
Best Local Similarity 40.0%; Pred. No. 3.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |  
Db 16 FTSAW 20

RESULT 11  
PCT-US93-08528-172  
Sequence 172, Application PC/TUS9308528  
GENERAL INFORMATION:  
APPLICANT: New York University  
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
NUMBER OF SEQUENCES: 348  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/08528  
FILING DATE: 09-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/943,236  
FILING DATE: 10-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, Kevin G.  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 172:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US93-08528-172

Query Match 70.8%; Score 17; DB 5; Length 34;  
Best Local Similarity 40.0%; Pred. No. 3.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |  
Db 16 FTTAW 20

RESULT 12  
US-08-467-023-137

; Sequence 137, Application US/08467023  
; Patent No. 6090386  
; GENERAL INFORMATION:  
; APPLICANT: Griffith, Irwin J.;  
; APPLICANT: Pollock, Joanne;  
; APPLICANT: Bond, Julian F.;  
; APPLICANT: Garman, Richard D;  
; APPLICANT: Kuo, Mei-Chang;  
; APPLICANT: Yeung, Siu-mei H.;  
; APPLICANT: Brauer, Andrew;  
; APPLICANT: Exley, Mark A.;  
; APPLICANT: Powers, Steven P.  
; TITLE OF INVENTION: Allergenic Proteins And Peptides From  
; TITLE OF INVENTION: Japanese Cedar Pollen  
; NUMBER OF SEQUENCES: 261  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.  
; STREET: 610 Lincoln St  
; CITY: Waltham  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,023  
; FILING DATE: June 6, 1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/350,225  
; FILING DATE: December 6, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jane E. Remillard  
; REGISTRATION NUMBER: 38,872  
; REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 137:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
; US-08-467-023-137  
  
Query Match 70.8%; Score 17; DB 3; Length 36;  
Best Local Similarity 40.0%; Pred. No. 3.8e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXXW 6  
| |  
Db 28 PSTAW 32  
  
RESULT 13  
US-09-330-914A-10  
; Sequence 10, Application US/09330914A  
; Patent No. 6432671  
; GENERAL INFORMATION:  
; APPLICANT: Flohe, Leopold  
; No. 6432671echeke, Everson  
; Kalisz, Henryk  
; Montemartini, Marisa  
; TITLE OF INVENTION: TRYPAEDOXIN, EXPRESSION PLASMID, PROCESS OF  
; PRODUCTION, METHOD OF USE, TEST KIT, AND  
; PHARMACEUTICAL COMPOSITION  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Broun  
; STREET: 233 South Wacker Drive/6300 Sears Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: Unites States of America  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/330,914A  
; FILING DATE: 11-Jun-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP97/06983  
; FILING DATE: 12-DEC-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, James P.  
; REGISTRATION NUMBER: 28,491  
; REFERENCE/DOCKET NUMBER: 29473/35678  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 37 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-09-330-914A-10  
  
Query Match 70.8%; Score 17; DB 4; Length 37;  
Best Local Similarity 40.0%; Pred. No. 3.8e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXXW 6  
| |  
Db 11 FSASW 15  
  
RESULT 14  
US-08-467-023-136  
; Sequence 136, Application US/08467023  
; Patent No. 6090386  
; GENERAL INFORMATION:  
; APPLICANT: Griffith, Irwin J.;  
; APPLICANT: Pollock, Joanne;  
; APPLICANT: Bond, Julian F.;  
; APPLICANT: Garman, Richard D;  
; APPLICANT: Kuo, Mei-Chang;  
; APPLICANT: Yeung, Siu-mei H.;  
; APPLICANT: Brauer, Andrew;  
; APPLICANT: Exley, Mark A.;  
; APPLICANT: Powers, Steven P.  
; TITLE OF INVENTION: Allergenic Proteins And Peptides From  
; TITLE OF INVENTION: Japanese Cedar Pollen  
; NUMBER OF SEQUENCES: 261  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.  
; STREET: 610 Lincoln St  
; CITY: Waltham  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,023  
FILING DATE: June 6, 1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/350,225  
FILING DATE: December 6, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane E. Remillard  
REGISTRATION NUMBER: 38,872  
REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 136:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 41 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-467-023-136

Query Match 70.8%; Score 17; DB 3; Length 41;  
Best Local Similarity 40.0%; Pred. No. 4.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |  
Db 33 FSTAW 37

RESULT 15  
US-08-467-023-135  
Sequence 135, Application US/08467023  
Patent No. 6090386  
GENERAL INFORMATION:  
APPLICANT: Griffith, Irwin J.;  
APPLICANT: Pollock, Joanne;  
APPLICANT: Bond, Julian F.;  
APPLICANT: Garman, Richard D;  
APPLICANT: Kuo, Mei-Chang;  
APPLICANT: Yeung, Siu-mei H.;  
APPLICANT: Brauer, Andrew;  
APPLICANT: Exley, Mark A.;  
APPLICANT: Powers, Steven P.  
TITLE OF INVENTION: Allergenic Proteins And Peptides From  
TITLE OF INVENTION: Japanese Cedar Pollen  
NUMBER OF SEQUENCES: 261  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.  
STREET: 610 Lincoln St  
CITY: Waltham  
STATE: MA  
COUNTRY: USA  
ZIP: 02154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,023  
FILING DATE: June 6, 1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/350,225  
FILING DATE: December 6, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane E. Remillard  
REGISTRATION NUMBER: 38,872

REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 135:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-467-023-135

Query Match 70.8%; Score 17; DB 3; Length 45;  
Best Local Similarity 40.0%; Pred. No. 4.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
| |  
Db 33 FSTAW 37

RESULT 16  
US-09-149-476-475  
Sequence 475, Application US/09149476  
Patent No. 6420526  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: P2002P1  
CURRENT APPLICATION NUMBER: US/09/149,476  
CURRENT FILING DATE: 1998-09-08  
EARLIER APPLICATION NUMBER: PCT/US98/04493  
EARLIER FILING DATE: 1998-03-06  
EARLIER APPLICATION NUMBER: 60/040,162  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,333  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/038,621  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,626  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,334  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,336  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,163  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/047,600  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,615  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,597  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,502  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,633  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,583  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,617  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,618  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,503  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,592  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,581  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,584  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,500





EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Query Match 70.8%; Score 17; DB 4; Length 45;  
Best Local Similarity 40.0%; Pred. No. 4.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
|  
Db 31 FSAW 35

## RESULT 17

US-09-369-247-129  
Sequence 129, Application US/09369247  
Patent No. 656992  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 44 Human Secreted Proteins  
FILE REFERENCE: P2024P1  
CURRENT APPLICATION NUMBER: US/09/369,247  
CURRENT FILING DATE: 1999-08-05  
EARLIER APPLICATION NUMBER: 60/074,118  
EARLIER FILING DATE: 1998-02-09  
EARLIER APPLICATION NUMBER: 60/074,157  
EARLIER FILING DATE: 1998-02-09  
EARLIER APPLICATION NUMBER: 60/074,137  
EARLIER FILING DATE: 1998-02-09  
EARLIER APPLICATION NUMBER: 60/074,341  
EARLIER FILING DATE: 1998-02-09  
EARLIER APPLICATION NUMBER: 60/074,141  
NUMBER OF SEQ ID NOS: 172  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 129  
LENGTH: 47  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-369-247-129

Query Match 70.8%; Score 17; DB 4; Length 47;  
Best Local Similarity 40.0%; Pred. No. 4.5e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
|  
Db 39 FSSW 43

## RESULT 18

US-08-118-270-209  
Sequence 209, Application US/08118270  
Patent No. 5508384  
GENERAL INFORMATION:  
APPLICANT: Murphy, Randall B.  
APPLICANT: Schuster, David I.  
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
NUMBER OF SEQUENCES: 348  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/118,270  
FILING DATE: 09-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/943,236  
FILING DATE: 10-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, Kevin G.  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: MURPHY=2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633

INFORMATION FOR SEQ ID NO: 209:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 49 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-118-270-209

Query Match 70.8%; Score 17; DB 1; Length 49;  
Best Local Similarity 40.0%; Pred. No. 4.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
|  
Db 36 FTSW 40

## RESULT 19

PCT-US93-08528-209  
Sequence 209, Application PC/TUS9308528  
GENERAL INFORMATION:  
APPLICANT: New York University  
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
NUMBER OF SEQUENCES: 348  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/08528  
FILING DATE: 09-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/943,236  
FILING DATE: 10-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, Kevin G.  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 209:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 49 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

```
; MOLECULE TYPE: peptide
PCT-US93-08428-209

Query Match      70.8%; Score 17; DB 5; Length 49;
Best Local Similarity 40.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXW 6
Db      16 FTSSW 40

RESULT 20
US-09-434-840-73
; Sequence 73, Application US/09434840
; Patent No. 6620985
; GENERAL INFORMATION:
; APPLICANT: Glazebrook, Jane
; APPLICANT: Jirage, Dayadevi
; APPLICANT: Tootle, Tina L
; APPLICANT: Zhou, Nan
; APPLICANT: Feyn, Bart
; TITLE OF INVENTION: PAD4 COMPOSITIONS AND METHODS THEREFOR
; FILE REFERENCE: 043503.0009
; CURRENT APPLICATION NUMBER: US/09/434,840
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: 09/190,733
; EARLIER FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 73
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Thermomyces lanuginosus
US-09-434-840-73

Query Match      70.8%; Score 17; DB 4; Length 54;
Best Local Similarity 40.0%; Pred. No. 4.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXW 6
Db      7 FTSSW 11

RESULT 21
US-09-733-643B-21
; Sequence 21, Application US/09733643B
; Patent No. 6734144
; GENERAL INFORMATION:
; APPLICANT: Laroche, Andre J.
; APPLICANT: Huang, Timothy Y
; APPLICANT: Lu, Zhen-Xiang
; APPLICANT: Frick, Michael M.
; APPLICANT: Huang, Hung Chang
; APPLICANT: Chong, Kuo Joan
; TITLE OF INVENTION: Coniothyrum minitans beta-(1,3) exoglucanase gene
; FILE REFERENCE: 24014US1
; CURRENT APPLICATION NUMBER: US/09/733,643B
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/170,168
; PRIOR FILING DATE: 1999-12-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 21
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: Exopg
US-09-733-643B-21

Query Match      70.8%; Score 17; DB 4; Length 54;
Best Local Similarity 40.0%; Pred. No. 4.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXW 6
Db      23 FAAW 27

RESULT 22
US-09-621-976-6592
; Sequence 6592, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6592
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6592

Query Match      70.8%; Score 17; DB 4; Length 56;
Best Local Similarity 40.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXW 6
Db      8 FTSSW 12

RESULT 23
US-09-270-767-35869
; Sequence 35869, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 35869
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-35869

Query Match      70.8%; Score 17; DB 4; Length 60;
Best Local Similarity 40.0%; Pred. No. 5.3e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 FXXW 6
Db      13 FTSSW 17

RESULT 24
US-09-270-767-51086
; Sequence 51086, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
```

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 51086  
; LENGTH: 60  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
; FEATURE:  
; OTHER INFORMATION: Xaa means any amino acid  
US-09-270-767-51086

Query Match 70.8%; Score 17; DB 4; Length 60;  
Best Local Similarity 40.0%; Pred. No. 5.3e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
|  
Db 13 FTSSW 17

RESULT 25

US-09-134-001C-4258  
; Sequence 4258, Application US/09134001C  
; Patent No. 6380370

; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 4258  
; LENGTH: 61  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-4258

Query Match 70.8%; Score 17; DB 3; Length 61;  
Best Local Similarity 40.0%; Pred. No. 5.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
|  
Db 14 FSTSW 18

RESULT 26

US-09-252-991A-28658  
; Sequence 28658, Application US/09252991A  
; Patent No. 6551795

; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 28658  
; LENGTH: 62  
; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-28658

Query Match 70.8%; Score 17; DB 4; Length 62;  
Best Local Similarity 40.0%; Pred. No. 5.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
|  
Db 58 FAASW 62

RESULT 27

US-09-621-976-5704  
; Sequence 5704, Application US/09621976  
; Patent No. 6639063

; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 5704  
; LENGTH: 62  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -43...-1  
US-09-621-976-5704

Query Match 70.8%; Score 17; DB 4; Length 62;  
Best Local Similarity 40.0%; Pred. No. 5.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
|  
Db 35 FTAASW 39

RESULT 28

US-09-248-796A-26247  
; Sequence 26247, Application US/09248796A  
; Patent No. 6747137

; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 26247  
; LENGTH: 62  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-26247

Query Match 70.8%; Score 17; DB 4; Length 62;  
Best Local Similarity 40.0%; Pred. No. 5.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
|  
Db 27 FSTSW 31

```
RESULT 29
US-09-902-510-11838
; Sequence 11838, Application US/09902540
; Patent No. 6432671
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16815
; SEQ ID NO 11838
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11838
Query Match      70.8%; Score 17; DB 4; Length 63;
Best Local Similarity 40.0%; Pred. No. 5.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 FXXXW 6
Db      27 FATAW 31

RESULT 30
US-09-621-976-6715
; Sequence 6715, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6715
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6715
Query Match      70.8%; Score 17; DB 4; Length 69;
Best Local Similarity 40.0%; Pred. No. 5.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 FXXXW 6
Db      62 FATTW 66

RESULT 31
US-09-248-796A-24056
; Sequence 24056, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinatlock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
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; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 24056
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-24056
Query Match      70.8%; Score 17; DB 4; Length 69;
Best Local Similarity 40.0%; Pred. No. 5.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 FXXXW 6
Db      62 FTTAW 66

RESULT 32
US-09-330-914A-4
; Sequence 4, Application US/09330914A
; Patent No. 6432671
; GENERAL INFORMATION:
; APPLICANT: Flohe, Leopold
; No. 6432671ecke, Everson
; Kalisz, Henryk
; Montemartini, Marisa
; TITLE OF INVENTION: TRYPAEDOXIN, EXPRESSION PLASMID, PROCESS OF
; PRODUCTION, METHOD OF USE, TEST KIT, AND
; PHARMACEUTICAL COMPOSITION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Broun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: Unites States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/330,914A
; FILING DATE: 11-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP97/06983
; FILING DATE: 12-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, James P.
; REGISTRATION NUMBER: 28,491
; REFERENCE/DOCKET NUMBER: 29473/35678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-330-914A-4
Query Match      70.8%; Score 17; DB 4; Length 80;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
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Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 FXXXW 6
Db 8 FSASW 12
RESULT 33
US-09-270-767-37303
; Sequence 37303, Application US/092270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37303
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-37303
Query Match 70.8%; Score 17; DB 4; Length 80;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 FXXXW 6
Db 41 FTASW 45
RESULT 34
US-09-270-767-52520
; Sequence 52520, Application US/092270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52520
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-52520
Query Match 70.8%; Score 17; DB 4; Length 80;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 FXXXW 6
Db 41 FTASW 45
RESULT 35
US-09-248-796A-24759
; Sequence 24759, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
```

```
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 24759
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-24759
Query Match 70.8%; Score 17; DB 4; Length 80;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 FXXXW 6
Db 72 FTTAW 76
RESULT 36
US-09-248-796A-19864
; Sequence 19864, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19864
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19864
Query Match 70.8%; Score 17; DB 4; Length 82;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 FXXXW 6
Db 74 FTTAW 78
RESULT 37
US-08-353-476-78
; Sequence 78, Application US/08353476
; Patent No. 5871902
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/353,476  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bencen, Gerard H  
; REGISTRATION NUMBER: 35,746  
; REFERENCE/DOCKET NUMBER: GP-100  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (904) 375-8100  
; TELEFAX: 904) 372-5800  
; INFORMATION FOR SEQ ID NO: 78:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 84 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
US-08-353-476-78

Query Match 70.8%; Score 17; DB 2; Length 84;  
Best Local Similarity 40.0%; Pred. No. 6.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6  
|  
Db 31 FSTTW 35

RESULT 38  
US-08-679-493A-97  
; Sequence 97, Application US/08679493A  
; Patent No. 6303295  
; GENERAL INFORMATION:  
; APPLICANT: Taylor, Ethan W.  
; TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS  
; FILE REFERENCE: 55-95  
; CURRENT APPLICATION NUMBER: US/08/679,493A  
; PRIOR FILING DATE: 1996-07-12  
; PRIOR FILING DATE: 1995-07-14  
; PRIOR APPLICATION NUMBER: 60/001203  
; PRIOR FILING DATE: 1995-09-01  
; PRIOR APPLICATION NUMBER: 60/003,112  
; NUMBER OF SEQ ID NOS: 216  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 97  
; LENGTH: 84  
; TYPE: PRT  
; ORGANISM: bovine papillomavirus type 8  
US-08-679-493A-97

Query Match 70.8%; Score 17; DB 3; Length 84;  
Best Local Similarity 40.0%; Pred. No. 6.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6  
|  
Db 31 FSTTW 35

RESULT 39  
US-09-583-110-3199  
; Sequence 199, Application US/09583110  
; Patent No. 6699703  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al.  
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus  
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

; FILE REFERENCE: PATH00-07A  
; CURRENT APPLICATION NUMBER: US/09/583,110  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/107,433  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/085,131  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: US 60/051,553  
; PRIOR FILING DATE: 1997-07-02  
; NUMBER OF SEQ ID NOS: 5322  
; SEQ ID NO 3199  
; LENGTH: 86  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-09-583-110-3199

Query Match 70.8%; Score 17; DB 4; Length 86;  
Best Local Similarity 40.0%; Pred. No. 6.8e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6  
|  
Db 4 FSSAW 8

RESULT 40  
US-09-621-976-6168  
; Sequence 6168, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 6168  
; LENGTH: 89  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-621-976-6168

Query Match 70.8%; Score 17; DB 4; Length 89;  
Best Local Similarity 40.0%; Pred. No. 7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6  
|  
Db 58 FSASW 62

Search completed: October 18, 2005, 15:32:10  
Job time : 32.2941 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:14:39 ; Search time 125.471 Seconds  
(without alignments)  
27.742 Million cell updates/sec

Title: US-09-214-371-11  
Perfect score: 24  
Sequence: 1 XFXXWXXX 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : A\_Geneseq\_16Dec04: \*  
1: Geneseqp1980s: \*  
2: Geneseqp1990s: \*  
3: Geneseqp2000s: \*  
4: Geneseqp2001s: \*  
5: Geneseqp2002s: \*  
6: Geneseqp2003as: \*  
7: Geneseqp2003bs: \*  
8: Geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	17	70.8	9	7	ADC07129	Adc07129 Honeybee
2	17	70.8	9	7	ADC07134	Adc07134 Painted l
3	17	70.8	10	3	AAB10010	Aab10010 H. pylori
4	17	70.8	10	4	AAB86090	Aab86090 H. pylori
5	17	70.8	10	4	AAB86058	Aab86058 H. pylori
6	17	70.8	11	7	ADC07163	Adc07163 Painted l
7	17	70.8	13	4	AAE05735	Aae05735 Complemen
8	17	70.8	13	6	ABG75574	Abg75574 CDR3 pept
9	17	70.8	14	4	AAM98088	Aam98088 Human pep
10	17	70.8	15	2	AAR97874	Aar97874 Japan ced
11	17	70.8	15	2	AAR97875	Aar97875 Japan ced
12	17	70.8	15	2	AAW57758	Aaw57758 Residues
13	17	70.8	19	5	AAE23038	Aae23038 Human thi
14	17	70.8	20	2	AAW42165	Aaw42165 T-cell ep
15	17	70.8	20	4	AAG62999	Aag62999 Complemen
16	17	70.8	25	7	ADE25429	Ade25429 Plant gro
17	17	70.8	27	4	AAM18617	Aam18617 Peptide #
18	17	70.8	27	4	AAM31077	Aam31077 Peptide #
19	17	70.8	27	4	ABG52487	Abg52487 Human liv
20	17	70.8	27	5	ABG40522	Abg40522 Human pep
21	17	70.8	29	3	AAB09301	Aab09301 Hepatitis
22	17	70.8	32	4	AAG71365	Aag71365 Human gen
23	17	70.8	33	5	ABP60808	Abp60808 Sus scrof
24	17	70.8	33	8	ABO54713	Abo54713 Human gen
25	17	70.8	34	2	AAR50631	Aar50631 G-protein

26	17	70.8	34	2	AAR50593	Aar50593 G-protein
27	17	70.8	34	2	AAW02823	Aaw02823 G-protein
28	17	70.8	34	2	AAW02785	Aaw02785 G-protein
29	17	70.8	35	4	AAO08042	Aao08042 Human pol
30	17	70.8	36	2	AAR53693	Aar53693 Japanese
31	17	70.8	37	4	AAO08979	Aao08979 Human pol
32	17	70.8	38	3	AAY76339	Aay76339 Fragment
33	17	70.8	38	3	AAG10451	Aag10451 Arabidops
34	17	70.8	38	7	ADE11915	Ade11915 Human sec
35	17	70.8	40	2	AAY41113	Aay41113 TNFR/NGFR
36	17	70.8	40	3	AAG51555	Aag51555 Arabidops
37	17	70.8	40	4	AAM37764	Aam37764 Peptide #
38	17	70.8	40	4	AAB64755	Aab64755 Human sec
39	17	70.8	40	4	AAO06835	Aao06835 Human pol
40	17	70.8	40	4	AAM64830	Aam64830 Human bra
41	17	70.8	40	4	ABG59226	Abg59226 Human liv
42	17	70.8	40	5	ABG46611	Abg46611 Human pep
43	17	70.8	41	2	AAR53692	Aar53692 Japanese
44	17	70.8	41	4	AAO07778	Aao07778 Human pol
45	17	70.8	44	4	AAM15556	Aam15556 Peptide #
46	17	70.8	44	4	ABB34562	Abb34562 Peptide #
47	17	70.8	44	4	AAM28045	Aam28045 Peptide #
48	17	70.8	44	4	ABB29389	Abb29389 Peptide #
49	17	70.8	44	4	ABB19970	Abb19970 Protein #
50	17	70.8	44	4	AAM67745	Aam67745 Human bon
51	17	70.8	44	4	AAO12937	Aao12937 Human pol
52	17	70.8	44	4	AAM55349	Aam55349 Human bra
53	17	70.8	44	4	ABG49383	Abg49383 Human liv
54	17	70.8	45	2	AAR53691	Aar53691 Japanese
55	17	70.8	45	5	ABG95335	Abg95335 Human nov
56	17	70.8	45	6	ABO34529	Abo34529 Region of
57	17	70.8	45	7	ADI23190	Adi23190 Novel hum
58	17	70.8	45	8	ADH74192	Adh74192 Human sec
59	17	70.8	46	4	AAM27852	Aam27852 Peptide #
60	17	70.8	46	4	ABB29210	Abb29210 Peptide #
61	17	70.8	46	4	ABB19786	Abb19786 Protein #
62	17	70.8	46	4	AAM67559	Aam67559 Human bon
63	17	70.8	46	4	AAM55165	Aam55165 Human bra
64	17	70.8	46	4	AAM03130	Aam03130 Peptide #
65	17	70.8	47	2	AAY30880	Aay30880 Human sec
66	17	70.8	47	5	ABP51359	Abp51359 Human MDD
67	17	70.8	49	2	AAR50668	Aar50668 G-protein
68	17	70.8	49	2	AAW02860	Aaw02860 G-protein
69	17	70.8	50	5	ABP05131	Abp05131 Human ORF
70	17	70.8	51	4	AAU58484	Aau58484 Propionib
71	17	70.8	51	6	ABM55003	Abm55003 Propionib
72	17	70.8	52	3	AAB45468	Aab45468 Human sec
73	17	70.8	52	4	AAU56768	Aau56768 Propionib
74	17	70.8	52	6	ABM53287	Abm53287 Propionib
75	17	70.8	53	3	AAB16526	Aab16526 Bacteriop
76	17	70.8	53	4	AAO08445	Aao08445 Human pol
77	17	70.8	53	6	ABJ18951	Abj18951 Pathogen
78	17	70.8	53	6	ABM71514	Abm71514 Staphyloc
79	17	70.8	54	3	AAU56440	Aau56440 Helicobac
80	17	70.8	54	7	ADH62390	Adh62390 Thermomyc
81	17	70.8	55	4	AAE01321	Aae01321 Human gen
82	17	70.8	55	6	ADA98194	Ada98194 Human sec
83	17	70.8	55	6	ADA44043	Ada44043 Human sec
84	17	70.8	55	7	ADC20359	Adc20359 Human sec
85	17	70.8	55	7	ADF10696	Adf10696 Human sec
86	17	70.8	56	3	AAB27801	Aab27801 Human sec
87	17	70.8	56	3	AAG41143	Aag41143 Zea mays
88	17	70.8	56	4	AAE05519	Aae05519 Human TNF
89	17	70.8	56	4	AAU64706	Aau64706 Propionib
90	17	70.8	56	5	ABP11292	Abp11292 Human ORF
91	17	70.8	56	6	ABM61225	Abm61225 Propionib
92	17	70.8	58	4	AAO11806	Aao11806 Human pol
93	17	70.8	58	4	AAU46944	Aau46944 Propionib
94	17	70.8	58	6	ABM43463	Abm43463 Propionib
95	17	70.8	59	4	AAM90403	Aam90403 Human imm
96	17	70.8	60	4	AAU64940	Aau64940 Propionib
97	17	70.8	60	5	ABB79236	Abb79236 Human pro
98	17	70.8	60	6	ABM61459	Abm61459 Propionib

99 17 70.8 61 4 AA04154 Human gen  
100 17 70.8 61 4 AA45906 Propionib

ALIGNMENTS

RESULT 1  
ADC07129  
ID ADC07129 standard; peptide; 9 AA.

XX AC ADC07129;  
XX DT 18-DEC-2003 (first entry)  
XX DE Honeybee AKH peptide.  
XX KW lipid mobilisation; insect; adipokinetic hormone; AKH; anorectic;  
KW antidiabetic; hypotensive; cardiant; antiarthritic; cytostatic;  
KW nephrotropic; hepatotropic; analgesic; cerebroprotective; uropathic;  
KW obesity; type II diabetes; cholelithiasis; hypertension;  
KW coronary heart disease; atherosclerosis; glycogenosis; arthritis; cancer;  
KW renal failure; liver; chronic pain; sleep apnea; stroke;  
KW urinary incontinence; honeybee.

OS Synthetic.  
OS Apia mellifera.  
XX  
XX PH Key Location/Qualifiers  
FT Modified-site 1 /label= OTHER  
FT /note= "OTHER = Pyroglutamic acid"  
FT Misc-difference 9  
FT /note= "Preferably C-terminal amide"

XX PN WO2003066080-A1.  
XX PD 14-AUG-2003.  
XX PF 07-FEB-2003; 2003WO-US003800.  
XX PR 07-FEB-2002; 2002US-00072419.  
XX PA (BLMB-) BLM GROUP.  
XX PI Schacter BZ, Schacter LP;  
XX WPI; 2003-712542/67.  
XX PT Pharmaceutical composition useful for promoting weight loss, comprises an  
PT insect adipokinetic hormone, having a pyroglutamate residue at its amino  
PT terminus.

PS Claim 29; Page 20; 82pp; English.  
XX  
XX CC The invention relates to a novel method of promoting lipid mobilisation  
CC in a human which comprises administering an insect adipokinetic hormone  
CC (AKH). The hormone of the invention demonstrates anorectic, antidiabetic,  
CC hypotensive, cardiant, antiarthritic, cytostatic, nephrotropic,  
CC hepatotropic, analgesic, cerebroprotective and uropathic activities. The  
CC method of the invention may be useful for treating obesity, type II  
CC diabetes, cholelithiasis, hypertension, coronary heart disease,  
CC atherosclerosis, types I to VI glycogenosis, arthritis, cancer, renal  
CC failure, liver disease, chronic pain, sleep apnea, stroke and urinary  
CC incontinence. The current sequence is that of the honeybee AKH peptide of  
CC the invention.

XX SQ Sequence 9 AA;  
Query Match 70.8%; Score 17; DB 7; Length 9;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
Db 4 FTSSW 8  
RESULT 2  
ADC07134  
ID ADC07134 standard; peptide; 9 AA.  
XX AC ADC07134;  
XX DT 18-DEC-2003 (first entry)  
XX DE Painted lady AKH peptide.  
XX KW lipid mobilisation; insect; adipokinetic hormone; AKH; anorectic;  
KW antidiabetic; hypotensive; cardiant; antiarthritic; cytostatic;  
KW nephrotropic; hepatotropic; analgesic; cerebroprotective; uropathic;  
KW obesity; type II diabetes; cholelithiasis; hypertension;  
KW coronary heart disease; atherosclerosis; glycogenosis; arthritis; cancer;  
KW renal failure; liver; chronic pain; sleep apnea; stroke;  
KW urinary incontinence; painted lady.  
OS Synthetic.  
OS Vanessa cardui.  
XX  
XX PH Key Location/Qualifiers  
FT Modified-site 1 /label= OTHER  
FT /note= "OTHER = Pyroglutamic acid"  
FT Misc-difference 9  
FT /note= "Preferably C-terminal amide"

XX PN WO2003066080-A1.  
XX PD 14-AUG-2003.  
XX PF 07-FEB-2003; 2003WO-US003800.  
XX PR 07-FEB-2002; 2002US-00072419.  
XX PA (BLMB-) BLM GROUP.  
XX PI Schacter BZ, Schacter LP;  
XX WPI; 2003-712542/67.

XX PT Pharmaceutical composition useful for promoting weight loss, comprises an  
PT insect adipokinetic hormone, having a pyroglutamate residue at its amino  
PT terminus.  
XX PS Claim 29; Page 20; 82pp; English.  
XX  
XX CC The invention relates to a novel method of promoting lipid mobilisation  
CC in a human which comprises administering an insect adipokinetic hormone  
CC (AKH). The hormone of the invention demonstrates anorectic, antidiabetic,  
CC hypotensive, cardiant, antiarthritic, cytostatic, nephrotropic,  
CC hepatotropic, analgesic, cerebroprotective and uropathic activities. The  
CC method of the invention may be useful for treating obesity, type II  
CC diabetes, cholelithiasis, hypertension, coronary heart disease,  
CC atherosclerosis, types I to VI glycogenosis, arthritis, cancer, renal  
CC failure, liver disease, chronic pain, sleep apnea, stroke and urinary  
CC incontinence. The current sequence is that of the painted lady AKH  
CC peptide of the invention.

XX SQ Sequence 9 AA;  
Query Match 70.8%; Score 17; DB 7; Length 9;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 FXXW 6  
Db 4 FTSSW 8

Db	4 FTSSW 8	
RESULT 3		
AAB10010		
ID	AAB10010 standard; protein; 10 AA.	
XX		
AC	AAB10010;	
XX		
DT	01-NOV-2000 (first entry)	
XX		
DE	H. pylori beta-urease-binding antibody heavy chain CDR1 protein #2.	
XX		
KW	Acid-resistant microorganism; detection; faecal; intestine; infection;	
KW	monoclonal antibody; heavy chain; complementarity determining region;	
KW	CDR; beta-urease.	
XX		
OS	Unidentified.	
XX		
PN	WO200026671-A1.	
XX		
PD	11-MAY-2000.	
XX		
PF	29-OCT-1999; 99WO-EP008212.	
XX		
PR	29-OCT-1998; 98EP-00120517.	
PR	06-NOV-1998; 98EP-00120687.	
XX		
PA	(CONN-) CONNEX GMBH.	
XX		
PI	Reiter C, Cullmann G, Friedrichs U, Heppner P, Lakner M;	
PI	Ringeis A;	
XX		
DR	WPI; 2000-365747/31.	
DR	N-PSDB; AAA40166.	
XX		
PT	Detecting infection by acid-fast microbes for diagnosis of Helicobacter	
PT	pylori, comprises reacting a fecal sample with two binding reagents for	
PT	antigens that survive intestinal passage.	
XX		
PS	Claim 26; Page 22; 84pp; German.	
XX		
CC	This invention describes a novel method for the detection of a mammalian	
CC	infection by an acid-resistant microorganism (A) by treating a faecal	
CC	sample with at least two different monoclonal antibodies (MAB) (or their	
CC	fragments or derivatives) or aptamers (collectively (I)) and detecting	
CC	formation of a complex (C) between (I) and the corresponding antigen of	
CC	(A). The first and second (I) bind to epitopes of different antigens	
CC	(Ag). These epitopes are present, after passage through the intestines,	
CC	in at least some mammals, and have either: (i) their native structure; or	
CC	(ii) a structure against which an antibody is produced by an animal	
CC	infected or immunized with (A), or its extract, lysate, derived protein	
CC	or fragment, or with a synthetic peptide. Practically all mammals display	
CC	at least one of the specified epitopes. The method is used to detect	
CC	infection by acid-fast bacteria, particularly of the genera Helicobacter,	
CC	Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus, M.	
CC	tuberculosis, C. jejuni and C. pylori. (I) may also be used	
CC	therapeutically. The method is direct and non-invasive, and provides an	
CC	inexpensive and easily standardizable diagnosis, despite possible	
CC	degradation of antigens during passage through the intestines. This	
CC	sequence represents a fragment of a H. pylori beta-urease-binding	
CC	antibody heavy chain complementarity determining region CDR1 which is	
CC	used to illustrate the method of the invention	
XX		
SQ	Sequence 10 AA;	
Query Match	70.8%; Score 17; DB 3; Length 10;	
Best Local Similarity	40.0%; Pred. No. 3.4e+03;	
Matches	2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
QY	2 FXXXW 6	
Db	4 FSTSW 8	
RESULT 4		
AAB86090		
ID	AAB86090 standard; peptide; 10 AA.	
XX		
AC	AAB86090;	
XX		
DT	17-JUL-2001 (first entry)	
XX		
DE	H. pylori beta-urease derived antibody light chain CDR1 #1.	
XX		
KW	Catalase; beta-urease; antibody; antigen; detection; infection; epitope;	
KW	acid-resistant microorganism; complementarity determining region; CDR;	
KW	feces; heavy chain; light chain.	
XX		
OS	Unidentified.	
XX		
PN	WO200127612-A2.	
XX		
PD	19-APR-2001.	
XX		
PF	12-OCT-2000; 2000WO-EP010057.	
XX		
PR	12-OCT-1999; 99EP-00120351.	
PR	16-MAR-2000; 2000EP-00105592.	
PR	31-MAR-2000; 2000EP-00107028.	
PR	10-MAY-2000; 2000EP-00110110.	
XX		
PA	(CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.	
XX		
PI	Reiter C, Cullmann G, Lakner M, Truee A, Dehnert S, Schwartz G;	
PI	Ringeis A;	
XX		
DR	WPI; 2001-282086/29.	
DR	N-PSDB; AAF88117.	
XX		
PT	Detecting infections by acid-resistant microorganisms, particularly for	
PT	diagnosing Helicobacter pylori, comprises immunochromatographic detection	
PT	of antigen in feces.	
XX		
PS	Claim 27; Page 27; 90pp; German.	
XX		
CC	This invention describes a novel method for detecting infection by an	
CC	acid-resistant microorganism (A), in a mammal, using	
CC	immunochromatography. The method is used to diagnose infection by an acid	
CC	-resistant microorganism (A), in a mammal, such as Helicobacter,	
CC	Campylobacter or Mycobacterium, particularly H. pylori (most preferred),	
CC	H. hepatica, C. jejuni and M. tuberculosis. The method is rapid, simple,	
CC	inexpensive and non-invasive, and may indicate the stage of infection. A	
CC	test strip used in the method may include a filter to eliminate particles	
CC	present in the sample and only a single receptor provides a reasonably	
CC	secure diagnosis, with specificity and selectivity improved by detecting	
CC	several epitopes (of catalase) or different antigens (catalase and beta-	
CC	urease). The method can be automated. This sequence represents a	
CC	complementarity determining region (CDR) from an antibody raised against	
CC	the H. pylori catalase or beta-urease antigen which is used to illustrate	
CC	the method of the invention	
XX		
SQ	Sequence 10 AA;	
Query Match	70.8%; Score 17; DB 4; Length 10;	
Best Local Similarity	40.0%; Pred. No. 3.4e+03;	
Matches	2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
QY	2 FXXXW 6	
Db	4 FSTSW 8	
RESULT 5		
AAB86058		
ID	AAB86058 standard; peptide; 10 AA.	
XX		



AC AAE05735;  
XX  
DT 24-SEP-2001 (first entry)  
XX  
DE Complementarity-determining region 3 (CDR3) of MoPhabs #7.  
XX  
KW CDR3; complementarity-determining region 3; monoclonal phage antibody;  
KW MoPhabs; antigen.  
XX  
OS Synthetic.  
XX  
PN US6265150-B1.  
XX  
PD 24-JUL-2001.  
XX  
PF 26-MAY-1998; 98US-00085072.  
XX  
PR 07-JUN-1995; 95US-00483633.  
PR 18-SEP-1997; 97US-00932892.  
XX  
PA (BECT ) BECTON DICKINSON & CO.  
PA (CRUC-) CRUCCELL HOLLAND BV.  
XX  
PI Terstappen LW, Logtenberg T;  
XX  
DR WPI; 2001-463929/50.  
XX  
XX Obtaining a phage particle, useful for obtaining human antibodies against  
PT known and novel surface antigens, by incubating a phage library with  
PT target cells to allow binding of the antibody fragment to the antigen.  
XX  
PS Example 6; Col 6; 6pp; English.  
XX  
CC The invention relates to a method of obtaining a phage particle which has  
CC an antibody fragment directed against an antigen associated with the  
CC surface of target cells in a heterogeneous cell population. The method  
CC involves incubating a library of phage particles with the target cells to  
CC allow binding of the antibody fragment expressed on the surface of the  
CC phage particles to the antigen associated with the target cells. The  
CC method is useful for obtaining human antibodies against known and novel  
CC surface antigens in their native configuration, expressed on  
CC phenotypically defined subpopulations of cells. The present sequence is  
CC complementarity-determining region 3 (CDR3) of monoclonal phage  
CC antibodies (MoPhabs) used in the exemplification of the invention  
XX  
SQ Sequence 13 AA;  
  
Query Match 70.8%; Score 17; DB 4; Length 13;  
Best Local Similarity 40.0%; Pred. No. 4.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXXW 6  
Db 6 FASSW 10  
  
RESULT 8  
ABG75574  
ID ABG75574 standard; peptide; 13 AA.  
XX  
AC ABG75574;  
XX  
DT 22-APR-2003 (first entry)  
XX  
DE CDR3 peptide sequence, #7, used in phage antibody construction.  
XX  
KW Phage; antibody; antigen; target cell; phage particle;  
KW cell-type specific phage antibody library; phage antibody; Phab;  
KW monoclonal phage antibody; MoPhab; blood cell; foetal bone marrow cell;  
KW complementarity determining region 3; CDR3; human.  
XX  
OS Homo sapiens.  
OS Synthetic.

XX US2002132228-A1.  
PN  
XX 19-SEP-2002.  
PD  
XX  
PF 24-MAY-2001; 2001US-00865048.  
XX  
PR 07-JUN-1995; 95US-00483633.  
PR 18-SEP-1997; 97US-00932892.  
PR 26-MAY-1998; 98US-00085072.  
XX  
PA (TERS/) TERSTAPPEN L W M M.  
PA (LOGT/) LOGTENBERG T.  
XX  
PI Terstappen LWM, Logtenberg T;  
XX  
DR WPI; 2003-174076/17.  
XX  
PT Obtaining phage having antibody specific for cell surface antigen of  
PT target cells in heterogeneous cell population, by incubating phage  
PT antibody library with target cells, and separating phage particles bound  
PT target cells.  
XX  
PS Example 6; Page 4; 5pp; English.  
XX  
CC The invention discloses a method for obtaining a phage comprising an  
CC antibody, or its fragment, directed against antigens associated with a  
CC target cells surface in a heterogeneous cell population. The method  
CC comprises providing a library of antibodies, or their fragments,  
CC expressed on the surface of phage particles, incubating the phage  
CC antibody library with the target cells, separating the target cells and  
CC phage particles associated with them from the phage particles not  
CC associated with the target cells and then recovering the phage particles.  
CC Also disclosed is a cell-type specific phage antibody library and an  
CC antibody, or antibody fragment, obtained using the method. The method is  
CC useful for obtaining a selection of phage antibodies (Phabs) and  
CC monoclonal phage antibodies (MoPhabs). The method is also useful for  
CC detecting known and novel structures on various populations of blood and  
CC foetal bone marrow cells. The sequence presented is an example of the  
CC partly randomised human complementarity determining region 3 (CDR3) used  
CC in the construction of the antibodies  
XX  
SQ Sequence 13 AA;  
  
Query Match 70.8%; Score 17; DB 6; Length 13;  
Best Local Similarity 40.0%; Pred. No. 4.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXXW 6  
Db 6 FASSW 10  
  
RESULT 9  
AAM98088  
ID AAM98088 standard; peptide; 14 AA.  
XX  
AC AAM98088;  
XX  
DT 24-JAN-2002 (first entry)  
XX  
DE Human peptide #1363 encoded by a SNP oligonucleotide.  
XX  
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;  
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease.  
XX  
OS Homo sapiens.





Query Match 70.8%; Score 17; DB 2; Length 15;  
Best Local Similarity 40.0%; Pred. No. 4.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
Db 4 FSTAW 8

RESULT 12  
AAW57758  
ID AAW57758 standard; peptide; 15 AA.  
XX  
AC AAW57758;  
XX  
DT 17-SEP-1998 (first entry)  
XX  
DE Residues 16-30 of Cry j 2.  
XX  
KW Cry j 2; Japanese cedar pollen antigen; allergy; immunotherapy;  
KW HLA class II molecule.  
XX  
OS Cryptomeria japonica.  
XX  
PN WO9820902-A1.  
XX  
PD 22-MAY-1998.  
XX  
PF 12-NOV-1997; 97WO-JP004129.  
XX  
PR 13-NOV-1996; 96JP-00302053.  
XX  
PA (MEIP ) MEIJI MILK PROD CO LTD.  
XX  
PI Sone T, Kume A, Dairiki K, Kino K;  
XX  
DR WPI; 1998-297617/26.  
XX  
PT Peptides derived from Japanese cedar pollen antigens are  
PT immunotherapeutic agents - useful for allergy treatment and typing HLA  
PT class II molecules in allergy sufferers.  
XX  
PS Claim 12; Page 29; 50pp; Japanese.  
XX  
CC This sequence represents residues 16-30 of the Cry j 2 protein, and is a  
CC peptide of the invention. The peptides are derived from Japanese cedar  
CC pollen antigens, and are used as immunotherapeutic agents in the  
CC treatment of allergy. The peptides can be used for identification and  
CC typing of the particular HLA class II molecules in an allergy sufferer,  
CC and also for peptide immunotherapy of an allergy. Using these peptides  
CC the immunotherapy can be targeted more specifically to the requirements  
CC of the individual patient, allowing more effective treatment of an  
CC allergy, including those patients for whom treatment with a conventional  
CC immunotherapeutic agent is ineffective  
XX  
SQ Sequence 15 AA;

Query Match 70.8%; Score 17; DB 2; Length 15;  
Best Local Similarity 40.0%; Pred. No. 4.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
Db 9 FSTAW 13

RESULT 13  
AAE23038  
ID AAE23038 standard; peptide; 19 AA.  
XX  
AC AAE23038;  
XX

DT 21-AUG-2002 (first entry)  
XX Human thioredoxin, 47916 peptide.  
XX  
KW Human; thioredoxin; 22108; 47916; haematopoietic disorder; leukaemia;  
KW cancer; lung; breast; thyroid; head; neck; prostate; genitourinary tract;  
KW cardiovascular disease; angina pectoris; arteriosclerosis; heart failure;  
KW brain disorder; brain abscess; meningitis; Alzheimer's disease; sarcoma;  
KW cytostatic; carcinoma; cardiac; neuroprotective; antiinflammatory;  
KW gene therapy; nootropic.  
XX  
OS Homo sapiens.  
XX  
PN WO200226803-A2.  
XX  
PD 04-APR-2002.  
XX  
PF 25-SEP-2001; 2001WO-US029967.  
XX  
PR 25-SEP-2000; 2000US-0235049P.  
XX  
PA (MILL-) MILLENIUM PHARM INC.  
XX  
PI Bandaru R, Kapeller-Libermann R;  
XX  
DR WPI; 2002-416475/44.  
XX  
PT New human thioredoxin nucleic acid and polypeptide molecules, designated  
PT 22108 and 47916, useful for diagnosing, preventing or treating cancer  
PT (e.g. carcinoma), cardiovascular diseases (e.g. heart failure) or brain  
PT disorders.  
XX  
PS Disclosure; Page 11; 124pp; English.  
XX  
CC The invention relates to human thioredoxin nucleic acid and polypeptide  
CC molecules, designated 22108 and 47916. The compound that modulates the  
CC activity or expression of 22108 and 47916 nucleic acid is useful for  
CC treating or preventing a disorder characterised by aberrant activity of  
CC 22108 and 47916-expressing cell, specifically for reducing or inhibiting  
CC the aberrant activity of the 22108 and 47916-expressing cancer cell. The  
CC 22108 and 47916 nucleic acid and polypeptide are useful for diagnosing,  
CC preventing or treating cancer in a subject (e.g. carcinoma, sarcoma,  
CC metastatic or haematopoietic disorders (e.g. leukaemia), or cancers of the  
CC lung, breast, thyroid, head neck, prostate or genito-urinary tract),  
CC cardiovascular diseases (e.g. angina pectoris, arteriosclerosis or heart  
CC failure) or brain disorders (e.g. brain abscess, meningitis, Alzheimer's  
CC diseases). The thioredoxin DNA is also useful in gene therapy. The  
XX present sequence is human thioredoxin, 47916 peptide  
SQ Sequence 19 AA;

Query Match 70.8%; Score 17; DB 5; Length 19;  
Best Local Similarity 40.0%; Pred. No. 5.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
Db 4 FSATW 8

RESULT 14  
AAW42165  
ID AAW42165 standard; peptide; 20 AA.  
XX  
AC AAW42165;  
XX  
DT 27-AUG-2003 (revised)  
DT 25-MAR-2003 (revised)  
DT 16-JUN-1998 (first entry)  
XX  
DE T-cell epitope peptide 45 from Japanese cypress pollen antigen Chao2.  
XX Japanese cypress pollen; antigen; T-cell epitope; Chao1; Chao2;  
KW



KW diagnosis; allergy; spring tree pollen disease; pollinosis.  
XX Chamaecyparis obtusa.  
OS WO9747648-A1.  
XX 18-DEC-1997.  
PD 12-JUN-1997; 97WO-JP002031.  
XX 14-JUN-1996; 96JP-00153527.  
PR (MEIP ) MEIJI MILK PROD CO LTD.  
XX Kino K, Dairiri K;  
PI WPI; 1998-052242/05.  
XX T-cell epitope peptide portion of Japanese cypress pollen antigens Chao1 and Chao2 - used for diagnosis and treatment of spring tree pollen disease.  
DR Claim 2; Page 36; 71pp; Japanese.  
XX The present sequence represents a T-cell epitope peptide from Japanese cypress pollen antigen Chao2. The present invention describes peptides which correspond to the T-cell epitope sites on Japanese cypress pollen antigens Chao1 and Chao2. The peptides can be used as a reagent for the diagnosis of allergy to Japanese cypress pollen, and as an antigen in the treatment and prevention of spring tree pollen disease in which the pollinosis involves reactivity to Japanese cypress pollen. (Updated on 25 -MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS field.)  
XX Sequence 20 AA;  
SQ Query Match 70.8%; Score 17; DB 2; Length 20;  
Best Local Similarity 40.0%; Pred. No. 5.8e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 FXXXW 6  
Db 8 FATTW 12  
RESULT 15  
AAG62999  
ID AAG62999 standard; peptide; 20 AA.  
XX  
AC AAG62999;  
XX 01-OCT-2001 (first entry)  
DT Complementarity determining region 3 (CDR3) of VH chain of clone G101.  
XX  
DE Antibody; light chain; VL; amyloid protein; blood brain barrier;  
XX endothelial cell; brain cell antigen; inflammation; adhesion molecule;  
KW transferrin receptor; neurological disease; Alzheimer's disease;  
KW prion disease; AIDS-related dementia; epilepsy; brain injury.  
XX Homo sapiens.  
OS WO200144300-A2.  
XX 21-JUN-2001.  
PD 27-NOV-2000; 2000WO-GB004501.  
XX 13-DEC-1999; 99US-0170599P.  
PR (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX Webster C, Osbourn J, Ward G, Miller K;

XX WPI; 2001-398131/42.  
DR Mixture or panel of antibodies for selecting specific binding members that cross the blood brain barrier, for use in delivering different molecules and treating neurological diseases.  
XX Claim 1; Page 76; 109pp; English.  
XX AAG62970-AAG63005 represent complementarity determining region 3 (CDR3) of VL and VH chains of antibodies of the invention. The specification describes a mixture or panel of 5 different specific binding members, each comprising an antibody VH and/or VL variable domain and capable, when displayed on the surface of filamentous bacteriophage particles or in the case of a specific binding member comprising the D5 VH and/or VL variable domain when bound to human serum amyloid protein, to pass through a mammalian blood brain barrier (BBB). The panel is useful for the selection of specific binding members with a desired property such as ability to cross BBB, ability to bind endothelial cells or other brain cell antigen, ability to bind areas of inflammation in the brain or BBB breakdown or ability to bind intracellular adhesion molecules and to bind transferrin receptor. The antibodies are useful in diagnosis, prophylaxis and treatment of human or animal body, including neurological diseases, such as Alzheimer's disease, prion disease, AIDS-related dementia, epilepsy and traumatic brain injury and any diseases involving inflammation occurring within the brain or central nervous system  
XX Sequence 20 AA;  
SQ Query Match 70.8%; Score 17; DB 4; Length 20;  
Best Local Similarity 40.0%; Pred. No. 5.8e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 FXXXW 6  
Db 4 FSSSW 8  
RESULT 16  
ADE25429  
ID ADE25429 standard; peptide; 25 AA.  
XX  
AC ADE25429;  
XX 29-JAN-2004 (first entry)  
DT Plant growth associated peptide #1.  
XX  
DE plant growth; plant growth trait modulation; Brassicaceae; Arabidopsis;  
XX Brassica; Zea; Oryza; Triticum; Hordeum; Lolium; Sorghum; Glycine;  
KW Medicago; Helianthus; Lactuca; Beta; Vitis; Solanum; Lycopersicon;  
KW Capsicum; Gossypium; Hevea; Linum; Prunus; Citrus; Populus; Pinus;  
KW Quercus.  
XX Magnoliophyta.  
OS US2003188343-A1.  
XX 02-OCT-2003.  
PD 07-JAN-2003; 2003US-00338777.  
XX 09-JAN-2002; 2002US-0347288P.  
PR (LYNX-) LYNX THERAPEUTICS INC.  
XX Bowen BA, Haudenschild CD, Buckler ES;  
PI WPI; 2003-803305/75.  
XX New isolated or recombinant polypeptide for use in modulating a plant growth trait in a flowering plant e.g. in Arabidopsis, Brassica, Zea, or Oryza.  
PT

XX Disclosure; Page 16; 81pp; English.

XX The invention describes an isolated or recombinant polypeptide (I) comprising a sequence: (a) comprising 1 of 30 sequences (S1), as given in the specification, or a conservative variant; (b) encoded by 1 of 30 sequences (S2), as given in the specification, or a conservative variant; (c) encoded by a sequence that hybridises under stringent conditions to S2; and (d) encoded by a sequence 70 % identical to S2. The expression or activity of (I) is modulated to modulate a plant growth trait in a flowering plant, of the family Brassicaceae, preferably in a plant that is Arabidopsis, Brassica, Zea, Oryza, Triticum, Hordeum, Lolium, Sorghum, Glycine, Medicago, Helianthus, Lactuca, Beta, Vitis, Solanum, Lycopersicon, Capsicum, Gossypium, Hevea, Linum, Prunus, Citrus, Populus, Pinus, or Quercus. A new method is used to detect genes for a plant growth trait. This is the amino acid sequence of region of ADE25056 used to demonstrate conservative substitutions occurring in the protein.

XX Sequence 25 AA;

SQ Query Match 70.8%; Score 17; DB 7; Length 25;  
Best Local Similarity 40.0%; Pred. No. 7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
20 FAASW 24

Db

RESULT 17  
AAM18617

ID AAM18617 standard; protein; 27 AA.

XX AAM18617;

AC AAM18617;

XX 12-OCT-2001 (first entry)

DT Peptide #5051 encoded by probe for measuring cervical gene expression.

XX Probe; human; microarray; gene expression; cervical epithelial cell; cervical cancer.

KW Homo sapiens.

XX WO200157278-A2.

PN 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US0000670.

PF 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488901/53.

DR Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.

XX Claim 27; SEQ ID NO 23443; 487pp; English.

PS The present invention relates to human single exon nucleic acid probes (SENPs: see AAI10068-AA128459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for

CC measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 27 AA;

SQ Query Match 70.8%; Score 17; DB 4; Length 27;  
Best Local Similarity 40.0%; Pred. No. 7.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
4 FSATW 8

Db

RESULT 18  
AAM31077

ID AAM31077 standard; protein; 27 AA.

XX AAM31077;

AC AAM31077;

XX 17-OCT-2001 (first entry)

DT Peptide #5114 encoded by probe for measuring placental gene expression.

XX Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder.

KW Homo sapiens.

XX WO200157272-A2.

PN 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US0000663.

PF 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

DR Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.

XX Claim 27; SEQ ID NO 31346; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENPs: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders

XX Sequence 27 AA;

SQ Query Match 70.8%; Score 17; DB 4; Length 27;  
Best Local Similarity 40.0%; Pred. No. 7.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
4 FSATW 8

Db 4 FSATW 8

RESULT 19  
ABG52487

ID ABG52487 standard; peptide; 27 AA.

XX  
AC ABG52487;

DT 25-FEB-2003 (first entry)

XX  
DE Human liver peptide, SEQ ID NO 31135.

XX  
KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;  
KW hypercholesterolaemia; coronary heart disease.

XX  
OS Homo sapiens.

XX  
PN WO200157273-A2.

XX  
PD 09-AUG-2001.

XX  
PF 30-JAN-2001; 2001WO-US0000664.

XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.

XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.

XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-488898/53.

PT Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human adult liver.

XX  
PS Claim 27; SEQ ID NO 31135; 658pp; English.

XX  
CC The invention relates to a single exon nucleic acid probe (SEN) (I) for  
CC measuring human gene expression in a sample derived from human adult  
CC liver, comprising one of 13109 defined nucleotide sequences given in the  
CC specification (or complements/ fragments). The probe hybridises at high  
CC stringency to a nucleic acid molecule expressed in the human adult liver.  
CC (I) may be used for predicting, measuring and displaying gene expression  
CC in samples derived from human adult liver. The genes identified may be  
CC involved in genetic liver diseases such as cirrhosis,  
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is  
CC associated with coronary heart disease. ABG47348-ABG59930 represent human  
CC liver single exon encoded peptides of the invention. Note: The sequence  
CC information for this patent does not appear in the printed specification  
CC but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX  
SQ Sequence 27 AA;

Query Match 70.8%; Score 17; DB 4; Length 27;  
Best Local Similarity 40.0%; Pred. NO. 7.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXXW 6  
| |  
| |

Db 4 FSATW 8

RESULT 20  
ABG40522

ID ABG40522 standard; peptide; 27 AA.

XX

AC ABG40522;

DT 19-AUG-2002 (first entry)

XX  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 30187.

XX  
KW Human; single exon probe; asthma; lung cancer; COPD; ILD;  
KW chronic obstructive pulmonary disease; interstitial lung disease;  
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;  
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
KW primary ciliary dyskinesia; pulmonary hypertension;  
KW hyaline membrane disease.

XX  
OS Homo sapiens.

XX  
PN WO200186003-A2.

XX  
PD 15-NOV-2001.

XX  
PF 30-JAN-2001; 2001WO-US0000665.

XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.

XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.

XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2002-114183/15.

PT Spatially-addressable set of single exon nucleic acid probes, used to  
PT measure gene expression in human lung samples.

XX  
PS Claim 27; SEQ ID NO 30187; 634pp; English.

XX  
CC The invention relates to a spatially-addressable set of single exon  
CC nucleic acid probes for measuring gene expression in a sample derived  
CC from human lung comprising single exon nucleic acid probes having one of  
CC 12614 nucleic acid sequences mentioned in the specification, or their  
CC complements or the 12387 open reading frames derived from the 12614  
CC probes. Also included are a microarray comprising the novel set of probes  
CC ; the novel set of probes which hybridise at high stringency to a nucleic  
CC acid expressed in the human lung; measuring gene expression in a sample  
CC derived from human lung, comprising (a) contacting the array with a  
CC collection of detectably labeled nucleic acids derived from human lung  
CC mRNA, and (b) measuring the label detectably bound to each probe of the  
CC array; identifying exons in a eukaryotic genome, comprising (a)  
CC algorithmically predicting at least one exon from genomic sequences of  
CC the eukaryote; and (b) detecting specific hybridisation of detectably  
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
CC having a fragment identical to the predicted exon, the probe is included  
CC in the above mentioned microarray; assigning exons to a single gene,  
CC comprising (a) identifying exons from genomic sequence by the method  
CC above and (b) measuring the expression of each of the exons in several  
CC tissues and/or cell types using hybridisation to a single exon  
CC microarrays having a probe with the exon, where a common pattern of  
CC expression of the exons in the tissues and/or cell types indicates that  
CC the exons should be assigned to a single gene; a peptide comprising one  
CC of 12011 sequences, mentioned in the specification, or encoded by the  
CC probes/open reading frames (ORF). The probes are used for gene expression  
CC analysis, and for identifying exons in a gene, particularly using human  
CC lung derived mRNA and for the study of lung diseases such as asthma, lung  
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-

CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary  
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,  
CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
CC present sequence is a peptide/protein encoded by a single exon probe of  
CC the invention. Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 27 AA;  
  
Query Match 70.8%; Score 17; DB 5; Length 27;  
Best Local Similarity 40.0%; Pred. No. 7.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXXW 6  
| |  
Db 4 FSATW 8  
  
RESULT 21  
AAB09301  
ID AAB09301 standard; protein; 29 AA.  
XX  
AC AAB09301;  
XX  
DT 06-AUG-2003 (revised)  
DT 30-AUG-2000 (first entry)  
XX  
DE Hepatitis GB virus protein sequence SEQ ID NO:428.  
XX  
KW Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic; infection;  
KW detection; characterisation; hepatitis.  
XX  
OS Hepatitis GB virus.  
XX  
PN US6051374-A.  
XX  
PD 18-APR-2000.  
XX  
PF 07-JUN-1995; 95US-00488445.  
XX  
PR 14-FEB-1994; 94US-00196030.  
PR 13-MAY-1994; 94US-00242654.  
PR 29-JUL-1994; 94US-00283314.  
PR 23-NOV-1994; 94US-00344185.  
PR 23-NOV-1994; 94US-00344190.  
PR 30-JAN-1995; 95US-00377557.  
XX  
PA (ABBO ) ABBOTT LAB.  
XX  
PI Dawson GJ, Leary TP, Muerhoff AS, Pilot-Matias TJ, Buijk SL;  
PI Mushahwar IK, Simons JN, Desai SM, Erker JC, Schlauder GG;  
XX  
DR WPI; 2000-338307/29.  
XX  
PT Detecting target hepatitis GB virus nucleic acid in a test sample  
PT suspected of containing HGBV comprises reacting the test sample the HGBV  
PT polynucleotide probe and detecting the complex that contains target HGBV.  
XX  
PS Example 18; Col 491-492; 369pp; English.  
XX  
CC The present invention describe a method for detecting target hepatitis GB  
CC virus (HGBV) nucleic acid (THN) in a test sample (T) suspected of  
CC containing HGBV. The method involves reacting (T) with a HGBV  
CC polynucleotide probe (I) containing 15 contiguous nucleotides, and which  
CC selectively hybridises to the HGBV genome or its full complement, and  
CC target HGBV. The method is used for detecting target HGBV nucleic acid in  
CC the test sample suspected of containing HGBV and for characterisation of  
CC newly ascertained etiological agent of non-A, non-B, non-C, non-D and non  
CC -E hepatitis causing agents collectively termed as hepatitis GB virus.  
CC AAA55270 to AAA55489 and AAB08985 to AAB09480 represent nucleotide and

CC protein sequences used in the exemplification of the present invention.  
CC (Updated on 06-AUG-2003 to correct OS field.)  
XX  
SQ Sequence 29 AA;  
  
Query Match 70.8%; Score 17; DB 3; Length 29;  
Best Local Similarity 40.0%; Pred. No. 7.8e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXXW 6  
| |  
Db 12 FASAW 16  
  
RESULT 22  
AAG71365  
ID AAG71365 standard; peptide; 32 AA.  
XX  
AC AAG71365;  
XX  
DT 30-JUL-2001 (first entry)  
XX  
DE Human gene 10-encoded secreted protein fragment, SEQ ID NO:216.  
XX  
KW Human; secreted protein; proliferative disorder; cancer; chromosome 1;  
KW foetal abnormality; developmental abnormality; haematopoietic disorder;  
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
KW inflammation; allergy; neurological disorder; Alzheimer's disease;  
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;  
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;  
KW cardiovascular disorder; angiogenic disorder; kidney disorder;  
KW gastrointestinal disorder; pregnancy-related disorder; tumour;  
KW endocrine disorder; infection; wound healing; vulnery; cell culture;  
KW chemotaxis; food additive; binding partner identification.  
XX  
OS Homo sapiens.  
XX  
PN WO200132674-A1.  
XX  
PD 10-MAY-2001.  
XX  
PF 25-OCT-2000; 2000WO-US029360.  
XX  
PR 29-OCT-1999; 99US-0162211P.  
PR 30-JUN-2000; 2000US-0215138P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, Komatsoulis GA, Young PE, Moore PA;  
XX  
DR WPI; 2001-291051/30.  
XX  
PT New nucleic acid molecule encoding a human secreted protein, useful for  
PT preventing, treating or ameliorating medical conditions such as  
PT rheumatoid arthritis, Alzheimer's disease and microbial infections.  
XX  
PS Disclosure; Page 27; 581pp; English.  
XX  
CC AAH31349-AAH31428 represent cDNAs corresponding to 26 human secreted  
CC protein genes, and AAG71243-AAG71319 represent the proteins they encode.  
CC AAG71320-AAG71403 represent human secreted protein fragments. The genes  
CC and their corresponding secreted proteins are useful for preventing,  
CC treating or ameliorating medical conditions, e.g., by protein or gene  
CC therapy. Pathological conditions can be diagnosed by determining the  
CC amount of the new protein in a sample or by determining the presence of  
CC mutations in the new genes. Specific uses are described for each of the  
CC 52 genes, based on the tissues in which they are most highly expressed,  
CC and include developing products for the diagnosis or treatment of  
CC proliferative disorders, cancer, tumours, foetal and developmental  
CC abnormalities, haematopoietic disorders, diseases of the immune system,  
CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,  
CC allergies, neurological disorders (e.g., Alzheimer's disease,  
CC Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin

disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein fragment referred to in the disclosure of the invention

Sequence 32 AA;

Query Match 70.8%; Score 17; DB 4; Length 32;  
 Best Local Similarity 40.0%; Pred. No. 8.5e+03;  
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6  
 Db 15 FAATW 19

RESULT 23  
 ABP60808  
 ID ABP60808 standard; protein; 33 AA.  
 XX  
 AC ABP60808;  
 XX  
 DT 06-SEP-2002 (first entry)  
 XX  
 DE Sus scrofa thiodoxin SEQ ID NO:157.  
 XX  
 KW Multimeric protein; redox protein; thiodoxin; thiodoxin reductase;  
 KW oil body; ophthalmological; antidiabetic; cytostatic; antipsoriatic;  
 KW vasotropic; vulnerary; antibacterial; immunosuppressive; antiulcer;  
 KW food product; milk; wheat; oxidative stress; cataract; diabetes;  
 KW chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;  
 KW bronchiolopulmonary disease; malignancy; reperfusion injury; wound healing;  
 KW gastro intestinal bleeding; intestinal bowel disease; ulcer;  
 KW gastro oesophageal reflux disease.  
 XX  
 OS Sus scrofa.  
 XX  
 XX WO200250289-A1.  
 PN  
 XX 27-JUN-2002.  
 PD  
 XX 19-DEC-2001; 2001WO-US050240.  
 PF  
 XX 19-DEC-2000; 2000US-00742900.  
 PR  
 PR 05-JUL-2001; 2001US-0302885P.  
 PR 04-DEC-2001; 2001US-00006038.  
 XX  
 XX (SEMB-) SEMBIOSYS GENETICS INC.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 XX  
 XX Van Rooijen G, Deckers H, Heifetz PB, Briggs SP, Dalmia BK;  
 PI Del Val G, Zaplachinski S, Moloney M;  
 XX WPI; 2002-508806/54.  
 DR  
 XX Producing oil body associated with recombinant multimeric protein complex  
 PT e.g. rodox proteins and immunoglobulins comprises producing recombinant  
 PT polypeptides capable of forming the complex in cells comprising oil  
 PT bodies.  
 XX Claim 81; Page 248; 362pp; English.  
 PS The present invention describes a method (M1) for producing an oil body  
 XX

associated with a recombinant multimeric protein complex (MPC). M1 comprises producing in a cell comprising oil bodies a first and second recombinant polypeptide (P1, P2), where P1 is capable of associating with P2 to form the MPC and associating the complex with an occlusion body (OB) through an OB-targeting-protein capable of associating with OB and P1. M1 is useful for producing an oil body associated with a recombinant MPC. The oil bodies are further formulated for use in the preparation of a food product such as milk or wheat based food product, personal care product which reduces the oxidative stress on the surface area of the human body or used to lighten the skin, or a pharmaceutical composition used to treat chronic obstructive pulmonary disease (COPD), cataracts, diabetes, envenomation, bronchiolopulmonary disease, psoriasis, malignancies, reperfusion injury, wound healing, sepsis, gastro intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to ABP60964 represent sequence given in the exemplification of the present invention

Sequence 33 AA;

Query Match 70.8%; Score 17; DB 5; Length 33;  
 Best Local Similarity 40.0%; Pred. No. 8.7e+03;  
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 FXXW 6  
 Db 26 FSATW 30

RESULT 24  
 ABO54713  
 ID ABO54713 standard; protein; 33 AA.  
 XX  
 AC ABO54713;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Human genome derived single exon protein #947.  
 DE  
 XX Human; gene expression; single exon probe; microarray;  
 KW alternative splicing event; genomic alteration.  
 KW  
 XX Homo sapiens.  
 OS  
 XX US2003194704-A1.  
 PN  
 XX 16-OCT-2003.  
 PD  
 XX 03-APR-2002; 2002US-00029386.  
 PF  
 XX 03-APR-2002; 2002US-00029386.  
 PR  
 XX (PENN/) PENN S G.  
 PA (RANK/) RANK D R.  
 PA (HANZ/) HANZEL D K.  
 XX  
 PI Penn SG, Rank DR, Hanzel DK;  
 XX WPI; 2004-119264/12.  
 DR  
 XX New human genome-derived single exon nucleic acid probes useful for human  
 PT gene expression analysis, for identifying or characterizing alternative  
 PT splicing events, for assessing genomic alterations or as tools for  
 PT surveying tissues.  
 XX Claim 45; SEQ ID NO 28347; 80pp; English.  
 PS The invention relates to a nucleic acid probe for measuring human gene  
 XX expression, comprising any of the 27,400 fully defined nucleotide  
 CC sequences in the specification, or their complements or fragments, and  
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences  
 CC fully defined in the specification. The probe is a single exon probe that  
 CC hybridises under high stringency conditions to a nucleic acid molecule

CC expressed in human cells or tissues. Also included are a spatially-  
CC addressable set of single exon nucleic acid probes for measuring human  
CC gene expression (comprising a plurality of single exon nucleic acid  
CC probes cited above, where each of the plurality of probes is separately  
CC and addressably isolatable or amplifiable from the plurality), a single  
CC exon microarray for measuring human gene expression, a method of  
CC measuring human gene expression, a vector comprising the single exon  
CC probe cited above, an ORF-encoded peptide comprising at least 8  
CC contiguous amino acids of any of the above-mentioned amino acid  
CC sequences (optionally with conservative amino acid substitutions), an  
CC isolated antibody that binds specifically to a peptide cited above,  
CC methods of selling and/or licensing single exon probes or microarrays to  
CC a customer desiring to measure gene expression, a method of providing  
CC human gene expression data by subscription, and a computer-readable  
CC storage medium which contains a database having a plurality of records  
CC (each record including data on the expression of a single exon probe  
CC cited above. The probe, methods and apparatus are useful in gene  
CC expression analysis. The probes may be used as tools for surveying  
CC tissues to detect the presence of expressed messages that contain their  
CC specific exon, or in constructing genome-derived single exon microarrays.  
CC In addition, the probes are used in identifying and characterising  
CC alternative splicing events, in detecting and characterising gross  
CC alterations in the genomic locus that includes their exon, in assessing  
CC smaller genomic alterations, in priming the synthesis of nucleic acids,  
CC or in expressing the ORF-encoded peptide. The present sequence is a human  
CC single exon probe protein of the invention. Note: The sequence data for  
CC this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=20030194704

SQ Sequence 33 AA;

Query Match 70.8%; Score 17; DB 8; Length 33;  
Best Local Similarity 40.0%; Pred. No. 8.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
| |  
Db 14 FSASW 18

RESULT 25

AAR50631  
ID AAR50631 standard; peptide; 34 AA.

XX AC AAR50631;

XX DT 08-MAY-1996 (first entry)

XX DE G-protein coupled receptor TM3 consensus polypeptide #77.

XX KW G-protein coupled receptor; ligand binding assay; transmembrane domain;  
KW psychotic disorder; schizophrenia; dopamine; CAMP; adenosine; thrombin;  
KW muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;  
KW rhodopsin; opsin; odorant; cytomegalovirus; serotonergic.

OS Synthetic.

XX PN WO9405695-A1.

XX PD 17-MAR-1994.

XX PF 09-SEP-1993; 93WO-US008528.

XX PR 10-SEP-1992; 92US-00943236.

XX PA (UUNY ) UNIV NEW YORK STATE.

XX PI Murphy RB, Schuster DI;

XX XX WPI; 1994-101120/12.

XX PT Polypeptides of G-coupled receptor proteins (GPRs) - useful for binding

PT GPR ligands or modulating GPR binding.

XX Claim 9; Page 28; 160pp; English.

CC Polypeptides AAR48768-81 and AAR50569-R50718 are based on the consensus  
CC transmembrane domain III sequence from G-protein coupled receptor (GPR).  
CC proteins, and can be used in G-protein coupled receptor ligand binding  
CC assays. The assay can be used to identify fragments pref. transmembrane  
CC fragments, from GPR proteins (see AAR48686-R48758 for examples) which  
CC retain biological activity such as binding a GPR ligand or modulating GPR  
CC ligand binding to a GPR (see AAR48759-R48758, AAR50569-R50807 and  
CC AAR89189-R89195 for examples of polypeptide fragments). The polypeptide  
CC fragments can be used in compositions for treating subjects suffering  
CC from a pathology related to a GPR abnormality e.g. a psychotic disorder  
CC such as schizophrenia

XX SQ Sequence 34 AA;

Query Match 70.8%; Score 17; DB 2; Length 34;  
Best Local Similarity 40.0%; Pred. No. 8.9e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXW 6  
| |  
Db 16 FTAW 20

RESULT 26

AAR50593  
ID AAR50593 standard; peptide; 34 AA.

XX AC AAR50593;

XX DT 03-MAY-1996 (first entry)

XX DE G-protein coupled receptor TM3 consensus polypeptide #39.

XX KW G-protein coupled receptor; ligand binding assay; transmembrane domain;  
KW psychotic disorder; schizophrenia; dopamine; CAMP; adenosine; thrombin;  
KW muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;  
KW rhodopsin; opsin; odorant; cytomegalovirus; serotonergic.

OS Synthetic.

XX PN WO9405695-A1.

XX PD 17-MAR-1994.

XX PF 09-SEP-1993; 93WO-US008528.

XX PR 10-SEP-1992; 92US-00943236.

XX PA (UUNY ) UNIV NEW YORK STATE.

XX PI Murphy RB, Schuster DI;

XX XX WPI; 1994-101120/12.

XX PT Polypeptides of G-coupled receptor proteins (GPRs) - useful for binding  
XX GPR ligands or modulating GPR binding.

XX PS Claim 9; Page 27; 160pp; English.

CC Polypeptides AAR48768-81 and AAR50569-R50718 are based on the consensus  
CC transmembrane domain III sequence from G-protein coupled receptor (GPR)  
CC proteins, and can be used in G-protein coupled receptor ligand binding  
CC assays. The assay can be used to identify fragments pref. transmembrane  
CC fragments, from GPR proteins (see AAR48686-R48758 for examples) which  
CC retain biological activity such as binding a GPR ligand or modulating GPR  
CC ligand binding to a GPR (see AAR48759-R48758, AAR50569-R50807 and  
CC AAR89189-R89195 for examples of polypeptide fragments). The polypeptide  
CC fragments can be used in compositions for treating subjects suffering  
CC from a pathology related to a GPR abnormality e.g. a psychotic disorder







OS Homo sapiens.  
XX WO200164835-A2.  
PN  
XX  
PD 07-SEP-2001.  
XX  
PF 26-FEB-2001; 2001WO-US004927.  
XX  
PR 28-FEB-2000; 2000US-00515126.  
PR 18-MAY-2000; 2000US-00577409.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Drmanac RT;  
XX  
DR WPI; 2001-514838/56.  
DR N-PSDB; AAI87973.  
XX  
PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing  
PT and treating e.g. leukemia, inflammation and immune disorders.  
XX  
PS Claim 20; SEQ ID NO 21934; 1399pp + Sequence Listing; English.  
XX  
XX The invention relates to human polynucleotides (AAI79941-AAI93841) and  
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, haematopoiesis regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activin/inhibin activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation. Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 35 AA;  
  
Query Match 70.8%; Score 17; DB 4; Length 35;  
Best Local Similarity 40.0%; Pred. No. 9.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXXW 6  
Db 3 FAATW 7  
  
RESULT 30  
AARS3693  
ID AARS3693 standard; protein; 36 AA.  
XX  
AC AARS3693;  
XX  
DT 25-MAR-2003 (revised)  
DT 01-FEB-1995 (first entry)  
XX  
XX Japanese cedar pollen allergen Cry j II fragment.  
DE  
XX Cedar pollinosis; diagnostic.  
KW  
XX Cryptomeria japonica.  
OS  
XX WO9411512-A2.  
PN  
XX  
PD 26-MAY-1994.  
XX  
PF 12-NOV-1993; 93WO-US011000.  
XX  
PR 12-NOV-1992; 92US-00975179.  
XX  
PA (IMMU-) IMMULOGIC PHARM CORP.  
XX

PI Kuo M, Yeung S, Brauer A, Pollock J;  
XX WPI; 1994-183513/22.  
DR  
XX Allergic Cry j II protein and fragments from Japanese cedar pollen -  
PT used to diagnose, treat and prevent Japanese cedar pollinosis.  
XX  
PS Disclosure; Page 47; 89pp; English.  
XX  
CC The sequence is of a Japanese cedar pollen allergen Cry j II fragment.  
CC The protein and fragments can be used for diagnosis and treatment of  
CC Japanese cedar pollinosis and to identify similar sequences in other  
CC plants. See also AAR53690-6. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
SQ Sequence 36 AA;  
  
Query Match 70.8%; Score 17; DB 2; Length 36;  
Best Local Similarity 40.0%; Pred. No. 9.3e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXXW 6  
Db 28 FSTAW 32  
  
RESULT 31  
AAO08979  
ID AAO08979 standard; protein; 37 AA.  
XX  
AC AAO08979;  
XX  
DT 06-NOV-2001 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 22871.  
XX  
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
KW nervous system disorders; arthritis; inflammation.  
XX  
OS Homo sapiens.  
XX  
PN WO200164835-A2.  
PD 07-SEP-2001.  
XX  
PF 26-FEB-2001; 2001WO-US004927.  
XX  
PR 28-FEB-2000; 2000US-00515126.  
PR 18-MAY-2000; 2000US-00577409.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Drmanac RT;  
XX  
DR WPI; 2001-514838/56.  
DR N-PSDB; AAI88910.  
XX  
PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing  
PT and treating e.g. leukemia, inflammation and immune disorders.  
XX  
PS Claim 20; SEQ ID NO 22871; 1399pp + Sequence Listing; English.  
XX  
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and  
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, haematopoiesis regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activin/inhibin activity and may be useful in the diagnosis and/or

CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation. Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 37 AA;  
Query Match 70.8%; Score 17; DB 4; Length 37;  
Best Local Similarity 40.0%; Pred. No. 9.5e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 FXXXW 6  
| |  
DB 6 FAATW 10  
RESULT 32  
AAAY76339  
ID AAY76339 standard; protein; 38 AA.  
XX  
AC AAY76339;  
XX  
DT 23-MAR-2000 (first entry)  
XX  
DE Fragment of human secreted protein encoded by gene 38.  
XX  
KW Human; secreted protein; cancer; tumour; developmental abnormality;  
KW foetal deficiency; blood disorder; immune system disorder; inflammation;  
KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;  
KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;  
KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;  
KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;  
KW therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO9958660-A1.  
XX  
PD 18-NOV-1999.  
XX  
PF 06-MAY-1999; 99WO-US009847.  
XX  
PR 12-MAY-1998; 98US-0085093P.  
PR 12-MAY-1998; 98US-0085094P.  
PR 12-MAY-1998; 98US-0085105P.  
PR 12-MAY-1998; 98US-0085180P.  
PR 18-MAY-1998; 98US-0085906P.  
PR 18-MAY-1998; 98US-0085920P.  
PR 18-MAY-1998; 98US-0085921P.  
PR 18-MAY-1998; 98US-0085922P.  
PR 18-MAY-1998; 98US-0085923P.  
PR 18-MAY-1998; 98US-0085924P.  
PR 18-MAY-1998; 98US-0085925P.  
PR 18-MAY-1998; 98US-0085927P.  
PR 18-MAY-1998; 98US-0085928P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX  
PI Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA;  
PI Olsen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR, Lafleur DW;  
PI Endress GA, Ebner R;  
XX  
DR WPI; 2000-062296/05.  
XX  
PT Now isolated human genes and the secreted polypeptides they encode,  
PT useful for diagnosis and treatment of e.g. cancers, neurological  
PT disorders, immune diseases, inflammation or blood disorders.  
XX  
PS Disclonure; Page 450; 475pp; English.  
XX  
CC AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes.  
CC AAY76124 to AAY76223 are the secreted proteins encoded by the 97 human  
CC genes. This sequence represents a fragment of one of the human secreted

CC proteins. The genes and their corresponding secreted polypeptides are  
CC useful for preventing, treating or ameliorating medical conditions, e.g.  
CC by protein or gene therapy. Also pathological conditions can be diagnosed  
CC by determining the amount of the new polypeptides in a sample or by  
CC determining the presence of mutations in the new genes. Specific uses are  
CC described for each of the 97 genes, based on which tissues they are most  
CC highly expressed in, and include developing products for the diagnosis or  
CC treatment of cancer, tumours, developmental abnormalities and foetal  
CC deficiencies, blood disorders, diseases of the immune system, autoimmune  
CC diseases, inflammation, allergies, Alzheimer's and cognitive disorders,  
CC schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,  
CC atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,  
CC digestive/endocrine disorders, infections and AIDS. The polypeptides are  
CC also useful for identifying their binding partners. The sequences shown  
CC in AAY76224 to AAY76424 represent fragments of the secreted proteins  
XX  
SQ Sequence 38 AA;  
Query Match 70.8%; Score 17; DB 3; Length 38;  
Best Local Similarity 40.0%; Pred. No. 9.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 FXXXW 6  
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DB 19 FAAAW 23  
RESULT 33  
AAG10451  
ID AAG10451 standard; protein; 38 AA.  
XX  
AC AAG10451;  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 8778.  
XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-00301439.  
XX  
PR 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
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PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
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PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.  
  
Query Match 70.8%; Score 17; DB 3; Length 38;  
Best Local Similarity 40.0%; Pred. No. 9.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXXW 6  
DB 23 FTTSW 27  
  
RESULT 34  
ADE11915  
ID ADE11915 standard; protein; 38 AA.  
XX AC ADE11915;  
XX 29-JAN-2004 (first entry)  
DT Human secreted polypeptide #169.  
DE  
XX Secreted protein; cancer; liver disorder; hepatitis; neural disorder;  
KW Alzheimer's disease; human.  
XX Synthetic.  
OS Homo sapiens.  
XX US2003100051-A1.  
PN 29-MAY-2003.  
PD  
XX 10-SEP-2001; 2001US-00948783.  
PF  
XX 12-MAY-1998; 98US-0085093P.  
PR 12-MAY-1998; 98US-0085094P.  
PR 12-MAY-1998; 98US-0085105P.  
PR 12-MAY-1998; 98US-0085180P.  
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PR 18-MAY-1998; 98US-0085925P.  
PR 18-MAY-1998; 98US-0085927P.  
PR 18-MAY-1998; 98US-0085928P.  
PR 06-MAY-1999; 99WO-US009847.  
PR 10-NOV-1999; 99US-00437658.  
PR 11-SEP-2000; 2000US-0231846P.  
PR 28-JUN-2001; 2001US-00892877.  
XX (RUBE/) RUBEN S M.  
PA (FLOR/) FLORENCE K A.  
PA (NIJJ/) NI J.  
PA (ROSE/) ROSEN C A.  
PA (CART/) CARTER K C.  
PA (MOOR/) MOORE P A.  
PA (OLSE/) OLSEN H S.  
PA (SHIY/) SHI Y.  
PA (YOUN/) YOUNG P E.  
PA (WEIY/) WEI Y.  
PA (BREW/) BREWER L A.  
PA (SOPP/) SOPPET D R.  
PA (LAF/) LAFLEUR D W.

PA (ENDR/) ENDRESS G A.  
PA (EBNE/) EBNER R.  
PA (BIRS/) BIRSE C E.  
XX Ruben SM, Florence KA, Ni J, Rosen CA, Carter KC, Moore PA;  
PI Olsen HS, Shi Y, Young PE, Wei Y, Brewer LA, Soppet DR, Lafleur DW;  
PI Endress GA, Ebner R, Birse CE;  
XX WPI; 2003-801210/75.  
DR  
XX New nucleic acid molecule, useful for preparing a medicament for  
PT preventing, treating or ameliorating a medical condition e.g. cancer,  
PT liver disorders or neural disorders.  
XX Claim 11; SEQ ID NO 287; 453pp; English.  
PS  
XX The invention relates to human secreted polypeptides and the  
CC polynucleotides encoding them. The sequences are useful for preparing  
CC medicaments for preventing, treating or ameliorating medical conditions  
CC e.g., cancer, liver disorders such as hepatitis or neural disorders such  
CC as Alzheimer's disease. This sequence represents a human secreted  
CC polypeptide of the invention.  
XX  
SQ Sequence 38 AA;  
  
Query Match 70.8%; Score 17; DB 7; Length 38;  
Best Local Similarity 40.0%; Pred. No. 9.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXXW 6  
DB 19 FFAAW 23  
  
RESULT 35  
AAY41113  
ID AAY41113 standard; peptide; 40 AA.  
XX AC AAY41113;  
XX 17-JAN-2000 (first entry)  
DT  
XX TNFR/NGFR cysteine-rich domain of T129 polypeptide.  
DE  
XX Tumor necrosis factor receptor; TNF; T129 protein; TANGO 129; human;  
KW cellular process; immunological disorder; abnormal lymphoid development;  
KW thymic development; T-cell mediated immune response; humoral B cell;  
KW skeletal muscle disorder; drug screening.  
XX Homo sapiens.  
OS  
XX WO9952924-A1.  
PN  
XX 21-OCT-1999.  
PD  
XX 08-APR-1999; 99WO-US007832.  
PF  
XX 09-APR-1998; 98US-00057951.  
PR  
XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
PA  
XX Holtzman D;  
PI  
XX WPI; 1999-620368/53.  
DR  
XX New isolated tumor necrosis factor receptor member used to develop  
PT products for treating, e.g. immunological disorders or disorders of the  
PT skeletal muscle.  
XX  
PS Example 3; Fig 2; 118pp; English.  
XX  
CC The invention provides an isolated human tumor necrosis factor (TNF)  
CC receptor member, T129 (also referred as TANGO 129). The T129 polypeptide

CC can be expressed by standard recombinant methodology. The T219  
CC polypeptides are useful as modulating agents in regulating a variety of  
CC cellular processes. Agents or modulators which have a stimulatory or  
CC inhibitory effect on T129 activity (e.g. T129 gene expression) as  
CC identified by a screening assay can be administered to individuals to  
CC treat (prophylactically or therapeutically) disorders, e.g. an  
CC immunological disorder associated with aberrant T129 activity, disorders  
CC associated with abnormal lymphoid and/or thymic development, T-cell  
CC mediated immune response, T-cell dependent help for B cells, and abnormal  
CC humoral B cell activity, and possibly disorders of the skeletal muscle.  
CC The products can also be used for detection, diagnosis, drug screening  
CC and production of transgenic animals. The present sequence represents a  
CC TNFR/NGFR cysteine-rich domain of T129 polypeptide  
XX  
SQ Sequence 40 AA;

Query Match 70.8%; Score 17; DB 2; Length 40;  
Best Local Similarity 40.0%; Pred. No. 1e+04;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FXXXW 6  
Db 6 FSAAW 10

RESULT 36  
AAG51555  
ID AAG51555 standard; protein; 40 AA.

XX AAG51555;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 65445.

KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 28-APR-1999; 99US-0130891P.  
PR 30-APR-1999; 99US-0131449P.  
PR 04-MAY-1999; 99US-0132048P.  
PR 05-MAY-1999; 99US-0132484P.  
PR 06-MAY-1999; 99US-0132485P.  
PR 07-MAY-1999; 99US-0132487P.  
PR 11-MAY-1999; 99US-0132863P.  
PR 14-MAY-1999; 99US-0134256P.  
PR 14-MAY-1999; 99US-0134218P.  
PR 14-MAY-1999; 99US-0134219P.  
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PR 14-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-0134768P.  
PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
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PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
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PR 20-JUL-1999; 99US-0144884P.  
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PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
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PR 27-JUL-1999; 99US-0145913P.

PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
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PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
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PR 13-AUG-1999; 99US-0148565P.  
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PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
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PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
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PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.

PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.  
  
Query Match 70.8%; Score 17; DB 3; Length 40;  
Best Local Similarity 40.0%; Pred.No. 1e+04;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXXW 6  
|  
Db 33 FSSAW 37  
  
RESULT 37  
AAM37764  
ID AAM37764 standard; protein; 40 AA.  
XX  
AC AAM37764;  
XX  
DT 17-OCT-2001 (first entry)  
XX  
DE Peptide #11801 encoded by probe for measuring placental gene expression.  
XX KW Probe; microarray; human; placenta; antenatal diagnosis;  
KW genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200157272-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US000663.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
(MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-488897/53.  
XX  
PT Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human placenta.  
XX  
PS Claim 27; SEQ ID NO 38033; 654pp; English.  
XX  
CC The present invention relates to single exon nucleic acid probes (SENP;  
CC see AAL31315-AA157546). The present sequence is a peptide encoded by one  
CC such probe. The probes are useful for producing a microarray for  
CC predicting, measuring and displaying gene expression in samples derived  
CC from human placenta. The probes are useful for antenatal diagnosis of  
CC human genetic disorders  
XX  
SQ Sequence 40 AA;  
  
Query Match 70.8%; Score 17; DB 4; Length 40;  
Best Local Similarity 40.0%; Pred.No. 1e+04;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 FXXXW 6  
|

Db	23 FTSSW 27	Db	8 FAATW 12
RESULT 38		RESULT 39	
AAB64755		AAO06835	
ID AAB64755 standard; protein; 40 AA.		ID AAO06835 standard; protein; 40 AA.	
XX		XX	
AC AAB64755;		AC AAO06835;	
XX		XX	
DT 23-MAR-2001 (first entry)		DT 06-NOV-2001 (first entry)	
XX		XX	
DE Human secreted protein sequence encoded by gene 36 SEQ ID NO:149.		DE Human polypeptide SEQ ID NO 20727.	
XX		XX	
KW Human; secreted protein; diagnosis; cytostatic; antirheumatic; antiarthritic; dermatological; cardiant; antiinflammatory; anti-ulcer;		KW Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis;	
KW gastrointestinal; solid tumour; rheumatoid arthritis; psoriasis;		KW tissue growth factor; immunomodulatory; cancer; leukaemia;	
KW diabetic retinopathy; myocardial angiogenesis; Crohn's disease; ulcer.		KW nervous system disorders; arthritis; inflammation.	
XX		XX	
OS Homo sapiens.		OS Homo sapiens.	
XX		XX	
PN WO200077237-A1.		PN WO200164835-A2.	
XX		XX	
PD 21-DEC-2000.		PD 07-SEP-2001.	
XX		XX	
PF 01-JUN-2000; 2000WO-US014928.		PF 26-FEB-2001; 2001WO-US004927.	
XX		XX	
PR 11-JUN-1999; 99US-0138633P.		PR 28-FEB-2000; 2000US-00515126.	
XX		PR 18-MAY-2000; 2000US-00577409.	
PA (HUMA-) HUMAN GENOME SCI INC.		XX	
PA (ROSE/) ROSEN C A.		PA (HYSE-) HYSEQ INC.	
XX		XX	
PI Rosen CA, Ruben SM, Komatsoulis GA;		PI Tang YT, Liu C, Drmanac RT;	
XX		XX	
DR WPI; 2001-071280/08.		DR WPI; 2001-514838/56.	
XX		DR N-PSDB; AAI86766.	
XX		XX	
PT Nucleic acids encoding 49 human secreted polypeptides, useful for preventing, diagnosing and/or treating diseases such as tumors, rheumatoid arthritis, psoriasis and diabetic retinopathy.		PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.	
PT		PT	
XX		XX	
PS Disclosure; Page 510; 520pp; English.		PS Claim 20; SEQ ID NO 20727; 1399pp + Sequence Listing; English.	
XX		XX	
CC The polynucleotide sequences given in AAF33037 to AAF33085 encode the human secreted proteins given in AAB64666 to AAB64714. AAB64715 to AAB64771 represent human secreted polypeptide sequences and proteins homologous to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include: cytostatic; antirheumatic; antiarthritic; dermatological; cardiant; antiinflammatory; gastrointestinal; and anti-ulcer. The polynucleotides and polypeptides can be used in the prevention, treatment and diagnosis of diseases associated with inappropriate polypeptide expression. Disorders that may be treated or prevented include solid tumours, rheumatoid arthritis, psoriasis, diabetic retinopathy, myocardial angiogenesis, Crohn's disease and ulcers. The polynucleotides and their complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples, and therefore which patients may be in need of restorative therapy. The polypeptides may also be used as antigens in the production of antibodies against the polypeptide and in assays to identify modulators (agonists and antagonists) of polypeptide expression and activity. The anti-polypeptide antibodies and antagonists may also be used to down regulate expression and activity. AAF33028 to AAF33036 and AAB64665 represent sequences used in the exemplification of the present invention		CC The invention relates to human polynucleotides (AAI79941-AAI33841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences	
XX		XX	
SQ Sequence 40 AA;		SQ Sequence 40 AA;	
Query Match	70.8%;	Query Match	70.8%;
Best Local Similarity	40.0%;	Best Local Similarity	40.0%;
Matches	2; Conservative	Matches	2; Conservative
	0; Mismatches		0; Mismatches
	3; Indels		3; Indels
	0; Gaps		0; Gaps
	0;		0;
QY	2 FXXXW 6	QY	2 FXXXW 6
Db	20 FATTW 24	Db	20 FATTW 24
RESULT 40		RESULT 40	
AAM64830		AAM64830	
ID AAM64830 standard; protein; 40 AA.		ID AAM64830 standard; protein; 40 AA.	
XX		XX	
AC AAM64830;		AC AAM64830;	
XX		XX	
DT 05-NOV-2001 (first entry)		DT 05-NOV-2001 (first entry)	



XX Human brain expressed single exon probe encoded protein SEQ ID NO: 36935.  
DE  
XX Human; brain expressed exon; gene expression analysis; probe; microarray;  
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.  
XX Homo sapiens.  
OS  
XX WO200157275-A2.  
PN  
XX  
XX PD  
XX 09-AUG-2001.  
XX  
XX PF 30-JAN-2001; 2001WO-US000667.  
XX  
XX PR 04-FEB-2000; 2000US-0180312P.  
XX PR 26-MAY-2000; 2000US-0207456P.  
XX PR 30-JUN-2000; 2000US-00608408.  
XX PR 03-AUG-2000; 2000US-00632366.  
XX PR 21-SEP-2000; 2000US-0234687P.  
XX PR 27-SEP-2000; 2000US-0236359P.  
XX PR 04-OCT-2000; 2000GB-00024263.  
XX  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
PI  
XX WPI; 2001-483446/52.  
DR  
XX Single exon nucleic acid probes for analyzing gene expression in human  
PT brains.  
XX  
XX Example 4; SEQ ID NO 36935; 650pp + Sequence Listing; English.  
PS  
XX The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC brain. They can be used to measure gene expression in brain cell samples,  
CC which may enable the diagnosis and improved treatment of nervous system  
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
CC epilepsy and cancers. The present sequence is a protein encoded by one of  
CC the probes of the invention  
XX  
XX SQ Sequence 40 AA;  
Query Match 70.8%; Score 17; DB 4; Length 40;  
Best Local Similarity 40.0%; Pred. No. 1e+04;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 FXXXW 6  
Db 23 FTSSW 27  
Search completed: October 18, 2005, 15:26:11  
Job time : 126.471 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:44:54 ; Search time 21.6471 Seconds  
(without alignments)  
35.558 Million cell updates/sec

Title: US-09-214-371-10  
Perfect score: 23  
Sequence: 1 FXXXXXXX 8

Scoring table: BLOSUM62  
Gapop 10.0 ; Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3886

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	73.9	9	2 A24244	adipokinetic hormo
2	16	69.6	8	2 A28004	adipokinetic hormo
3	16	69.6	10	2 A31571	hypertrehalosemic/
4	15	65.2	8	2 S10596	adipokinetic hormo
5	15	65.2	9	2 D57444	neuropeptide Grb-A
6	15	65.2	10	2 T17063	cytochrome-c oxida
7	15	65.2	10	2 T12325	cytochrome-c oxida
8	15	65.2	10	2 S53789	neuropeptide Pec-H
9	15	65.2	15	2 PH1613	Ig H chain V-D-J r
10	15	65.2	17	2 A34704	protein-tyrosine k
11	15	65.2	20	2 S77981	cytochrome-c oxida
12	15	65.2	20	2 PN0171	peptidylprolyl iso
13	15	65.2	20	2 PH1380	alpha-amylase (EC
14	14	60.9	8	2 A33995	adipokinetic hormo
15	14	60.9	8	2 A44960	neuropeptide led-C
16	14	60.9	8	2 B44960	neuropeptide led-C
17	14	60.9	8	2 A58620	adipokinetic hormo
18	14	60.9	8	2 S11545	adipokinetic hormo
19	14	60.9	8	2 S55310	adipokinetic hormo
20	14	60.9	8	2 A61348	red pigment-concen
21	14	60.9	8	2 S08995	hypertrehalosemic
22	14	60.9	8	2 S08996	hypertrehalosemic
23	14	60.9	8	2 A49823	adipokinetic hormo
24	14	60.9	8	2 B49823	adipokinetic hormo
25	14	60.9	8	2 A43976	hypertrehalosemic
26	14	60.9	8	2 B43976	hypertrehalosemic
27	14	60.9	8	2 A05169	neuropeptide M-I -
28	14	60.9	10	2 B33995	hypertrehalosemic h
29	14	60.9	10	2 S08997	hypertrehalosemic

30	14	60.9	10	2 A60421	hypertrehalosemic
31	14	60.9	10	2 S08998	hypertrehalosemic
32	14	60.9	10	2 A26381	hypertrehalosemic
33	14	60.9	10	2 JC1416	hypertrehalosemic
34	14	60.9	10	2 S09138	hypertrehalosemic
35	14	60.9	10	2 C39191	hypothetical prote
36	14	60.9	10	2 PT0322	Ig heavy chain CRD
37	14	60.9	10	2 T17066	cytochrome-c oxida
38	14	60.9	10	2 T17069	cytochrome-c oxida
39	14	60.9	10	2 T12329	cytochrome-c oxida
40	14	60.9	12	2 PT0274	Ig heavy chain CRD
41	14	60.9	12	2 PH1324	Ig heavy chain DJ
42	14	60.9	13	2 PC4391	cysteine proteinas
43	14	60.9	16	2 C37290	homeotic protein G
44	14	60.9	19	2 S32675	nitrogen fixation
45	14	60.9	20	2 FC1240	calcium-binding pr
46	13	56.5	9	2 PT0288	Ig heavy chain CRD
47	13	56.5	9	2 I46023	growth hormone rec
48	13	56.5	11	2 C53652	rh1R protein - pse
49	13	56.5	11	2 PT0302	Ig heavy chain CRD
50	12	52.2	8	2 T13818	cytochrome oxidase
51	12	52.2	10	1 RHLMGS	gonadoliberin - se
52	12	52.2	11	2 S05002	corazonin - Americ
53	12	52.2	18	2 S39009	oviductin - golden
54	11	47.8	3	3 F37196	bradykinin-potenti
55	11	47.8	4	2 A34626	RPCH-related neuro
56	11	47.8	4	2 B53284	T-cell receptor be
57	11	47.8	4	2 PT0661	T-cell receptor be
58	11	47.8	5	2 A32516	cholecystokinin-5
59	11	47.8	5	2 A60803	neuropeptide - sea
60	11	47.8	5	2 JH0253	gut pentapeptide -
61	11	47.8	5	2 PT0281	Ig heavy chain CRD
62	11	47.8	5	2 PT0308	Ig heavy chain CRD
63	11	47.8	5	2 PT0729	T-cell receptor be
64	11	47.8	5	2 PT0580	T-cell receptor be
65	11	47.8	5	2 G37196	bradykinin-potenti
66	11	47.8	6	2 S66195	alcohol dehydrogen
67	11	47.8	6	2 B34835	dnaA protein - Pse
68	11	47.8	6	2 A31263	dihydrofolate redu
69	11	47.8	6	2 B31263	dihydrofolate redu
70	11	47.8	6	2 B35640	cerebellar degener
71	11	47.8	6	2 PT0629	T-cell receptor be
72	11	47.8	6	2 PT0532	T-cell receptor be
73	11	47.8	6	2 PT0519	T-cell receptor be
74	11	47.8	6	2 PT0637	T-cell receptor be
75	11	47.8	6	2 PT0641	T-cell receptor be
76	11	47.8	6	2 PT0726	T-cell receptor be
77	11	47.8	6	2 F41946	T-cell receptor ga
78	11	47.8	6	2 PD0028	pev-kinin 2 - pena
79	11	47.8	6	2 A61068	locustakinin - mig
80	11	47.8	6	2 I79564	hypothetical TCU3
81	11	47.8	7	2 S21230	dermorphin (Trp-4,
82	11	47.8	7	2 S09652	hypothetical prote
83	11	47.8	7	2 PQ0727	H2 class I protein
84	11	47.8	7	2 E48394	glycoprotein compo
85	11	47.8	7	2 PH1602	Ig H chain V-D-J r
86	11	47.8	7	2 PT0526	T-cell receptor be
87	11	47.8	7	2 PT0628	T-cell receptor be
88	11	47.8	7	2 PT0642	T-cell receptor be
89	11	47.8	7	2 PT0722	T-cell receptor be
90	11	47.8	7	2 PT0688	T-cell receptor be
91	11	47.8	7	2 PT0586	T-cell receptor be
92	11	47.8	7	2 PT0728	T-cell receptor be
93	11	47.8	7	2 PX0008	glucuronosyltransf
94	11	47.8	7	2 B48394	major fat-globule
95	11	47.8	7	2 PD0029	pev-kinin 1 - pena
96	11	47.8	7	2 PN0649	pullulanase (EC 3.
97	11	47.8	7	2 S57274	triacylglycerol li
98	11	47.8	7	2 S33244	neuromodulatory pe
99	11	47.8	7	2 S33245	neuromodulatory pe
100	11	47.8	7	2 S33246	neuromodulatory pe
101	11	47.8	7	2 S33567	tubulin beta-3 cha
102	11	47.8	7	2 A58512	venom heptapeptide

103 47.8 7 2 A61081 tryptophyllin, bas  
104 47.8 7 4 I55382 hypothetical pepti  
105 47.8 7 4 A58725 virotoxin - destro  
106 47.8 8 2 S15422 adipokinetic hormo  
107 47.8 8 2 A58641 adipokinetic hormo  
108 47.8 8 2 PQ0012 cholecystokinin -  
109 47.8 8 2 A43001 cholecystokinin -  
110 47.8 8 2 PT0724 T-cell receptor be  
111 47.8 8 2 A38887 T-cell receptor ga  
112 47.8 8 2 A59495 Vesicle associated  
113 47.8 8 2 S19288 acylase - Kluuyvera  
114 47.8 8 2 A39308 glycine reductase  
115 47.8 8 2 C61512 variant surface gl  
116 47.8 8 2 D61512 variant surface gl  
117 47.8 8 2 JS0315 leucokinin V - Mad  
118 47.8 8 2 JS0316 leucokinin VI - Ma  
119 47.8 8 2 JS0317 leucokinin VII - M  
120 47.8 8 2 JS0318 leucokinin VIII -  
121 47.8 8 2 S21663 neuropeptide - flo  
122 47.8 8 2 A41117 acetylcholinestera  
123 47.8 8 2 A31570 angiotensin-conver  
124 47.8 9 1 AKLQM locustamyo inhibiti  
125 47.8 9 2 S07205 litorin 2-Glu - Au  
126 47.8 9 2 S07204 litorin I - Austra  
127 47.8 9 2 S07241 litorin - Rohde's  
128 47.8 9 2 A61357 phyllocaerulein -  
129 47.8 9 2 JS0302 xenopsin-related p  
130 47.8 9 2 A60320 Ig heavy chain CDR  
131 47.8 9 2 PT0231 Ig heavy chain CDR  
132 47.8 9 2 PT0270 Ig heavy chain CDR  
133 47.8 9 2 PT0272 Ig heavy chain CDR  
134 47.8 9 2 PT0299 Ig heavy chain CDR  
135 47.8 9 2 PT0324 Ig heavy chain CDR  
136 47.8 9 2 PT0634 T-cell receptor be  
137 47.8 9 2 PT0562 T-cell receptor be  
138 47.8 9 2 I58350 gene c-mpl protein  
139 47.8 9 2 S78426 52.5K protein - sp  
140 47.8 9 2 S56004 glucan 1,3-beta-gl  
141 47.8 9 2 A43848 cell surface adhes  
142 47.8 9 2 A57444 neuropeptide Grb-A  
143 47.8 9 2 B57444 neuropeptide Grb-A  
144 47.8 9 2 C57444 neuropeptide Grb-A  
145 47.8 9 2 A37027 macrophage chemota  
146 47.8 9 2 QDRB delta sleep-induci  
147 47.8 9 2 A60522 sperm-activating p  
148 47.8 10 1 XASNPC angiotensin-conver  
149 47.8 10 1 XAVIGB angiotensin-conver  
150 47.8 10 1 RHPGG gonadoliberin - pi  
151 47.8 10 1 RHSHG gonadoliberin - sh  
152 47.8 10 1 A61126 gonadoliberin - sp  
153 47.8 10 1 RHAQ1 gonadoliberin I -  
154 47.8 10 1 RHAQ2 gonadoliberin II -  
155 47.8 10 2 S71868 glutathione transf  
156 47.8 10 2 B46030 gonadoliberin II -  
157 47.8 10 2 JC1367 thyroliberin poten  
158 47.8 10 2 A60647 neuromedin C - bov  
159 47.8 10 2 PQ0177 neuromedin C - lau  
160 47.8 10 2 A61337 caerulein - frog (  
161 47.8 10 2 A13687 caerulein-like pep  
162 47.8 10 2 S59625 beta-galactosidase  
163 47.8 10 2 PQ0753 beta-fructofuranos  
164 47.8 10 2 S63696 DNA polymerase - y  
165 47.8 10 2 A49187 gonadotropin-relea  
166 47.8 10 2 A35556 hypothetical prote  
167 47.8 10 2 PT0245 Ig heavy chain CDR  
168 47.8 10 2 PT0289 Ig heavy chain CDR  
169 47.8 10 2 PT0310 Ig heavy chain CDR  
170 47.8 10 2 PH1344 Ig heavy chain DJ  
171 47.8 10 2 S23370 T-cell receptor al  
172 47.8 10 2 E49033 T-cell receptor ga  
173 47.8 10 2 F49033 T-cell receptor ga  
174 47.8 10 2 E41946 T-cell receptor ga  
175 47.8 10 2 C41946 T-cell receptor ga

176 11 47.8 10 2 B38887 T-cell receptor ga  
177 11 47.8 10 2 PH0916 T-cell receptor be  
178 11 47.8 10 2 PH0923 T-cell receptor be  
179 11 47.8 10 2 A40753 aldehyde ferredoxi  
180 11 47.8 10 2 A59272 peptide-N4-(N-acet  
181 11 47.8 10 2 S66248 processing enzyme,  
182 11 47.8 10 2 A27617 triose-phosphate i  
183 11 47.8 10 2 A46030 gonadoliberin I -  
184 11 47.8 10 2 A21114 gonadoliberin - ch  
185 11 47.8 10 2 B37196 bradykinin-potenti  
186 11 47.8 10 2 H37196 bradykinin-potenti  
187 11 47.8 10 2 F33932 Ig mu chain J regi  
188 11 47.8 10 2 T17054 cytochrome-c oxida  
189 11 47.8 10 2 T17075 cytochrome-c oxida  
190 11 47.8 10 2 T13976 cytochrome-c oxida  
191 11 47.8 10 2 T17057 cytochrome-c oxida  
192 11 47.8 10 2 T12303 cytochrome-c oxida  
193 11 47.8 10 2 T14019 cytochrome-c oxida  
194 11 47.8 10 2 T17060 cytochrome-c oxida  
195 11 47.8 10 2 T14043 cytochrome-c oxida  
196 11 47.8 10 2 T14054 cytochrome-c oxida  
197 11 47.8 10 2 T12308 cytochrome-c oxida  
198 11 47.8 10 2 T17072 cytochrome-c oxida  
199 11 47.8 10 2 T12312 cytochrome-c oxida  
200 11 47.8 10 2 T12316 cytochrome-c oxida  
201 11 47.8 10 2 T14212 cytochrome-c oxida  
202 11 47.8 10 2 T12321 cytochrome-c oxida  
203 11 47.8 10 2 T14215 cytochrome-c oxida  
204 11 47.8 10 2 T14223 cytochrome-c oxida  
205 11 47.8 10 2 T14219 cytochrome-c oxida  
206 11 47.8 10 2 A59173 cytochrome-c oxida  
207 11 47.8 10 2 S39030 cytochrome-c oxida  
208 11 47.8 11 1 LFTWWE lysyl-bradykinin -  
209 11 47.8 11 2 S66196 probable trpEG lea  
210 11 47.8 11 2 B49164 alcohol dehydrogen  
211 11 47.8 11 2 S32575 chromogranin-B - r  
212 11 47.8 11 2 H54346 ribosomal protein  
213 11 47.8 11 2 PT0249 pyruvate synthase  
214 11 47.8 11 2 PT0273 Ig heavy chain CDR  
215 11 47.8 11 2 PH1343 Ig heavy chain CDR  
216 11 47.8 11 2 S68649 Ig heavy chain DJ  
217 11 47.8 11 2 A33571 spermadhesin AQN-3  
218 11 47.8 11 2 D41946 follistatin - bovi  
219 11 47.8 11 2 B41946 T-cell receptor ga  
220 11 47.8 11 2 C38887 T-cell receptor ga  
221 11 47.8 11 2 T41946 T-cell receptor ga  
222 11 47.8 11 2 A49037 TcR gamma V-J regi  
223 11 47.8 11 2 B49037 TcR gamma V-J regi  
224 11 47.8 11 2 C49037 TcR gamma V-J regi  
225 11 47.8 11 2 S70338 napin small chain  
226 11 47.8 11 2 C59151 protein-tyrosine k  
227 11 47.8 11 2 JQ2307 hypothetical 1.5K  
228 11 47.8 11 2 JQ2317 hypothetical 1.5K  
229 11 47.8 11 2 PQ0731 unidentified 5.7/3  
230 11 47.8 11 2 S45698 gamma-MSH-like pro  
231 11 47.8 11 2 A34662 Achatina cardio-ex  
232 11 47.8 11 2 A59146 conotoxin au5a - c  
233 11 47.8 11 2 B59146 conotoxin au5b - c  
234 11 47.8 11 2 T12264 cytochrome-c oxida  
235 11 47.8 11 2 T12253 cytochrome-c oxida  
236 11 47.8 11 2 T12244 cytochrome-c oxida  
237 11 47.8 11 2 T12248 cytochrome-c oxida  
238 11 47.8 11 2 T17081 cytochrome-c oxida  
239 11 47.8 11 2 T17078 cytochrome-c oxida  
240 11 47.8 12 1 UOGM2 alpha-conotoxin Im  
241 11 47.8 12 1 A53709 phospholipase A2 (  
242 11 47.8 12 2 A29169 gene HEXA protein  
243 11 47.8 12 2 JS0423 urotensin II-A pep  
244 11 47.8 12 2 S42765 urotensin II - tel  
245 11 47.8 12 2 PH1675 Ig heavy chain V r  
246 11 47.8 12 2 S26548 T-cell receptor be  
247 11 47.8 12 2 S26553 T-cell receptor be  
248 11 47.8 12 2 S26553 T-cell receptor be

249	11	47.8	12	2	A26093	microbial collagen	322	11	47.8	14	2	S03530	Ig heavy chain J r
250	11	47.8	12	2	G64003	hypothetical prote	323	11	47.8	14	2	I54284	Ci-inhibitor - hum
251	11	47.8	12	2	S69123	proton-translocati	324	11	47.8	14	2	PT0223	Ig heavy chain DJ
252	11	47.8	12	2	A40763	sucrose-6-phosphat	325	11	47.8	14	2	PH1348	Ig heavy chain DJ
253	11	47.8	12	2	PH1308	Ig heavy chain DJ	326	11	47.8	14	2	PH1327	Ig heavy chain DJ
254	11	47.8	12	2	S43957	Ig mu chain V regi	327	11	47.8	14	2	PH1356	Ig heavy chain DJ
255	11	47.8	12	2	A49033	T-cell receptor de	328	11	47.8	14	2	PH1332	Ig heavy chain DJ
256	11	47.8	12	2	B49033	T-cell receptor de	329	11	47.8	14	2	PH1322	Ig heavy chain DJ
257	11	47.8	12	2	S25039	Ig heavy chain V r	330	11	47.8	14	2	PH1757	T cell receptor al
258	11	47.8	12	2	H41946	T-cell receptor ga	331	11	47.8	14	2	PH1758	T cell receptor al
259	11	47.8	12	2	A42324	cytochrome P450c27	332	11	47.8	14	2	PH1759	T cell receptor al
260	11	47.8	12	2	I57678	gene rPLP-A protei	333	11	47.8	14	2	PH1766	T cell receptor al
261	11	47.8	12	2	I41235	glutamine-tRNA lig	334	11	47.8	14	2	PH1767	T cell receptor al
262	11	47.8	12	2	JS0424	urotensin II-B pep	335	11	47.8	14	2	PH1768	T cell receptor al
263	11	47.8	12	2	A49637	MHC class II histo	336	11	47.8	14	2	PH1769	T cell receptor al
264	11	47.8	12	2	I77529	estrogen receptor	337	11	47.8	14	2	S57572	T cell receptor V-
265	11	47.8	12	2	S43170	kinesin light chai	338	11	47.8	14	2	S58426	spermadhesin AWN h
266	11	47.8	12	2	PN0046	ATP synthase D cha	339	11	47.8	14	2	PH1625	Ig H chain V-D-J r
267	11	47.8	12	2	I58273	thyroglobulin - ra	340	11	47.8	14	2	PH1626	Ig H chain V-D-J r
268	11	47.8	12	2	PQ0776	NADH2 dehydrogenas	341	11	47.8	14	2	PH1627	Ig H chain V-D-J r
269	11	47.8	13	1	XAVI9B	angiotensin-conver	342	11	47.8	14	2	PH1594	Ig H chain V-D-J r
270	11	47.8	13	1	MTCMAD	melanotropin alpha	343	11	47.8	14	2	PH0801	T-cell receptor al
271	11	47.8	13	1	PTH0AD	melanotropin alpha	344	11	47.8	14	2	PH0747	T-cell receptor be
272	11	47.8	13	2	PQ0445	urotensin II - lau	345	11	47.8	14	2	F49037	TCR delta chain V-
273	11	47.8	13	2	PH1676	Ig heavy chain V r	346	11	47.8	14	2	B44854	L-2,4-diaminobuty
274	11	47.8	13	2	B28810	glutathione transf	347	11	47.8	14	2	PT0026	calotropin DI - mu
275	11	47.8	13	2	PT0293	Ig heavy chain CRD	348	11	47.8	14	2	S33801	chaperone, TCPI-re
276	11	47.8	13	2	PT0304	Ig heavy chain CRD	349	11	47.8	14	2	S33802	chaperone, TCPI-re
277	11	47.8	13	2	S57567	T cell receptor V-	350	11	47.8	14	2	PT0029	karatasin - karata
278	11	47.8	13	2	S23372	T-cell receptor al	351	11	47.8	14	2	S14336	mastoparan B - hor
279	11	47.8	13	2	PH0138	T-cell receptor be	352	11	47.8	14	2	A47421	leukotriene B-4 12
280	11	47.8	13	2	S61798	T-cell-specific tr	353	11	47.8	14	2	S68095	calcium-binding pr
281	11	47.8	13	2	B56864	dipeptidyl-peptida	354	11	47.8	14	2	S39931	S-allele-associate
282	11	47.8	13	2	B25448	Ig kappa-1 chain,	355	11	47.8	14	2	A44515	Trp EG leader pept
283	11	47.8	13	2	PH1636	Ig H chain V-D-J r	356	11	47.8	14	2	JH0328	probursin tetradec
284	11	47.8	13	2	PH1620	Ig H chain V-D-J r	357	11	47.8	15	2	B26997	unspecific monooxy
285	11	47.8	13	2	G37266	Ig heavy chain C r	358	11	47.8	15	2	A26997	unspecific monooxy
286	11	47.8	13	2	D37267	Ig heavy chain C r	359	11	47.8	15	2	PQ0195	Sfil-glycoprotein
287	11	47.8	13	2	B26406	Ig kappa chain J r	360	11	47.8	15	2	PQ0174	stylar glycoprotei
288	11	47.8	13	2	PH0928	T-cell receptor be	361	11	47.8	15	2	PQ0175	stylar glycoprotei
289	11	47.8	13	2	A47630	Ig kappa chain J r	362	11	47.8	15	2	S21202	glucan 1,4-alpha-g
290	11	47.8	13	2	I51905	collecting duct wa	363	11	47.8	15	2	S21240	alpha-glucosidase
291	11	47.8	13	2	S54344	glyceraldehyde-3-p	364	11	47.8	15	2	S21241	oligo-1,6-glucosid
292	11	47.8	13	2	A59491	epithelial dog all	365	11	47.8	15	2	S24159	leukocyte elastase
293	11	47.8	13	2	I54984	aeg-46.5 protein -	366	11	47.8	15	2	PQ0232	cystatin CI-4a - m
294	11	47.8	13	2	PC2369	early nodulin 40 -	367	11	47.8	15	2	PH1319	Ig heavy chain DJ
295	11	47.8	13	2	S60046	glutathione transf	368	11	47.8	15	2	S26791	Ig heavy chain V r
296	11	47.8	13	2	A61514	factor X activator	369	11	47.8	15	2	PS0382	Ig heavy chain J r
297	11	47.8	13	2	A60379	glutathione transf	370	11	47.8	15	2	S39012	proteinase - Therm
298	11	47.8	13	2	S32551	serine proteinase	371	11	47.8	15	2	T46625	hypothetical prote
299	11	47.8	13	2	S66558	hypothetical prote	372	11	47.8	15	2	S08209	hypothetical prote
300	11	47.8	13	2	A86126	bombesin-like pept	373	11	47.8	15	2	PQ0750	self-incompatibili
301	11	47.8	13	2	A60409	tryptophyllin-13 -	374	11	47.8	15	2	B56891	gamma 2 gliadin -
302	11	47.8	13	2	A05174	bombesin - fire-be	375	11	47.8	15	2	S10388	Ig heavy chain J r
303	11	47.8	14	1	BSTD	mastoparan X - hor	376	11	47.8	15	2	S10386	Ig heavy chain J r
304	11	47.8	14	1	QMVHXX	polistes mastopara	377	11	47.8	15	2	A47628	Fc gamma receptor
305	11	47.8	14	1	QMWAPP	trp operon leader	378	11	47.8	15	2	PH1365	Ig heavy chain DJ
306	11	47.8	14	1	LFEBWC	trp operon leader	379	11	47.8	15	2	PH1366	Ig heavy chain DJ
307	11	47.8	14	1	LFEBWT	trp operon leader	380	11	47.8	15	2	PH1342	Ig heavy chain DJ
308	11	47.8	14	1	LFECW	trp operon leader	381	11	47.8	15	2	PH1318	Ig heavy chain DJ
309	11	47.8	14	2	PC2373	probable IMP dehyd	382	11	47.8	15	2	PH1320	Ig heavy chain DJ
310	11	47.8	14	2	A60622	somatostatin - spo	383	11	47.8	15	2	S43956	Ig mu chain V regi
311	11	47.8	14	2	A60840	somatostatin I - E	384	11	47.8	15	2	PH1762	T cell receptor al
312	11	47.8	14	2	C60414	somatostatin - sli	385	11	47.8	15	2	PH1788	T cell receptor al
313	11	47.8	14	2	B60842	somatostatin I - c	386	11	47.8	15	2	G49655	T-cell-receptor be
314	11	47.8	14	2	S00172	somatostatin I - s	387	11	47.8	15	2	PQ0073	T-cell receptor be
315	11	47.8	14	2	PH1677	Ig heavy chain V r	388	11	47.8	15	2	A45103	7 alpha-hydroxy-4-
316	11	47.8	14	2	PH1705	Ig heavy chain V r	389	11	47.8	15	2	PH1616	Ig H chain V-D-J r
317	11	47.8	14	2	PT0077	proteochondroitin c	390	11	47.8	15	2	PH1590	Ig H chain V-D-J r
318	11	47.8	14	2	E90858	trp operon leader	391	11	47.8	15	2	PH1612	Ig H chain V-D-J r
319	11	47.8	14	2	B85761	trp operon leader	392	11	47.8	15	2	PH0782	T-cell receptor al
320	11	47.8	14	2	A35105	hypothetical prote	393	11	47.8	15	2	E49037	TCR delta chain V-
321	11	47.8	14	2	PC1215	homeotic protein E	394	11	47.8	15	2	PL0109	complement factor

395	11	47.8	15	2	S02381	probable membrane	468	11	47.8	17	2	PH1357	Ig heavy chain DJ
396	11	47.8	15	2	PH0216	agarase (EC 3.2.1.1.	469	11	47.8	17	2	PH1630	Ig H chain V-D-J r
397	11	47.8	15	2	S21411	nodulation protein	470	11	47.8	17	2	PS0384	Ig heavy chain J r
398	11	47.8	15	2	S33781	acetolactate synth	471	11	47.8	17	2	A46592	lactase-phlorizin
399	11	47.8	15	2	B60763	endo-1,3-beta-gluc	472	11	47.8	17	2	A44560	terephthalate 1,2-
400	11	47.8	15	2	A48372	benzoyl-CoA ligase	473	11	47.8	17	2	A27636	cytotoxin B - Clos
401	11	47.8	15	2	T09463	ribosomal protein	474	11	47.8	17	2	A38824	tachyplesin I - ho
402	11	47.8	15	2	PA0036	glycine cleavage s	475	11	47.8	17	2	JX0125	tachyplesin III -
403	11	47.8	15	2	PA0099	phenotypic variati	476	11	47.8	17	2	PC1318	large granule L6 c
404	11	47.8	15	2	PX0031	mixed lymphocyte r	477	11	47.8	17	2	S10786	enamelin, 26K - bo
405	11	47.8	15	2	C84035	hypothetical prote	478	11	47.8	17	2	I53392	CD33 antigen homol
406	11	47.8	15	4	I38032	hypothetical MN1/T	479	11	47.8	17	2	I67524	CD33 antigen homol
407	11	47.8	16	1	A49761	locustapyrokinin -	480	11	47.8	17	2	I67526	CD33 antigen homol
408	11	47.8	16	1	MTDFBS	melanotropin beta	481	11	47.8	17	2	A61211	anantin - Streptom
409	11	47.8	16	2	E41425	cytochrome P450 IF	482	11	47.8	17	2	B48943	phage antigenic de
410	11	47.8	16	2	S03405	hydrogenase (EC 1.	483	11	47.8	17	2	E59137	protein pfd3 - gol
411	11	47.8	16	2	I57530	gene c-fms protein	484	11	47.8	17	2	A29834	trp leader peptide
412	11	47.8	16	2	A60551	leukocyte elastase	485	11	47.8	18	1	MTDFBC	melanotropin beta
413	11	47.8	16	2	A29541	little gastrin - C	486	11	47.8	18	1	MTHOB	melanotropin beta
414	11	47.8	16	2	S03532	Ig heavy chain J r	487	11	47.8	18	2	S23799	sorbitol dehydroge
415	11	47.8	16	2	D49021	Ig heavy chain J7	488	11	47.8	18	2	S24780	protein-tyrosine k
416	11	47.8	16	2	A36300	T-cell receptor ga	489	11	47.8	18	2	S74195	epoxide hydrolase
417	11	47.8	16	2	PS0383	Ig heavy chain J r	490	11	47.8	18	2	G02018	proteasome chain L
418	11	47.8	16	2	S26746	Ig heavy chain J r	491	11	47.8	18	2	S04229	N4-(beta-N-acetyl
419	11	47.8	16	2	S66613	protein p12E - Fri	492	11	47.8	18	2	D49570	plasma membrane ca
420	11	47.8	16	2	S28213	glutathione transf	493	11	47.8	18	2	S43834	DNA topoisomerase
421	11	47.8	16	2	PT0237	Ig heavy chain CDR	494	11	47.8	18	2	PH1368	Ig heavy chain DJ
422	11	47.8	16	2	PT0282	Ig heavy chain CDR	495	11	47.8	18	2	PH1323	Ig heavy chain DJ
423	11	47.8	16	2	PT0296	Ig heavy chain CDR	496	11	47.8	18	2	S03528	Ig heavy chain J1
424	11	47.8	16	2	PH1346	Ig heavy chain DJ	497	11	47.8	18	2	A32220	T-cell receptor de
425	11	47.8	16	2	S23184	redoxendonuclease	498	11	47.8	18	2	A25941	Ig heavy chain J-H
426	11	47.8	16	2	PH1637	Ig H chain V-D-J r	499	11	47.8	18	2	S29264	ovoheremerythrin - d
427	11	47.8	16	2	PH1638	Ig H chain V-D-J r	500	11	47.8	18	2	S55501	thrombospondin pre
428	11	47.8	16	2	PH1604	Ig H chain V-D-J r	501	11	47.8	18	2	S52125	gamma2-gliadin P25
429	11	47.8	16	2	A48839	T-cell receptor al	502	11	47.8	18	2	C56211	progesterone recep
430	11	47.8	16	2	PH0748	T-cell receptor be	503	11	47.8	18	2	I40062	NTL1 protein - cur
431	11	47.8	16	2	D49037	TcR delta chain V-	504	11	47.8	18	2	S21669	shikimate 5-dehydr
432	11	47.8	16	2	A46236	transforming prote	505	11	47.8	18	2	T03799	1H-4-oxoquinoline
433	11	47.8	16	2	S33589	beta-crystallin A4	506	11	47.8	18	2	S19914	leader peptide trp
434	11	47.8	16	2	B44820	7K protein - Esche	507	11	47.8	18	2	I52623	choline O-acetyltr
435	11	47.8	16	2	PC1299	subtilisin (EC 3.4	508	11	47.8	18	2	PT0239	hypothetical prote
436	11	47.8	16	2	A24099	crystal protein, 2	509	11	47.8	18	2	PT0286	Ig heavy chain CDR
437	11	47.8	16	2	T44936	calmodulin kinase	510	11	47.8	18	2	PH1349	Ig heavy chain CDR
438	11	47.8	16	2	A20190	hypodermin B - ear	511	11	47.8	18	2	PH1350	Ig heavy chain DJ
439	11	47.8	16	2	A48630	bothrojaracin - ja	512	11	47.8	18	2	S43958	Ig mu chain V regi
440	11	47.8	16	2	I37452	protein kinase - h	513	11	47.8	18	2	A40256	interleukin-7 rece
441	11	47.8	16	2	S13898	alkaline phosphata	514	11	47.8	18	2	I35141	T-cell receptor de
442	11	47.8	16	2	B23692	transcription fact	515	11	47.8	18	2	C49254	TcR C gamma 1 chai
443	11	47.8	16	2	E37290	homeotic protein G	516	11	47.8	18	2	G49037	24k serine protein
444	11	47.8	16	2	S05703	homeotic protein c	517	11	47.8	18	2	A61577	gluten - wheat
445	11	47.8	16	4	I79565	hypothetical TcL3/	518	11	47.8	18	2	S20322	polyphemusin I - A
446	11	47.8	17	1	GMSH	gastrin - sheep	519	11	47.8	18	2	JU0124	polyphemusin II -
447	11	47.8	17	2	S66198	alcohol dehydrogen	520	11	47.8	18	2	JU0125	hypothetical prote
448	11	47.8	17	2	A60071	gastrin - rhesus m	521	11	47.8	18	2	A35678	hypothetical prote
449	11	47.8	17	2	S24570	Ig heavy chain J r	522	11	47.8	18	2	S27141	neuropeptide A - b
450	11	47.8	17	2	H49048	T-cell receptor be	523	11	47.8	18	2	A24749	ancovenin - Strept
451	11	47.8	17	2	I49048	T-cell receptor be	524	11	47.8	19	1	EWSMAN	cytochrome P450-C-
452	11	47.8	17	2	S03531	Ig heavy chain J5	525	11	47.8	19	2	A28702	L-lactate dehydrog
453	11	47.8	17	2	S26747	Ig heavy chain J r	526	11	47.8	19	2	I45957	glutathione transf
454	11	47.8	17	2	S26744	Ig heavy chain J r	527	11	47.8	19	2	S71871	protein kinase (EC
455	11	47.8	17	2	B44873	caldesmon - rabbit	528	11	47.8	19	2	PC1251	testin II - rat (f
456	11	47.8	17	2	I57941	beta 3-adrenergic	529	11	47.8	19	2	S60633	H+-transporting tw
457	11	47.8	17	2	I51910	SP-A2 - human (fra	530	11	47.8	19	2	PH1304	Ig heavy chain DJ
458	11	47.8	17	2	A41053	glutamate receptor	531	11	47.8	19	2	PT0244	Ig heavy chain CDR
459	11	47.8	17	2	E40442	integrase homolog	532	11	47.8	19	2	PH1304	T-cell receptor be
460	11	47.8	17	2	S18534	hypothetical prote	533	11	47.8	19	2	G49048	Ig heavy chain DJ
461	11	47.8	17	2	B44923	carboxypeptidase 3	534	11	47.8	19	2	PH1307	Ig mu chain V regi
462	11	47.8	17	2	S19614	globin - polychaet	535	11	47.8	19	2	S43960	Ig kappa chain V r
463	11	47.8	17	2	S03533	Ig heavy chain J r	536	11	47.8	19	2	A28814	amyloid protein -
464	11	47.8	17	2	PT0234	Ig heavy chain CRD	537	11	47.8	19	2	I53673	genome polypotein
465	11	47.8	17	2	PT0235	Ig heavy chain CRD	538	11	47.8	19	2	B61409	beta-galactoside-b
466	11	47.8	17	2	PH1367	Ig heavy chain DJ	539	11	47.8	19	2	PX0062	
467	11	47.8	17	2	PH1331	Ig heavy chain DJ	540	11	47.8	19	2		

541	11	47.8	19	2	S02269	glycogen(starch) s	614	11	47.8	20	2	PH1358	Ig heavy chain DJ
542	11	47.8	19	2	B56613	virion morphogenes	615	11	47.8	20	2	PH1341	Ig heavy chain DJ
543	11	47.8	19	2	S63489	dissimilatory sulf	616	11	47.8	20	2	PH1326	Ig heavy chain DJ
544	11	47.8	19	2	T50329	wd-repeat protein	617	11	47.8	20	2	PC2248	lambda 112 protein
545	11	47.8	19	2	S60110	hypothetical prote	618	11	47.8	20	2	S60350	kallikrein, pankre
546	11	47.8	19	2	PH1352	Ig heavy chain DJ	619	11	47.8	20	2	S15861	estrogen receptor
547	11	47.8	19	2	PH1353	Ig heavy chain DJ	620	11	47.8	20	2	A38689	1-phosphatidylinos
548	11	47.8	19	2	PH1339	Ig heavy chain DJ	621	11	47.8	20	2	PQ0071	T-cell receptor be
549	11	47.8	19	2	PH1315	Ig heavy chain DJ	622	11	47.8	20	2	S56756	link protein - rat
550	11	47.8	19	2	PH1330	Ig heavy chain DJ	623	11	47.8	20	2	S68341	procathepsin L - g
551	11	47.8	19	2	S57515	T cell receptor be	624	11	47.8	20	2	S66222	defensin AMP2 - Da
552	11	47.8	19	2	S57516	T cell receptor be	625	11	47.8	20	2	C56894	intracrystalline c
553	11	47.8	19	2	S03519	T-cell receptor ga	626	11	47.8	20	2	D84716	hypothetical prote
554	11	47.8	19	2	I46654	T-cell receptor de	627	11	47.8	20	2	T44453	acetyl-CoA synthet
555	11	47.8	19	2	PH1624	Ig H chain V-D-J r	628	11	47.8	20	2	A44927	major outer membra
556	11	47.8	19	2	PH0793	T-cell receptor al	629	11	47.8	20	2	S45637	oxidoreductase - p
557	11	47.8	19	2	I49037	Tcr delta chain V-	630	11	47.8	20	2	S63490	dissimilatory sulf
558	11	47.8	19	2	B46592	lactase-phlorizin	631	11	47.8	20	2	A40451	dormancy-related p
559	11	47.8	19	2	A48354	nonstructural prot	632	11	47.8	20	2	S29636	jacalin beta-I cha
560	11	47.8	19	2	I40063	shikimate 5-dehydr	633	11	47.8	20	2	S29635	jacalin beta chain
561	11	47.8	19	2	A44854	L-2,4-diaminobutyr	634	11	47.8	20	2	S03987	agglutinin beta-2
562	11	47.8	19	2	S29212	protein C - oat (f	635	11	47.8	20	2	S35460	allin lyase (EC 4
563	11	47.8	19	2	S19532	globin - polychaet	636	11	47.8	20	2	PC2084	serine proteinase
564	11	47.8	19	2	S19613	globin - polychaet	637	11	47.8	20	2	S38763	S-adenosyl-L-mathi
565	11	47.8	19	2	JX0124	tachyplesin I prec	638	11	47.8	20	2	A34817	collagenolytic pro
566	11	47.8	19	2	I52721	gene hMLH1 protein	639	11	47.8	20	2	A56899	serum heterodimer,
567	11	47.8	19	2	S12268	Qa-2 antigen - mou	640	11	47.8	20	2	A47105	dystroglycan - Chi
568	11	47.8	19	2	A60505	hemoglobin C1 beta	641	11	47.8	20	2	A61506	alpha-1-antitrypsi
569	11	47.8	19	2	A58700	actagardine [valid	642	11	47.8	20	2	A56894	intracrystalline c
570	11	47.8	19	4	I54264	rhodopsin single b	643	11	47.8	20	2	B56894	intracrystalline c
571	11	47.8	20	2	A23739	cytochrome P450 MU	644	11	47.8	20	2	A85659	hypothetical prote
572	11	47.8	20	2	S21176	testosterone 6beta	645	11	47.8	20	2	AE0120	insertion element
573	11	47.8	20	2	A60728	cytochrome P450 3A	646	11	47.8	20	2	AC0269	probable trp opero
574	11	47.8	20	2	B61080	5-carboxymethyl-2-	647	11	47.8	20	2	B60505	hemoglobin A1-2 be
575	11	47.8	20	2	B37520	glutathione transf	648	11	47.8	20	2	S08605	hypothetical prote
576	11	47.8	20	2	S29099	glutathione transf	649	11	47.8	20	2	S27142	hypothetical prote
577	11	47.8	20	2	S29100	glutathione transf	650	11	47.8	20	2	DIRT	dental fluid tra
578	11	47.8	20	2	S71869	glutathione transf	651	8	34.8	12	2	A28856	fructose-bisphosph
579	11	47.8	20	2	S30381	glutathione transf	652	7	30.4	15	2	E41383	23K variable hist
580	11	47.8	20	2	PQ0751	self-incompatibili	653	7	30.4	20	2	I70108	microsomal triglyc
581	11	47.8	20	2	PH0111	style glycoprotein	654	6	26.1	3	3	S68328	blood cell protein
582	11	47.8	20	2	PH0110	style glycoprotein	655	6	26.1	4	1	ECXAA	antho-RFamide neur
583	11	47.8	20	2	PC2347	base nonspecific a	656	6	26.1	4	2	D41654	hypothetical prote
584	11	47.8	20	2	S33787	pancreatic elastas	657	6	26.1	4	2	S53508	starvation-induced
585	11	47.8	20	2	A56900	chymotrypsin I (EC	658	6	26.1	4	2	A25844	autho-RF amide neu
586	11	47.8	20	2	B61333	chymotrypsin (EC 3	659	6	26.1	4	2	S39390	myosin-light-chain
587	11	47.8	20	2	I49423	cytotoxic T-lympho	660	6	26.1	4	2	JQ1273	neuropeptide Antho
588	11	47.8	20	2	S46205	comosain (EC 3.4.2	661	6	26.1	4	2	A35779	neuropeptide Antho
589	11	47.8	20	2	S46204	ananain (EC 3.4.22	662	6	26.1	4	2	A60418	PMRFamide - polych
590	11	47.8	20	2	C54052	phosphoribosyl-AMP	663	6	26.1	4	2	A32480	achatin-I - giant
591	11	47.8	20	2	A37111	ribulose-bisphosph	664	6	26.1	4	2	ECNK	cardioexcitatory n
592	11	47.8	20	2	C49164	chromogranin-B - r	665	6	26.1	5	2	A44955	alkanal monooxygen
593	11	47.8	20	2	PT0248	Ig heavy chain CDR	666	6	26.1	5	2	S70615	endo-1,4-beta-xyla
594	11	47.8	20	2	F49048	T-cell receptor be	667	6	26.1	5	2	PS0324	ribulose-bisphosph
595	11	47.8	20	2	A49048	T-cell receptor be	668	6	26.1	5	2	B45525	actin I - malaria
596	11	47.8	20	2	PL0192	Ig lambda 2 chain	669	6	26.1	5	2	B61445	Leu-enkephalin - b
597	11	47.8	20	2	S39049	cytotoxin-binding	670	6	26.1	5	2	A61445	Met-enkephalin - b
598	11	47.8	20	2	B33761	actin - Acanthamo	671	6	26.1	5	2	B61168	cocoonase (EC 3.4.
599	11	47.8	20	2	A05313	apolipoprotein A-I	672	6	26.1	5	2	PT0278	Ig heavy chain CRD
600	11	47.8	20	2	A36045	thrombospondin hom	673	6	26.1	5	2	A44692	fulicin - giant Af
601	11	47.8	20	2	S03335	photosystem II pho	674	6	26.1	5	2	JS0319	subesophageal gang
602	11	47.8	20	2	PW0003	chlorophyll a/b-bi	675	6	26.1	5	2	PT0644	T-cell receptor be
603	11	47.8	20	2	S04988	gag core shell pro	676	6	26.1	5	4	A58728	serrawettin W2 - S
604	11	47.8	20	2	A44773	pollen allergen I	677	6	26.1	6	2	A61049	halo-toxin - Pseud
605	11	47.8	20	2	A60372	pollen allergen Po	678	6	26.1	6	2	A60986	N-formyl oligopept
606	11	47.8	20	2	D37396	pollen allergen Fe	679	6	26.1	6	2	S11024	hydrogensulfite re
607	11	47.8	20	2	I64036	hypothetical prote	680	6	26.1	6	2	I51317	bHLH transcription
608	11	47.8	20	2	T46626	hypothetical prote	681	6	26.1	6	2	I37263	Y protein - human
609	11	47.8	20	2	S16202	pyroline-5-carbox	682	6	26.1	6	2	I59142	platelet-derived g
610	11	47.8	20	2	D25507	proteinase inhibit	683	6	26.1	6	2	A41946	T-cell receptor ga
611	11	47.8	20	2	PC1152	equinatoxin 1D - s	684	6	26.1	6	2	A27696	contraction-inhibi
612	11	47.8	20	2	S10876	hypothetical prote	685	6	26.1	6	2	B27696	contraction-inhibi
613	11	47.8	20	2	S58382	hypothetical prote	686	6	26.1	6	2	A43129	neuropeptide GNPFR

687 6 26.1 7 1 NYPG7 hypothalamic hepta  
688 6 26.1 7 1 A61324 dermorphin - Rohde  
689 6 26.1 7 2 A60224 Met-enkephalin-Arg  
690 6 26.1 7 2 S36662 dermorphin (Lys-7)  
691 6 26.1 7 2 PH1408 Ig heavy chain V r  
692 6 26.1 7 2 B39127 phosphotransferase  
693 6 26.1 7 2 I40504 hypothetical prote  
694 6 26.1 7 2 H33038 180K exoantigen -  
695 6 26.1 7 2 S68004 hucolin, 75K chain  
696 6 26.1 7 2 E33932 Ig mu chain D regi  
697 6 26.1 7 2 PT0665 T-cell receptor be  
698 6 26.1 7 2 A59489 protein kinase C i  
699 6 26.1 7 2 B35890 RNA-directed DNA p  
700 6 26.1 7 2 A25269 sex pheromone cAM3  
701 6 26.1 7 2 A30812 sex pheromone cCF1  
702 6 26.1 7 2 S17976 glucose isomerase  
703 6 26.1 7 2 PC2132 FMRFamide-related  
704 6 26.1 7 2 B44787 calliFMRFamide 11  
705 6 26.1 7 2 S08606 hypothetical prote  
706 6 26.1 8 2 A32523 peptidyl-dipeptida  
707 6 26.1 8 2 PH1407 Ig heavy chain V r  
708 6 26.1 8 2 FL0184 capsid protein VP-  
709 6 26.1 8 2 PA0032 protein QA300040 -  
710 6 26.1 8 2 S13661 polygalacturonase  
711 6 26.1 8 2 B33099 158K exoantigen -  
712 6 26.1 8 2 A39892 P element, P cytot  
713 6 26.1 8 2 B45800 serum albumin - do  
714 6 26.1 8 2 A42057 fibroblast growth  
715 6 26.1 8 2 PH0803 T-cell receptor al  
716 6 26.1 8 2 PC4372 telomeric and tetr  
717 6 26.1 8 2 S66236 Na+-transporting A  
718 6 26.1 8 2 S37141 rpsA protein - Erw  
719 6 26.1 8 2 S21273 cellulase (EC 3.2.  
720 6 26.1 8 2 A37521 R-phycoerythrin ga  
721 6 26.1 8 2 S11078 glucose-6-phosphat  
722 6 26.1 8 2 PT0030 inulinase (EC 3.2.  
723 6 26.1 8 2 A46306 spasmogenic toxin  
724 6 26.1 8 2 A23967 leucopyrokinin - M  
725 6 26.1 8 2 S66646 cardioacceleratory  
726 6 26.1 8 2 B27867 homeotic protein U  
727 6 26.1 8 2 H41978 calliFMRFamide 8 -  
728 6 26.1 8 2 D47393 neuropeptide calla  
729 6 26.1 8 2 E47393 neuropeptide calla  
730 6 26.1 8 2 S71919 aspartate transami  
731 6 26.1 8 2 A14683 trypsin (EC 3.4.21  
732 6 26.1 8 2 A61328 thymic humoral fac  
733 6 26.1 8 2 A28719 cytochrome-c oxida  
734 6 26.1 8 2 S65381 telomeric and tetr  
735 6 26.1 8 2 PC4373 MHC class I histoc  
736 6 26.1 8 2 A59028 leghemoglobin III  
737 6 26.1 8 2 S20162 sperm-activating p  
738 6 26.1 8 2 F60588 neuropeptide B - b  
739 6 26.1 8 2 B24749 sperm-activating p  
740 6 26.1 8 2 E60588 sperm-activating p  
741 6 26.1 8 2 G60588 tumor-associated a  
742 6 26.1 8 2 S43972 tumor-associated a  
743 6 26.1 8 2 S43971 conopressin G - co  
744 6 26.1 9 2 A28495 calsequestrin, car  
745 6 26.1 9 2 A61230 fibrinogen beta ch  
746 6 26.1 9 2 D24180 fibrinogen beta ch  
747 6 26.1 9 2 C24180 fibrinogen beta B -  
748 6 26.1 9 2 E28854 fibrinopeptide B -  
749 6 26.1 9 2 F28854 fibrinopeptide B -  
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751 6 26.1 9 2 D58503 translation elonga  
752 6 26.1 9 2 S66607 quinoline 2-oxidor  
753 6 26.1 9 2 S63491 dissimilatory sulf  
754 6 26.1 9 2 S36898 ribosomal protein  
755 6 26.1 9 2 T31612 hypothetical prote  
756 6 26.1 9 2 S39766 cardioactive pepti  
757 6 26.1 9 2 S65433 bradykinin - horn  
758 6 26.1 9 2 PT0225 Ig heavy chain CDR  
759 6 26.1 9 2 PT0315 Ig heavy chain CRD

760 6 26.1 9 2 S36850 Ig heavy chain V r  
761 6 26.1 9 2 G41946 T-cell receptor ga  
762 6 26.1 9 2 A42266 peptidylglycine mo  
763 6 26.1 9 2 I52974 seminal vesicle pr  
764 6 26.1 9 2 S39767 cardioactive pepti  
765 6 26.1 9 2 S39040 lysine-conopressin  
766 6 26.1 9 2 S58502 kidney and bladder  
767 6 26.1 9 2 S19523 orf AB protein - S  
768 6 26.1 9 2 A31576 xylose isomerase (  
769 6 26.1 9 2 S13333 alpha/beta-gliadin  
770 6 26.1 9 2 PC2021 oxytocin-related p  
771 6 26.1 9 2 A26363 cardioactive pepti  
772 6 26.1 9 2 A61620 locustamyotropin I  
773 6 26.1 9 2 S27233 cardioactive pepti  
774 6 26.1 9 2 A41978 calliFMRFamide 1 -  
775 6 26.1 9 2 A44787 calliFMRFamide 10  
776 6 26.1 9 2 D44787 calliFMRFamide 13  
777 6 26.1 9 2 B41978 calliFMRFamide 2 -  
778 6 26.1 9 2 C41978 calliFMRFamide 3 -  
779 6 26.1 9 2 D41978 calliFMRFamide 4 -  
780 6 26.1 9 2 E41978 calliFMRFamide 5 -  
781 6 26.1 9 2 F41978 calliFMRFamide 6 -  
782 6 26.1 9 2 G41978 calliFMRFamide 7 -  
783 6 26.1 9 2 S10920 venom protein HR-3  
784 6 26.1 9 2 JN0027 [Phe-6]-mosact - s  
785 6 26.1 9 2 B20569 serum amyloid P-co  
786 6 26.1 9 2 S77984 cytochrome-c oxida  
787 6 26.1 9 2 PT0080 60K Ca binding pro  
788 6 26.1 9 2 A61386 macrophage inhibit  
789 6 26.1 9 2 B39504 octamer-binding pr  
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791 6 26.1 9 2 S10784 enamelin i - bovin  
792 6 26.1 9 2 A28924 fructose-bisphosph  
793 6 26.1 9 2 PD0443 3-oxoacid CoA-tran  
794 6 26.1 9 2 PC7074 translation elonga  
795 6 26.1 9 2 A43065 hydroxyproline-3-b  
796 6 26.1 9 2 PD0027 pev-tachykinin - p  
797 6 26.1 9 2 G85802 hypothetical prote  
798 6 26.1 9 2 S15850 vitamin D3 26-mono  
799 6 26.1 9 2 A26744 bradykinin-like pe  
800 6 26.1 9 2 A61057 Thr-6 bradykinin -  
801 6 26.1 9 2 A60579 bradykinin-like pe  
802 6 26.1 9 2 S19329 sperm-activating p  
803 6 26.1 9 2 B60246 ornitho-kinin - ch  
804 6 26.1 9 2 A61363 bradykinin - commo  
805 6 26.1 9 2 A61358 bradykinin-like pe  
806 6 26.1 10 1 ECLQ1M tachykinin I - mig  
807 6 26.1 10 1 ECLQ3M tachykinin III - m  
808 6 26.1 10 1 ECLQ4M tachykinin IV - mi  
809 6 26.1 10 1 SPPGNK neuromedin K - pig  
810 6 26.1 10 1 GMR0L2 leucosulfakinin-II  
811 6 26.1 10 2 S28055 cytochrome b559 co  
812 6 26.1 10 2 S15118 dihydrofolate redu  
813 6 26.1 10 2 S39392 calpain (EC 3.4.22  
814 6 26.1 10 2 A60624 angiotensin I - Ja  
815 6 26.1 10 2 A60410 angiotensin I - beta-neoendorphin  
816 6 26.1 10 2 JN0024 neurokinin A - chi  
817 6 26.1 10 2 S39374 mannose receptor -  
818 6 26.1 10 2 A61617 ecdysteroid UDPglu  
819 6 26.1 10 2 S66458 ferredoxin - Rhizo  
820 6 26.1 10 2 S70721 heat shock protein  
821 6 26.1 10 2 S48182 bacterioferritin -  
822 6 26.1 10 2 H28027 protein P11 - curl  
823 6 26.1 10 2 C61440 polygalacturonase  
824 6 26.1 10 2 S65432 angiotensin I - ho  
825 6 26.1 10 2 PT0230 Ig heavy chain CDR  
826 6 26.1 10 2 PT0251 Ig heavy chain CRD  
827 6 26.1 10 2 PT0284 Ig heavy chain CRD  
828 6 26.1 10 2 B45482 platelet activatin  
829 6 26.1 10 2 S23371 T-cell receptor al  
830 6 26.1 10 2 S66214 cartilage oligomer  
831 6 26.1 10 2 S71948 matrix metalloprot  
832 6 26.1 10 2 C39398 Fc mu (IgM) recept



833	6	26.1	10	2	A37268	Ig heavy chain C r	906	6	26.1	10	2	I60588	sperm-activating p
834	6	26.1	10	2	S36849	Ig heavy chain V r	907	6	26.1	10	2	B60589	sperm-activating p
835	6	26.1	10	2	PH0807	T-cell receptor al	908	6	26.1	10	2	C61033	ranatachykinin C -
836	6	26.1	10	2	PT0215	T-cell receptor be	909	6	26.1	10	2	B61033	ranatachykinin B -
837	6	26.1	10	2	S65385	cytochrome-c oxida	910	6	26.1	10	2	S27178	neurokinin A-relat
838	6	26.1	10	2	S68033	cytochrome P450 1A	911	6	26.1	10	2	A32543	cardioexcitatory n
839	6	26.1	10	2	D37397	hypothetical prote	912	6	26.1	10	4	S14943	UGA3 leader peptid
840	6	26.1	10	2	B46453	e antigen p20e pre	913	6	26.1	11	1	ECLQ2M	tachykinin II - mi
841	6	26.1	10	2	G58501	48K bile/gallblad	914	6	26.1	11	1	A60654	substance P - guin
842	6	26.1	10	2	I39702	nopaline synthase	915	6	26.1	11	1	EOOC	eledoisin - musky
843	6	26.1	10	2	S06964	hypothetical prote	916	6	26.1	11	1	EOCC	eledoisin - curled
844	6	26.1	10	2	S18396	probable glucose-6	917	6	26.1	11	1	SPHO	substance P - hors
845	6	26.1	10	2	S70251	nitrogenase (EC 1.	918	6	26.1	11	1	GMROL	leucosulfakinin -
846	6	26.1	10	2	I40032	trpE protein - Bac	919	6	26.1	11	1	G42762	proteasome endopep
847	6	26.1	10	2	A60476	S-layer protein -	920	6	26.1	11	2	A33917	dihydroorotase (EC
848	6	26.1	10	2	I44644	neurotoxin-associa	921	6	26.1	11	2	JN0023	substance P - chic
849	6	26.1	10	2	A39745	endo-glucosylceram	922	6	26.1	11	2	A38841	rhodopsin homolog
850	6	26.1	10	2	PC2044	beta-Kirilowin - M	923	6	26.1	11	2	D58502	27K bile and gallb
851	6	26.1	10	2	B59272	peptide-N4-(N-acet	924	6	26.1	11	2	A58502	38K kidney stone p
852	6	26.1	10	2	S38304	lectin GNL1 alpha	925	6	26.1	11	2	S33782	acetolactate synth
853	6	26.1	10	2	S38305	lectin GNL2 alpha	926	6	26.1	11	2	E60691	phycobilisome 8K 1
854	6	26.1	10	2	D28027	protein P7 - curle	927	6	26.1	11	2	D60691	phycobilisome 9K 1
855	6	26.1	10	2	B61440	polygalacturonase	928	6	26.1	11	2	PC2372	58K heat shock pro
856	6	26.1	10	2	D61440	polygalacturonase	929	6	26.1	11	2	B41835	translation elonga
857	6	26.1	10	2	PN0165	triose-phosphate i	930	6	26.1	11	2	S19301	endo-1,4-beta-xyla
858	6	26.1	10	2	A58365	neuropeptide FFRFa	931	6	26.1	11	2	PA0028	protein QA300042 -
859	6	26.1	10	2	B60656	leucosulfakinin II	932	6	26.1	11	2	T06383	hypothetical prote
860	6	26.1	10	2	A43977	FMRFamide-like pro	933	6	26.1	11	2	PU0029	33K protein 3218 -
861	6	26.1	10	2	C44787	calliFMRFamide 12	934	6	26.1	11	2	S78026	ribosomal protein
862	6	26.1	10	2	A56633	neomysuppressin -	935	6	26.1	11	2	I33098	173K exoantigen -
863	6	26.1	10	2	D46285	formaldehyde dehyd	936	6	26.1	11	2	B60769	Ig H2 chain - Paci
864	6	26.1	10	2	A30823	bothropstoxin - ja	937	6	26.1	11	2	I52980	glucocerebrosidase
865	6	26.1	10	2	A90917	angiotensin precur	938	6	26.1	11	2	PT0250	Ig heavy chain CRD
866	6	26.1	10	2	A90345	angiotensin precur	939	6	26.1	11	2	PT0287	Ig heavy chain CRD
867	6	26.1	10	2	S65387	cytochrome-c oxida	940	6	26.1	11	2	S57575	T cell receptor V-
868	6	26.1	10	2	T13838	cytochrome-c oxida	941	6	26.1	11	2	S23364	T-cell receptor al
869	6	26.1	10	2	A44871	monodehydroascorba	942	6	26.1	11	2	S23373	T-cell receptor al
870	6	26.1	10	2	S74147	glyceraldehyde-3-p	943	6	26.1	11	2	S51732	T-cell receptor al
871	6	26.1	10	2	B33710	ornithine decarbox	944	6	26.1	11	2	A54348	N-acetylglucosamin
872	6	26.1	10	2	A60527	sperm-activating p	945	6	26.1	11	2	PD0442	NIPSNAP2 protein -
873	6	26.1	10	2	B49581	sialokinin II - ye	946	6	26.1	11	2	PH1376	T antigen variant
874	6	26.1	10	2	A49581	sialokinin I - yel	947	6	26.1	11	2	PT0214	T-cell receptor be
875	6	26.1	10	2	H60787	sperm-activating p	948	6	26.1	11	2	I60434	68kDa neurofilamen
876	6	26.1	10	2	G60787	sperm-activating p	949	6	26.1	11	2	S53436	beta-D-galactosida
877	6	26.1	10	2	F60787	sperm-activating p	950	6	26.1	11	2	PH0906	T-cell receptor be
878	6	26.1	10	2	E60787	sperm-activating p	951	6	26.1	11	2	C58501	42K bile stone pro
879	6	26.1	10	2	C60787	sperm-activating p	952	6	26.1	11	2	S58244	pyrroloquinoline g
880	6	26.1	10	2	A60787	sperm-activating p	953	6	26.1	11	2	S35490	type II site-speci
881	6	26.1	10	2	D60787	sperm-activating p	954	6	26.1	11	2	B39853	LuxC protein - Pho
882	6	26.1	10	2	B60787	sperm-activating p	955	6	26.1	11	2	PC2330	cycloinulooligosac
883	6	26.1	10	2	D60588	sperm-activating p	956	6	26.1	11	2	A44755	20alpha-hydroxyste
884	6	26.1	10	2	B60588	sperm-activating p	957	6	26.1	11	2	A35594	buccalin - Califor
885	6	26.1	10	2	C60588	sperm-activating p	958	6	26.1	11	2	S69349	neuropeptide Ffami
886	6	26.1	10	2	I60527	sperm-activating p	959	6	26.1	11	2	A60656	perisulfakinin - A
887	6	26.1	10	2	A60588	sperm-activating p	960	6	26.1	11	2	I41978	calliFMRFamide 9 -
888	6	26.1	10	2	A60788	sperm-activating p	961	6	26.1	11	2	S33300	probable substance
889	6	26.1	10	2	D60527	sperm-activating p	962	6	26.1	11	2	D42965	talain - chicken (f
890	6	26.1	10	2	C39572	sperm-activating p	963	6	26.1	11	2	E57789	gallbladder stone
891	6	26.1	10	2	F60527	sperm-activating p	964	6	26.1	11	2	S13279	Ile-Ser-bradykinin
892	6	26.1	10	2	C60527	sperm-activating p	965	6	26.1	11	2	A32428	amine oxidase (cop
893	6	26.1	10	2	E60527	sperm-activating p	966	6	26.1	11	2	PN0042	stathmin - mouse (
894	6	26.1	10	2	G60527	sperm-activating p	967	6	26.1	11	2	A48973	glucoamylase A1 (E
895	6	26.1	10	2	E39572	sperm-activating p	968	6	26.1	11	2	S09074	cytochrome P450-4b
896	6	26.1	10	2	D60788	sperm-activating p	969	6	26.1	11	2	A57458	gene Gax protein -
897	6	26.1	10	2	E60788	sperm-activating p	970	6	26.1	11	2	S07203	uperolein - frog (
898	6	26.1	10	2	C60788	sperm-activating p	971	6	26.1	11	2	B26744	megascoliakinin -
899	6	26.1	10	2	A24867	scyllorhinin I - s	972	6	26.1	11	2	C60409	kassinin-like pept
900	6	26.1	10	2	S23307	neurokinin A - rai	973	6	26.1	11	2	E60409	substance P-like p
901	6	26.1	10	2	S23186	neurokinin A - Atl	974	6	26.1	11	2	B60409	kassinin-like pept
902	6	26.1	10	2	S07202	phylomedulin - tw	975	6	26.1	11	2	F60409	substance P-like p
903	6	26.1	10	2	F60589	sperm-activating p	976	6	26.1	11	2	D60409	kassinin-like pept
904	6	26.1	10	2	C60589	sperm-activating p	977	6	26.1	11	2	YHHU	morphogenetic neur
905	6	26.1	10	2	D60589	sperm-activating p	978	6	26.1	11	2	YHBO	morphogenetic neur

979 6 26.1 11 2 YHJFYH morphogenetic neur  
980 6 26.1 11 2 YHXAE morphogenetic neur  
981 6 26.1 11 2 S23308 substance P - rain  
982 6 26.1 11 2 S23306  
983 6 26.1 11 2 S07207 Crinia-angiotensin  
984 6 26.1 11 2 S07201 physalaemin - frog  
985 6 26.1 11 2 A61365 phyllokinin - Rohd  
986 6 26.1 11 2 A61033 ranatachykinin A -  
987 6 26.1 11 2 D61033 ranatachykinin D -  
988 6 26.1 11 2 YHRT morphogenetic neur  
989 6 26.1 11 4 S41909 hypothetical prote  
990 6 26.1 11 4 PC2124 aminotransferase C  
991 6 26.1 11 4 S52252 hypothetical prote  
992 6 26.1 12 1 A43975 locustamyotropin -  
993 6 26.1 12 1 LFCEDE pyrE leader peptid  
994 6 26.1 12 2 S17869 glutathione transf  
995 6 26.1 12 2 C36201 l-aminocyclopropan  
996 6 26.1 12 2 A61309 glycoprotein hormo  
997 6 26.1 12 2 S26552 T-cell receptor be  
998 6 26.1 12 2 S26549 T-cell receptor be  
999 6 26.1 12 2 S26544  
1000 6 26.1 12 2 S25056 Ig heavy chain - m

## ALIGNMENTS

## RESULT 1

A24244  
adipokinetic hormone - bollworm  
N;Alternate names: Hez-AKH  
C;Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)  
C;Date: 31-Mar-1988 #sequence\_revision 23-Mar-1995 #text\_change 09-Jul-2004  
C;Accession: A24244  
R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway  
Biochem. Biophys. Res. Commun. 135, 622-628, 1986  
A;Title: Isolation and primary structure of a peptide from the corpora cardiaca of Helio  
A;Reference number: A24244; MUID:86186794; PMID:3964263  
A;Accession: A24244  
A;Molecule type: protein  
A;Residues: 1-9 <JAF>  
A;Cross-references: UNIPROT:P08901  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 73.9%; Score 17; DB 2; Length 9;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
| |  
Db 4 FTSSW 8

## RESULT 2

A28004  
adipokinetic hormone G - two-spotted cricket  
N;Alternate names: AKH-G  
C;Species: Gryllus bimaculatus (two-spotted cricket)  
C;Date: 30-Jun-1989 #sequence\_revision 24-Oct-1997 #text\_change 09-Jul-2004  
C;Accession: A28004  
R;Gaede, G.; Rinehart, K.L.  
Biochem. Biophys. Res. Commun. 149, 908-914, 1987  
A;Title: Primary sequence analysis by fast atom bombardment mass spectrometry of a pepti  
A;Reference number: A28004; MUID:88106553; PMID:3426616  
A;Accession: A28004  
A;Molecule type: protein  
A;Residues: 1-8 <GAE>  
A;Cross-references: UNIPROT:P14086  
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 69.6%; Score 16; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
| |  
Db 4 FSTGW 8

## RESULT 3

A31571  
hypertrehalosemic/adipokinetic hormone - bollworm  
N;Alternate names: Hez-HrTH  
C;Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)  
C;Date: 30-Jun-1989 #sequence\_revision 23-Mar-1995 #text\_change 09-Jul-2004  
C;Accession: A31571  
R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Bird, T.G.; Tseng, C.M.; Zhang, Y.S.  
Biochem. Biophys. Res. Commun. 155, 344-350, 1988  
A;Title: Isolation and primary structure of a neuropeptide hormone from Heliothis zea wit  
A;Reference number: A31571; MUID:88326324; PMID:3415690  
A;Accession: A31571  
A;Molecule type: protein  
A;Residues: 1-10 <JAF>  
A;Cross-references: UNIPROT:P16353  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;10/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 69.6%; Score 16; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 6.3e+02;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
| |  
Db 4 FSSGW 8

## RESULT 4

S10596  
adipokinetic hormone - pond skimmer  
C;Species: Libellula auripennis  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C;Accession: S10596  
R;Gaede, G.  
Biol. Chem. Hoppe-Seyler 371, 475-483, 1990  
A;Title: The putative ancestral peptide of the adipokinetic/red-pigment-concentrating hor  
A;Reference number: S10596; MUID:90359055; PMID:2390213  
A;Accession: S10596  
A;Molecule type: protein  
A;Residues: 1-8 <BIO>  
A;Cross-references: UNIPROT:P25418  
C;Comment: This peptide has both adipokinetic and hypertrehalosemic activities.  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 65.2%; Score 15; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
| |  
Db 4 FTPSW 8

## RESULT 5

D57444

neuropeptide Grb-AST B4 - two-spotted cricket  
C;Species: Gryllus bimaculatus (two-spotted cricket)  
C;Date: 26-Jan-1996 #sequence\_revision 26-Jan-1996 #text\_change 09-Jul-2004  
C;Accession: D57444  
R;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.  
J. Biol. Chem. 270, 21103-21108, 1995  
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cr  
A;Reference number: A57444; MUID:95403341; PMID:7673141  
A;Accession: D57444  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-9 <LOR>  
A;Cross-references: UNIPROT:Q7M3N6

Query Match 65.2%; Score 15; DB 2; Length 9;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5  
|  
Db 5 FHGSW 9

RESULT 6  
T17063  
cytochrome-c oxidase (EC 1.9.3.1) chain I - Hoplocercus spinosus mitochondrion (fragment  
C;Species: mitochondrion Hoplocercus spinosus  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T17063  
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.  
J. Mol. Evol. 44, 660-674, 1997  
A;Title: Evolutionary shifts in three major structural features of the mitochondrial gen  
A;Reference number: Z18674; MUID:97315309; PMID:9169559  
A;Accession: T17063  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-10 <MAC>  
A;Cross-references: UNIPROT:Q79897; EMBL:U82683; NID:g3603124; PID:g3603127; PIDN:AAC622  
C;Genetics:  
A;Genome: mitochondrion  
A;Note: COI  
C;Keywords: mitochondrion; oxidoreductase

Query Match 65.2%; Score 15; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 1.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5  
|  
Db 2 FISRW 6

RESULT 7  
T12325  
cytochrome-c oxidase (EC 1.9.3.1) chain I - Leliocephalus carinatus mitochondrion (fragme  
C;Species: mitochondrion Leliocephalus carinatus  
C;Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 09-Jul-2004  
C;Accession: T12325  
R;Schulte, J.A.; Macey, J.R.; Larson, A.; Papenfuss, T.J.  
Mol. Phylogenet. Evol. 10, 367-376, 1998  
A;Title: Molecular tests of phylogenetic taxonomies: A general procedure and example usi  
A;Reference number: Z17488; MUID:99162288; PMID:10051389  
A;Accession: T12325  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-10 <SCH>  
A;Cross-references: UNIPROT:Q9ZYT2; EMBL:AF049864; NID:g4105754; PID:g4105757; PIDN:AAD0  
C;Genetics:  
A;Genome: mitochondrion  
A;Note: COI  
C;Keywords: mitochondrion; oxidoreductase

Query Match 65.2%; Score 15; DB 2; Length 10;

Best Local Similarity 40.0%; Pred. No. 1.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5  
|  
Db 2 FITRW 6

RESULT 8  
S53789  
neuropeptide Pec-HrTH - Platyleura capensis  
C;Species: Platyleura capensis  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C;Accession: S53789  
R;Gaede, G.; Janssens, M.P.E.  
Biol. Chem. Hoppe-Seyler 375, 803-809, 1994  
A;Title: Cicadas contain novel members of the AKH/RPCH family peptides with hypertrehalo  
A;Reference number: S53789; MUID:95225985; PMID:7710694  
A;Accession: S53789  
A;Molecule type: protein  
A;Residues: 1-10 <GAE>  
A;Cross-references: UNIPROT:Q7M465  
C;Keywords: blocked amino end; blocked carboxyl end

Query Match 65.2%; Score 15; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 1.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5  
|  
Db 4 FSPSW 8

RESULT 9  
PH1613  
Ig H chain V-D-J region (clone B-less 17) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C;Accession: PH1613  
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
A;Reference number: PH1580; MUID:93301609; PMID:8315387  
A;Accession: PH1613  
A;Molecule type: DNA  
A;Residues: 1-15 <LEV>  
A;Experimental source: bone marrow pre-B lymphocyte  
C;Keywords: immunoglobulin

Query Match 65.2%; Score 15; DB 2; Length 15;  
Best Local Similarity 40.0%; Pred. No. 1.5e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5  
|  
Db 10 FTMLW 14

RESULT 10  
A34704  
protein-tyrosine kinase (EC 2.7.1.112) 1, neuron-specific - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 06-Jul-1990 #sequence\_revision 06-Jul-1990 #text\_change 09-Jul-2004  
C;Accession: A34704  
R;Pyper, J.M.; Bolen, J.B.  
Mol. Cell. Biol. 10, 2035-2040, 1990  
A;Title: Identification of a novel neuronal C-SRC exon expressed in human brain.  
A;Reference number: A34704; MUID:90220588; PMID:1691439  
A;Accession: A34704  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-17 <PYP>  
A;Cross-references: UNIPROT:Q14925

C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

Query Match 65.2%; Score 15; DB 2; Length 17;  
Best Local Similarity 40.0%; Pred. No. 1.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 10 FTRFW 14

## RESULT 11

S77981

cytochrome-c oxidase (EC 1.9.3.1) chain Va.1 - bigeye tuna (fragment)

C;Species: Thunnus obesus (bigeye tuna)

C;Date: 17-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004

C;Accession: S77981

R;Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.

submitted to the Protein Sequence Database, June 1997

A;Reference number: S77980

A;Accession: S77981

A;Molecule type: protein

A;Residues: 1-20 <ARN>

A;Cross-references: UNIPROT:P80972

A;Experimental source: heart; liver

C;Genetics:

A;Genome: nuclear

C;Function:

A;Pathway: oxidative phosphorylation; respiratory chain

C;Superfamily: mammalian cytochrome-c oxidase chain Va

C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 65.2%; Score 15; DB 2; Length 20;  
Best Local Similarity 40.0%; Pred. No. 1.9e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 11 FDRW 15

## RESULT 12

PN0171

peptidylprolyl isomerase (EC 5.2.1.8) b, cytosolic - fungus (Fusarium sporotrichioides)

N;Contains: cyclophilin

C;Species: Fusarium sporotrichioides

C;Date: 05-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 02-Sep-2000

C;Accession: PN0171

R;Fukaya, N.; Chow, L.P.; Sugitara, Y.; Taugita, A.; Ueno, Y.; Tabuchi, K.

submitted to JIPID, May 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides

A;Reference number: PN0160

A;Accession: PN0171

A;Molecule type: protein

A;Residues: 1-20 <PUK>

A;Experimental source: strain M-1-1

C;Superfamily: peptidylprolyl isomerase; cyclophilin homology

C;Keywords: cis-trans-isomerase; cyclosporin A binding; cytosol

Query Match 65.2%; Score 15; DB 2; Length 20;  
Best Local Similarity 40.0%; Pred. No. 1.9e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 6 FDIW 10

## RESULT 13

PH1380

alpha-amylase (EC 3.2.1.1) (Haim sensitive) - Bacillus sp. (fragment)

C;Species: Bacillus sp.

C;Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 09-Jul-2004

C;Accession: PH1380

R;Kawaguchi, T.; Nagae, H.; Murao, S.; Arai, M.

Biosci. Biotechnol. Biochem. 56, 1792-1796, 1992

A;Title: Purification and some properties of a Haim-sensitive alpha-amylase from newly isolated

A;Reference number: PH1380; MUID:93113087; PMID:1369074

A;Accession: PH1380

A;Molecule type: protein

A;Residues: 1-20 <KAW>

A;Cross-references: UNIPROT:Q9R5E8

A;Experimental source: strain N0.195

C;Comment: This enzyme has an optimum pH of 7.0.

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 65.2%; Score 15; DB 2; Length 20;  
Best Local Similarity 40.0%; Pred. No. 1.9e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 13 PSWTW 17

## RESULT 14

A33995

adipokinetin hormone - black horse fly

C;Species: Tabanus atratus (black horse fly)

C;Date: 23-Mar-1990 #sequence\_revision 23-Mar-1990 #text\_change 09-Jul-2004

C;Accession: A33995

R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang, Y.

Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989

A;Title: Primary structure of two neurotrophic hormones with adipokinetin and hypotrehalose

A;Reference number: A33995; MUID:90046758; PMID:2813385

A;Accession: A33995

A;Molecule type: protein

A;Residues: 1-8 <JAF>

A;Cross-references: UNIPROT:P14595

C;Superfamily: adipokinetin hormone

C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neurotrophic; pyroglutamic

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted

F;8/Modified site: amidated carboxyl end (Trp) #status predicted

Query Match 60.9%; Score 14; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 4 FTGWM 8

## RESULT 15

A44960

neurotrophic peptide Led-CC-I - Colorado potato beetle

C;Species: Leptinotarsa decemlineata (Colorado potato beetle)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004

C;Accession: A44960

R;Gaede, G.; Kellner, R.

Peptides 10, 1287-1289, 1989

A;Title: The metabolic neurotrophic peptides of the corpus cardiacum from the potato beetle and

A;Reference number: A44960; MUID:90160053; PMID:2576128

A;Accession: A44960

A;Molecule type: protein

A;Residues: 1-8 <GAE>

A;Cross-references: UNIPROT:P04548

C;Superfamily: adipokinetin hormone

C;Keywords: blocked carboxyl end; corpora cardiaca; hormone; neurotrophic; pyroglutamic

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 8;

Best Local Similarity 40.0%; Pred. No. 2.8e+05; Mismatches 3; Indels 0; Gaps 0;  
Matches 2; Conservative 0;

QY 1 FXXW 5  
|  
Db 4 FSPW 8

## RESULT 16

B44960  
neuropeptide Led-CC-II - Colorado potato beetle  
C;Species: Leptinotarsa decemlineata (Colorado potato beetle)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C;Accession: B44960  
R;Gaede, G.; Kellner, R.  
Peptides 10, 1287-1289, 1989  
A;Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle and  
A;Reference number: A44960; MUID:90160053; PMID:2576128  
A;Accession: B44960

A;Molecule type: protein

A;Residues: 1-8 <GAE>

A;Cross-references: UNIPROT:P04549

C;Superfamily: adipokinetic hormone

C;Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 8;

Best Local Similarity 40.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5  
|  
Db 4 FTPW 8

## RESULT 17

A58620  
adipokinetic hormone - damselfly (Ischnura senegalensis)  
C;Species: Ischnura senegalensis  
C;Date: 28-Oct-1997 #sequence\_revision 31-Oct-1997 #text\_change 09-Jul-2004  
C;Accession: A58620  
R;Janssens, M.P.E.; Kellner, R.; Gaede, G.  
Biochem. J. 302, 539-543, 1994

A;Title: A novel adipokinetic octapeptide found in the damselflies Pseudagrion inconspic  
A;Reference number: S55310; MUID:94379987; PMID:8093008

A;Accession: A58620

A;Molecule type: protein

A;Residues: 1-8 <JAN>

A;Cross-references: UNIPROT:Q7M4H6

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 8;

Best Local Similarity 40.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5  
|  
Db 4 FTPW 8

## RESULT 18

S11545  
adipokinetic hormone - nestling-sucking blowfly  
C;Species: Protophormia terraenovae (nestling-sucking blowfly)  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
C;Accession: S11545  
R;Gaede, G.; Wilps, H.; Kellner, R.  
Biochem. J. 269, 309-313, 1990

A;Title: Isolation and structure of a novel charged member of the red-pigment-concentrat

erraenovae (Diptera).

A;Reference number: S11545; MUID:90351345; PMID:2386478

A;Accession: S11545

A;Molecule type: protein

A;Residues: 1-8 <GAE>

A;Cross-references: UNIPROT:P61856

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 8;

Best Local Similarity 40.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5  
|  
Db 4 FSPW 8

## RESULT 19

S55310

adipokinetic hormone - damselfly (Pseudagrion inconspicuum)

N;Alternate names: Psi-AKH

C;Species: Pseudagrion inconspicuum

C;Date: 19-Mar-1997 #sequence\_revision 31-Oct-1997 #text\_change 09-Jul-2004

C;Accession: S55310

R;Janssens, M.P.E.; Kellner, R.; Gaede, G.

Biochem. J. 302, 539-543, 1994

A;Title: A novel adipokinetic octapeptide found in the damselflies Pseudagrion inconspic

A;Reference number: S55310; MUID:94379987; PMID:8093008

A;Accession: S55310

A;Molecule type: protein

A;Residues: 1-8 <JAN>

A;Cross-references: UNIPROT:Q7M4H7

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 8;

Best Local Similarity 40.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5  
|  
Db 4 FTPW 8

## RESULT 20

A61348

red pigment-concentrating hormone - northern shrimp

N;Alternate names: blanching hormone

C;Species: Pandalus borealis (northern shrimp)

C;Date: 02-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 09-Jul-2004

C;Accession: A61348; S07139

R;Fornlund, P.; Josefsson, L.

Science 177, 173-175, 1972

A;Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.

A;Reference number: A61348; MUID:72228738; PMID:5041363

A;Accession: A61348

A;Molecule type: protein

A;Residues: 1-8 <FER1>

A;Cross-references: UNIPROT:P08939

R;Fornlund, P.

Biochim. Biophys. Acta 371, 304-311, 1974

A;Title: Structure of the red-pigment-concentrating hormone of the shrimp, Pandalus bore

A;Reference number: S07139; MUID:75054965; PMID:4433569

A;Accession: S07139

A;Molecule type: protein

A;Residues: 'E', 2-8 <FER2>

A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have

C;Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in pi

zed pigment-containing cells.  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutamic  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 4 FSPGW 8

RESULT 21  
S08995  
hypertrehalosemic hormone I - oriental cockroach  
N;Alternate names: Pea-CAH-I  
C;Species: Blatta orientalis (oriental cockroach)  
C;Date: 30-Jun-1992 #sequence\_revision 24-Oct-1997 #text\_change 09-Jul-2004  
C;Accession: S08995  
R;Gaede, G.; Rinehart, K.L.  
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990  
A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora  
entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard  
A;Reference number: S08995; MUID:90253659; PMID:2340112  
A;Accession: S08995  
A;Molecule type: protein  
A;Residues: 1-8 <GAE>  
A;Cross-references: UNIPROT:P04548  
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 4 FSPNW 8

RESULT 22  
S08996  
hypertrehalosemic hormone II - oriental cockroach  
N;Alternate names: Pea-CAH-II  
C;Species: Blatta orientalis (oriental cockroach)  
C;Date: 30-Jun-1992 #sequence\_revision 24-Oct-1997 #text\_change 09-Jul-2004  
C;Accession: S08996  
R;Gaede, G.; Rinehart, K.L.  
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990  
A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora  
entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard  
A;Reference number: S08995; MUID:90253659; PMID:2340112  
A;Accession: S08996  
A;Molecule type: protein  
A;Residues: 1-8 <GAE>  
A;Cross-references: UNIPROT:P04549  
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 4 FSPNW 8

Db 4 FTPNW 8  
|

RESULT 23  
A49823  
adipokinetic hormone I - American cockroach  
N;Alternate names: periplanetin CC-1  
C;Species: Periplaneta americana (American cockroach)  
C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 09-Jul-2004  
C;Accession: A49823  
R;Scarborough, R.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller, C.J.  
Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984  
A;Title: Isolation and primary structure of two peptides with cardioacceleratory and hyp  
A;Reference number: A49823; MUID:84298179; PMID:6591205  
A;Accession: A49823  
A;Molecule type: protein  
A;Residues: 1-8 <SCA>  
A;Cross-references: UNIPROT:P04548  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 4 FSPNW 8

RESULT 24  
B49823  
adipokinetic hormone II - American cockroach  
N;Alternate names: neuropeptide M-II; periplanetin CC-1  
C;Species: Periplaneta americana (American cockroach)  
C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 09-Jul-2004  
C;Accession: B49823; A05170  
R;Scarborough, R.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller, C.J.  
Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984  
A;Title: Isolation and primary structure of two peptides with cardioacceleratory and hyp  
A;Reference number: A49823; MUID:84298179; PMID:6591205  
A;Accession: B49823  
A;Molecule type: protein  
A;Residues: 1-8 <SCA>  
A;Cross-references: UNIPROT:P04549  
R;Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.L.  
Biochem. Biophys. Res. Commun. 124, 350-358, 1984  
A;Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mass  
A;Reference number: A90118; MUID:85046530; PMID:6548628  
A;Accession: A05170  
A;Molecule type: protein  
A;Residues: 'E', 2-8 <WIT>  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 4 FTPNW 8

RESULT 25  
A43976  
hypertrehalosemic hormone - yellow mealworm  
C;Species: Tenebrio molitor (yellow mealworm)



C;Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 09-Jul-2004  
C;Accession: A43976  
R;Gaede, G.; Rosinski, G.  
Peptides 11, 455-459, 1990  
A;Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid beetle  
A;Reference number: A43976; MUID:90341081; PMID:2381871  
A;Accession: A43976  
A;Molecule type: protein  
A;Residues: 1-8 <GAE>  
A;Cross-references: UNIPROT:P25419  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5  
|  
Db 4 FSPNW 8

RESULT 26  
B43976  
hypertrehalosemic hormone - beetle (Zophobas rugipes)  
C;Species: Zophobas rugipes  
C;Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 09-Jul-2004  
C;Accession: B43976  
R;Gaede, G.; Rosinski, G.  
Peptides 11, 455-459, 1990  
A;Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid beetle  
A;Reference number: A43976; MUID:90341081; PMID:2381871  
A;Accession: B43976  
A;Molecule type: protein  
A;Residues: 1-8 <GAE>  
A;Cross-references: UNIPROT:P25419  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5  
|  
Db 4 FSPNW 8

RESULT 27  
A05169  
neuropeptide M-I - American cockroach  
C;Species: Periplaneta americana (American cockroach)  
C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 09-Jul-2004  
C;Accession: A05169  
R;Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.I.  
Biochem. Biophys. Res. Commun. 124, 350-358, 1984  
A;Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mass spectrometry  
A;Reference number: A90118; MUID:85046530; PMID:6548628  
A;Accession: A05169  
A;Molecule type: protein  
A;Residues: 1-8 <WIT>  
A;Cross-references: UNIPROT:P04548  
C;Keywords: neuropeptide

Query Match 60.9%; Score 14; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5  
|  
Db 4 FSPNW 8

Db 4 FSPNW 8

RESULT 28  
B33995  
hypertrehalosemic hormone - black horse fly  
C;Species: Tabanus atratus (black horse fly)  
C;Date: 23-Mar-1990 #sequence\_revision 23-Mar-1990 #text\_change 09-Jul-2004  
C;Accession: B33995  
R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang, Y.  
Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989  
A;Title: Primary structure of two neuropeptide hormones with adipokinetic and hypotrehalosemic activities  
A;Reference number: A33995; MUID:90046758; PMID:2813385  
A;Accession: B33995  
A;Molecule type: protein  
A;Residues: 1-10 <JAF>  
A;Cross-references: UNIPROT:P14596  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted  
F;10/Modified site: amidated carboxyl end (Tyr) #status predicted

Query Match 60.9%; Score 14; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5  
|  
Db 4 FTPGW 8

RESULT 29  
S08997  
hypertrehalosemic neuropeptide Bld-HrTH - cockroach (Gromphadorina portentosa)  
C;Species: Gromphadorina portentosa  
C;Date: 30-Jun-1992 #sequence\_revision 14-Sep-1994 #text\_change 09-Jul-2004  
C;Accession: S08997  
R;Gaede, G.; Rinehart, K.L.  
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990  
A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpora cardiaca and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry  
A;Reference number: S08995; MUID:90253659; PMID:2340112  
A;Accession: S08997  
A;Molecule type: protein  
A;Residues: 1-10 <GAE>  
A;Cross-references: UNIPROT:P10939  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5  
|  
Db 4 FSPGW 8

RESULT 30  
A60421  
hypertrehalosemic hormone - German cockroach  
N;Alternate names: Bld-HrTH  
C;Species: Blattella germanica (German cockroach)  
C;Date: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 09-Jul-2004  
C;Accession: A60421; S09137  
R;Veenstra, J.A.; Camps, F.  
Neuropeptides 15, 107-109, 1990  
A;Title: Structure of the hypertrehalosemic neuropeptide of the German cockroach, Blattella germanica  
A;Reference number: A60421; MUID:91179584; PMID:2080017  
A;Accession: A60421



A;Molecule type: protein  
A;Residues: 1-10 <VEE>  
A;Cross-references: UNIPROT:P10939  
R;Gaede, G.; Rinehart, K.L.  
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990  
A;Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corpora entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment  
A;Reference number: S08995; MUID:90253659; PMID:2340112  
A;Accession: S09137  
A;Molecule type: protein  
A;Residues: 1-10 <GAE>  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
| |  
Db 4 FSPGW 8

RESULT 31  
S08998  
hypertrehalosemic neuropeptide Bld-HrTH - Madeira cockroach  
C;Species: Leucophaea maderae (Madeira cockroach)  
C;Date: 30-Jun-1992 #sequence\_revision 14-Sep-1994 #text\_change 09-Jul-2004  
C;Accession: S08998  
R;Gaede, G.; Rinehart, K.L.  
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990  
A;Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corpora entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment  
A;Reference number: S08995; MUID:90253659; PMID:2340112  
A;Accession: S08998  
A;Molecule type: protein  
A;Residues: 1-10 <GAE>  
A;Cross-references: UNIPROT:P10939  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
| |  
Db 4 FSPGW 8

RESULT 32  
A26381  
hypertrehalosemic hormone - gray cockroach  
C;Species: Nauphoeta cinerea (gray cockroach)  
C;Date: 31-Mar-1988 #sequence\_revision 24-Oct-1997 #text\_change 09-Jul-2004  
C;Accession: A26381  
R;Gaede, G.; Rinehart Jr., K.L.  
Biochem. Biophys. Res. Commun. 141, 774-781, 1986  
A;Title: Amino acid sequence of a hypertrehalosaemic neuropeptide from the corpus cardiale  
A;Reference number: A26381; MUID:87100208; PMID:3801028  
A;Accession: A26381  
A;Molecule type: protein  
A;Residues: 1-10 <GAD>  
A;Cross-references: UNIPROT:P10939  
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
| |  
Db 4 FSPGW 8

RESULT 33  
JC1416  
hypertrehalosemic hormone I - stick insect (Carausius morosus)  
N;Alternate names: neuropeptide Cam-HrTH-I  
N;Contains: hypertrehalosemic factor II  
C;Species: Carausius morosus  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C;Accession: JC1416; S07157  
R;Gaede, G.; Kellner, R.; Rinehart, K.L.; Proefke, M.L.  
Biochem. Biophys. Res. Commun. 189, 1303-1309, 1992  
A;Title: A tryptophan-substituted member of the AKH/RPCH family isolated from a stick insect  
A;Reference number: JC1416; MUID:93129188; PMID:1482345  
A;Accession: JC1416  
A;Molecule type: protein  
A;Residues: 1-10 <GAE1>  
A;Cross-references: UNIPROT:P11385  
R;Gaede, G.; Rinehart Jr., K.L.  
Biol. Chem. Hoppe-Seyler 368, 67-75, 1987  
A;Title: Primary structure of the hypertrehalosaemic factor II from the corpus cardiacum  
A;Reference number: S07157; MUID:87157103; PMID:3828078  
A;Accession: S07157  
A;Molecule type: protein  
A;Residues: 'Z', 2-10 <GAE2>  
C;Comment: Hypertrehalosemic factor II lacks the tryptophan modification.  
C;Comment: This peptide raises hemolymph levels of trehalose in the cockroach Periplaneta  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; glycoprotein; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;8/Binding site: carbohydrate (Trp) (covalent) #status experimental  
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
| |  
Db 4 FTPNW 8

RESULT 34  
S09138  
hypertrehalosemic hormone II - stick insect (Extatosoma tiaratum)  
N;Alternate names: Cam-HrTH-II  
C;Species: Extatosoma tiaratum  
C;Date: 30-Jun-1992 #sequence\_revision 24-Oct-1997 #text\_change 09-Jul-2004  
C;Accession: S09138  
R;Gaede, G.; Rinehart, K.L.  
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990  
A;Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corpora entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment  
A;Reference number: S08995; MUID:90253659; PMID:2340112  
A;Accession: S09138  
A;Molecule type: protein  
A;Residues: 1-10 <GAE>  
A;Cross-references: UNIPROT:P11385  
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have  
C;Superfamily: adipokinetic hormone  
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 60.9%; Score 14; DB 2; Length 10;



PT0274  
Ig heavy chain CDR3 region (clone 3-109B) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C;Accession: PT0274  
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j  
A;Reference number: PT0222; MUID:91108337; PMID:1899102  
A;Accession: PT0274  
A;Molecule type: DNA  
A;Residues: 1-12 <YAM>  
A;Experimental source: B lymphocyte  
C;Keywords: heterotetramer; immunoglobulin

Query Match 60.9%; Score 14; DB 2; Length 12;  
Best Local Similarity 20.0%; Pred.No. 2.3e+03;  
Matches 1; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
 : |  
Db 3 YSSSW 7

Search completed: October 18, 2005, 15:59:21  
Job time : 30.6471 secs

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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:32:19 ; Search time 104.471 Seconds  
(without alignments)  
39.213 Million cell updates/sec

Title: US-09-214-371-10  
Perfect score: 23  
Sequence: 1 FXXXWXXX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 12050

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : UniProt 03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	73.9	9	1 AKH HELZE	P67787 heliothis z
2	17	73.9	13	2 Q9XL12	Q9xli2 bemisia tab
3	16	69.6	8	1 AKHG GRYBI	P67785 gryllus bim
4	16	69.6	8	1 AKH ROMMI	P67786 romalea mic
5	16	69.6	10	1 HTF_HELZE	P16353 heliothis z
6	16	69.6	11	2 Q6E5N4	Q6e5n4 mantheyus p
7	16	69.6	11	2 Q9G649	Q9g649 otocryptis
8	16	69.6	17	2 O15276	O15276 homo sapien
9	16	69.6	17	2 Q7Y1X8	Q7y1x8 lilium long
10	16	69.6	19	2 Q91329	Q91329 human immun
11	16	69.6	19	2 Q9WJBI	Q9wjbi human immun
12	16	69.6	20	2 Q6LD18	Q6ld18 mus musculus
13	15	65.2	8	1 AKH LIBAU	P25418 libellula a
14	15	65.2	9	2 Q7M3N6	Q7m3n6 gryllus bim
15	15	65.2	9	2 Q8WGE6	Q8wge6 procambarus
16	15	65.2	10	1 AKHX LOCFI	P81626 locusta mig
17	15	65.2	10	2 Q7M465	Q7m465 platypieura
18	15	65.2	10	2 Q70F01	Q70f01 sus scrofa
19	15	65.2	10	2 Q79897	Q79897 hoplocercus
20	15	65.2	10	2 P92707	P92707 platysaurus
21	15	65.2	10	2 Q6UJL5	Q6ujl5 strophurus
22	15	65.2	10	2 Q6WBU4	Q6wbu4 sceloporur
23	15	65.2	10	2 Q6X0E7	Q6x0e7 anolis marc
24	15	65.2	10	2 Q71DW3	Q71dw3 polychrus m
25	15	65.2	10	2 Q71DW6	Q71dw6 polychrus a
26	15	65.2	10	2 Q71DW9	Q71dw9 anisolepis
27	15	65.2	10	2 Q71E17	Q71e17 morunasauru
28	15	65.2	10	2 Q71E20	Q71e20 enyalioides
29	15	65.2	10	2 Q92YT2	Q9zyt2 leiocephalu
30	15	65.2	11	2 Q8WES0	Q8wes0 ceratophora
31	15	65.2	11	2 Q9G365	Q9g365 calotes emm

32	15	65.2	11	2 Q9G368	Q9g368 draco blanf
33	15	65.2	11	2 Q9G5Y9	Q9g5y9 pseudocalot
34	15	65.2	11	2 Q9G5Z2	Q9g5z2 pseudocalot
35	15	65.2	11	2 Q9G601	Q9g601 bronchocela
36	15	65.2	11	2 Q9G625	Q9g625 calotes ver
37	15	65.2	11	2 Q9G628	Q9g628 calotes mys
38	15	65.2	11	2 Q9G631	Q9g631 calotes nig
39	15	65.2	11	2 Q9G634	Q9g634 calotes lio
40	15	65.2	11	2 Q9G640	Q9g640 calotes cey
41	15	65.2	11	2 Q9G643	Q9g643 calotes cal
42	15	65.2	11	2 Q9G646	Q9g646 sitana pont
43	15	65.2	12	2 Q6WR31	Q6wr31 mycteria am
44	15	65.2	12	2 Q6WR52	Q6wr52 asio otus (
45	15	65.2	12	2 Q6WR67	Q6wr67 neomorphus
46	15	65.2	12	2 Q6WR73	Q6wr73 coccyzus er
47	15	65.2	12	2 Q6WR79	Q6wr79 cuculus can
48	15	65.2	14	2 Q71H30	Q71h30 andrena bra
49	15	65.2	16	2 Q760I9	Q760i9 aspergillus
50	15	65.2	19	2 Q7S645	Q7s645 neurospora
51	15	65.2	20	1 COXA_THUOB	P80972 thunnus obe
52	15	65.2	20	2 Q95MK5	Q95mk5 varecia var
53	15	65.2	20	2 Q673D5	Q673d5 dehalococco
54	15	65.2	20	2 Q9R5E8	Q9r5e8 bacillus sp
55	14	60.9	8	1 AKH_PROTE	P61856 protophormi
56	14	60.9	8	1 AKH_TABAT	P14595 tabanus atr
57	14	60.9	8	1 HTF1_PERAM	P04548 periplaneta
58	14	60.9	8	1 HTF2_PERAM	P04549 periplaneta
59	14	60.9	8	1 HTF_TENMO	P67789 tenebrio mo
60	14	60.9	8	1 HTF_ZOPRU	P67790 zophobas ru
61	14	60.9	8	1 RPCH_PANBO	P08939 pandalus bo
62	14	60.9	8	2 Q7M4H6	Q7m4h6 ischnura se
63	14	60.9	8	2 Q7M4H7	Q7m4h7 pseudagrion
64	14	60.9	10	1 HTF1_ROMMI	P18110 romalea mic
65	14	60.9	10	1 HTF2_CARMO	P62542 carausius m
66	14	60.9	10	1 HTF2_EXTTI	P62543 extatosoma
67	14	60.9	10	1 HTF_BLAG	P84220 blattella g
68	14	60.9	10	1 HTF_GROPO	P84221 gromphadori
69	14	60.9	10	1 HTF_LEUWA	P84219 leucophaea
70	14	60.9	10	1 HTF_NAUCI	P84218 nauphoeta c
71	14	60.9	10	1 HTF_TABAT	P14596 tabanus atr
72	14	60.9	10	2 Q79885	O79885 anolis pate
73	14	60.9	10	2 Q79903	O79903 oplurus cuv
74	14	60.9	10	2 Q79906	O79906 phrynosoma
75	14	60.9	10	2 Q8W7U4	Q8w7u4 anolis nite
76	14	60.9	10	2 Q8W8Q2	Q8w8q2 anolis punc
77	14	60.9	10	2 Q8W8Q3	Q8w8q3 anolis nite
78	14	60.9	10	2 Q8W8Q4	Q8w8q4 anolis punc
79	14	60.9	10	2 Q8W969	Q8w969 anolis orto
80	14	60.9	10	2 Q8W970	Q8w970 anolis nite
81	14	60.9	10	2 Q8W971	Q8w971 anolis fusc
82	14	60.9	10	2 Q8WDG6	Q8wdg6 anolis trac
83	14	60.9	10	2 Q8WDH0	Q8wdh0 anolis limi
84	14	60.9	10	2 Q8WDH2	Q8wdh2 anolis lemu
85	14	60.9	10	2 Q8WDH4	Q8wdh4 anolis carp
86	14	60.9	10	2 Q8WDH6	Q8wdh6 anolis wood
87	14	60.9	10	2 Q8WDH8	Q8wdh8 anolis mest
88	14	60.9	10	2 Q8WDI8	Q8wdi8 anolis tran
89	14	60.9	10	2 Q6WBN7	Q6wbn7 sceloporur
90	14	60.9	10	2 Q6WBR1	Q6wbr1 sceloporur
91	14	60.9	10	2 Q6WBR4	Q6wbr4 sceloporur
92	14	60.9	10	2 Q6WBS3	Q6wbs3 sceloporur
93	14	60.9	10	2 Q6WBT8	Q6wbt8 sceloporur
94	14	60.9	10	2 Q6WBU1	Q6wbu1 sceloporur
95	14	60.9	10	2 Q6WBW2	Q6wbw2 phrynosoma
96	14	60.9	10	2 Q6WBW5	Q6wbw5 phrynosoma
97	14	60.9	10	2 Q6WBW8	Q6wbw8 phrynosoma
98	14	60.9	10	2 Q6WBX1	Q6wbx1 phrynosoma
99	14	60.9	10	2 Q6WBX4	Q6wbx4 phrynosoma
100	14	60.9	10	2 Q6WZN6	Q6wzn6 anolis cybo
101	14	60.9	10	2 Q6X061	Q6x061 anolis haet
102	14	60.9	10	2 Q6X071	Q6x071 anolis shre
103	14	60.9	10	2 Q6X0C3	Q6x0c3 anolis whit
104	14	60.9	10	2 Q6X0D2	Q6x0d2 anolis armo

105	14	60.9	10	2	Q6X0D8	Q6x0d8 anolis long	178	14	60.9	19	2	Q44506	Q44506 anabaena va
106	14	60.9	10	2	Q71DR5	Q71dr5 leiocephalu	179	14	60.9	19	2	Q6QLM2	Q6qlm2 influenza a
107	14	60.9	10	2	Q71DR8	Q71dr8 leiocephalu	180	14	60.9	20	1	CRTC_SPIOL	P30806 spinacia ol
108	14	60.9	10	2	Q71DS4	Q71ds4 tropidurus	181	14	60.9	20	1	GBB4_RAT	O35353 rattus norv
109	14	60.9	10	2	Q71DS7	Q71ds7 tropidurus	182	14	60.9	20	2	Q95WJ7	Q95mj7 tarsius syr
110	14	60.9	10	2	Q71DT0	Q71dt0 uranoscodon	183	14	60.9	20	2	Q95WJ8	Q95mj8 galago moho
111	14	60.9	10	2	Q71DT3	Q71dt3 tropidurus	184	14	60.9	20	2	Q95WJ9	Q95mj9 pan troglod
112	14	60.9	10	2	Q71DT6	Q71dt6 uracentron	185	14	60.9	20	2	Q95WK0	Q95mk0 pongo pygma
113	14	60.9	10	2	Q71DT9	Q71dt9 stenocercus	186	14	60.9	20	2	Q95WK1	Q95mk1 colobus ang
114	14	60.9	10	2	Q71DU2	Q71du2 stenocercus	187	14	60.9	20	2	Q95WK2	Q95mk2 papio cynoc
115	14	60.9	10	2	Q71DU5	Q71du5 stenocercus	188	14	60.9	20	2	Q95WK3	Q95mk3 ateles belz
116	14	60.9	10	2	Q71DU8	Q71du8 sceloporos	189	14	60.9	20	2	Q95WK4	Q95mk4 cheirogaleu
117	14	60.9	10	2	Q71DW0	Q71dw0 phrynosoma	190	14	60.9	20	2	Q95WK6	Q95mk6 eulemur cor
118	14	60.9	10	2	Q71DX5	Q71dx5 urostrophus	191	14	60.9	20	2	Q9TRA4	Q9tra4 sus scrofa
119	14	60.9	10	2	Q71DX8	Q71dx8 enyalius le	192	14	60.9	20	2	Q66548	Q66548 human herpe
120	14	60.9	10	2	Q71DY1	Q71dy1 pristidactyl	193	13	56.5	6	1	EI01_LITRU	P82096 litoria rub
121	14	60.9	10	2	Q71DY4	Q71dy4 leiosaurus	194	13	56.5	9	2	Q28121	Q28121 bos taurus
122	14	60.9	10	2	Q71DY7	Q71dy7 leiosaurus	195	13	56.5	15	2	Q6JQC4	Q6jccq4 tetraleurod
123	14	60.9	10	2	Q71DZ0	Q71dz0 diplolaemus	196	13	56.5	15	2	Q6JCS2	Q6jcs2 aieuroplatu
124	14	60.9	10	2	Q71DZ3	Q71dz3 diplolaemus	197	13	56.5	16	2	Q697F2	Q697f2 bemisia sp.
125	14	60.9	10	2	Q71E08	Q71e08 anolis cybo	198	13	56.5	16	2	Q9XNP6	Q9xnp6 boophilus m
126	14	60.9	10	2	Q71E11	Q71e11 chalarodon	199	13	56.5	18	2	Q7S173	Q7s173 neurospora
127	14	60.9	10	2	Q71E23	Q71e23 corytophane	200	13	56.5	18	2	Q8RU82	Q8ru82 zea mays (m
128	14	60.9	10	2	Q71E35	Q71e35 basiliscus	201	13	56.5	19	2	Q9TU41	Q9tu41 loxodontu a
129	14	60.9	10	2	Q71SD0	Q71sd0 liolaemus w	202	13	56.5	19	2	Q9TU42	Q9tu42 mammutus p
130	14	60.9	10	2	Q9T8U8	Q9t8u8 liolaemus p	203	13	56.5	19	2	Q99722	Q99722 lamprotorni
131	14	60.9	10	2	Q9T8X1	Q9t8x1 liolaemus a	204	13	56.5	20	2	Q90X92	Q90x92 gallus gall
132	14	60.9	10	2	Q9ZY56	Q9zy56 stenocercus	205	12	52.2	8	2	Q7GEM6	Q7gem6 branchiosto
133	14	60.9	12	2	Q6WR34	Q6wr34 phoenicopte	206	12	52.2	10	1	GON1_PETMA	P04378 petromyzon
134	14	60.9	12	2	Q6WR37	Q6wr37 buteo jamai	207	12	52.2	10	2	Q6UJL2	Q6ujl2 strophurus
135	14	60.9	12	2	Q6WR43	Q6wr43 scolopax mi	208	12	52.2	11	1	CA31_LITCI	P82089 litoria cit
136	14	60.9	12	2	Q6WR55	Q6wr55 crinifer pi	209	12	52.2	11	1	CA32_LITCI	P82090 litoria cit
137	14	60.9	12	2	Q6WR58	Q6wr58 musophaga v	210	12	52.2	11	1	CORZ_PERAM	P11496 periplaneta
138	14	60.9	12	2	Q6WR82	Q6wr82 urocolius m	211	12	52.2	11	2	Q6E5M8	Q6esm8 ptyctolaemu
139	14	60.9	12	2	Q6WR88	Q6wr88 coracias sp	212	12	52.2	11	2	Q9G359	Q9g359 japalura fl
140	14	60.9	12	2	Q6WR91	Q6wr91 trogon curu	213	12	52.2	11	2	Q9G607	Q9g607 aphanlotis
141	14	60.9	12	2	Q6WR94	Q6wr94 tockus eryt	214	12	52.2	12	2	P92680	Q92680 trimeresuru
142	14	60.9	12	2	Q6WR97	Q6wr97 anseranas s	215	12	52.2	16	2	Q9N237	Q9n237 pan troglod
143	14	60.9	12	2	Q6WRA0	Q6wra0 chauna torq	216	12	52.2	17	2	Q8MJ33	Q8mj33 sus scrofa
144	14	60.9	12	2	Q6WRA3	Q6wra3 megapodius	217	12	52.2	17	2	Q9TR22	Q9tr22 bos taurus
145	14	60.9	12	2	Q6WRA6	Q6wra6 alectura la	218	12	52.2	18	2	Q9QW51	Q9qw51 mus sp. . a
146	14	60.9	12	2	Q6WRA9	Q6wra9 crax rubra	219	12	52.2	19	2	Q7REE1	Q7reel plasmodium
147	14	60.9	12	2	Q8HN63	Q8hn63 sayornis ph	220	11	47.8	2	1	GWA_SEPOF	P83570 sepia offic
148	14	60.9	12	2	Q8HN66	Q8hn66 acryllium v	221	11	47.8	4	1	OCP3_OTIMI	P58649 octopus min
149	14	60.9	12	2	Q53579	Q53579 rhodobacter	222	11	47.8	5	1	BPP7_BOTIN	P30425 bothrops in
150	14	60.9	13	1	BML2_BOMVA	P84211 bombina var	223	11	47.8	5	1	UF01_MOUSE	P38639 mus musculu
151	14	60.9	13	1	YPNP_PHOLU	P41122 photorhabdu	224	11	47.8	6	1	LOK1_LOCM1	P41491 locusta mig
152	14	60.9	13	2	Q7M1F5	Q7mlf5 freesia ref	225	11	47.8	7	1	BRHP_CONIM	P58803 conus imper
153	14	60.9	13	2	Q66NE7	Q66ne7 borrelia bu	226	11	47.8	7	1	TPFY_PACDA	P83455 pachymedusa
154	14	60.9	13	2	Q718T2	Q718t2 newcastle d	227	11	47.8	7	1	TY51_LITRU	P82065 litoria rub
155	14	60.9	15	2	Q6LC27	Q6lc27 homo sapien	228	11	47.8	7	1	WWA1_ACHFU	P35919 achatina fu
156	14	60.9	15	2	Q9UC22	Q9uc22 homo sapien	229	11	47.8	7	1	WWA2_ACHFU	P35920 achatina fu
157	14	60.9	15	2	Q53580	Q53580 rhodobacter	230	11	47.8	7	1	WWA3_ACHFU	P35921 achatina fu
158	14	60.9	15	2	Q9R5D6	Q9r5d6 chromatium	231	11	47.8	7	2	Q9BRY4	Q9bry4 homo sapien
159	14	60.9	16	2	Q79B06	Q79b06 helicobacte	232	11	47.8	7	2	Q95945	Q95945 saccharomyc
160	14	60.9	16	2	Q9R4F2	Q9r4f2 streptomyce	233	11	47.8	7	2	Q49223	O49223 glycine max
161	14	60.9	16	2	Q9QW76	Q9qw76 mus sp. hom	234	11	47.8	7	2	Q8XMS9	Q8kms9 enterobacte
162	14	60.9	16	2	Q8QGA1	Q8qga1 brachydanio	235	11	47.8	7	2	Q8GL00	Q8gl00 borrelia bu
163	14	60.9	17	2	Q8MIG9	Q8mig9 cynopterus	236	11	47.8	7	2	Q8GL04	Q8gl04 borrelia bu
164	14	60.9	17	2	Q9QUU4	Q9quj4 mus sp. mep	237	11	47.8	7	2	Q8JEB1	Q8je81 human immun
165	14	60.9	17	2	Q6QLL7	Q6ql17 influenza a	238	11	47.8	8	1	ACI_THUAL	P18691 thunnus alb
166	14	60.9	17	2	Q6QLL9	Q6ql19 influenza a	239	11	47.8	8	1	AKH_GEOST	P84241 geotrupes s
167	14	60.9	17	2	Q6QLM0	Q6qlm0 influenza a	240	11	47.8	8	1	AKH_MELML	P84240 melolontha
168	14	60.9	17	2	Q6QLM1	Q6qlm1 influenza a	241	11	47.8	8	1	AKH_PACMA	P84242 pachnoda ma
169	14	60.9	18	2	Q8NOX8	Q8n0x8 homo sapien	242	11	47.8	8	1	C125_CYPDO	P83661 cyphononyx
170	14	60.9	18	2	Q71U72	Q71u72 homo sapien	243	11	47.8	8	1	CKKN_DASV1	P68125 dasyurus vi
171	14	60.9	18	2	Q9ZYW4	Q9zyw4 habrobracon	244	11	47.8	8	1	CKKN_MACEU	P68126 macropus eu
172	14	60.9	18	2	Q9ZYX7	Q9zyx7 perga conde	245	11	47.8	8	1	COW2_CONPU	P58785 conus purpu
173	14	60.9	19	2	P83003	P83003 entamoeba h	246	11	47.8	8	1	LCK1_LEUMA	P21140 leucophaea
174	14	60.9	19	2	Q9N1W2	Q9nlw2 equus cabal	247	11	47.8	8	1	LCK2_LEUMA	P21141 leucophaea
175	14	60.9	19	2	Q9T2V5	Q9t2v5 crithidia f	248	11	47.8	8	1	LCK3_LEUMA	P21142 leucophaea
176	14	60.9	19	2	Q9ZYW7	Q9zyw7 aphidius ro	249	11	47.8	8	1	LCK4_LEUMA	P21143 leucophaea
177	14	60.9	19	2	Q9ZYW8	Q9zyw8 ichneutes b	250	11	47.8	8	1	LCK5_LEUMA	P19987 leucophaea

251	11	47.8	8	1	LCK6_LEUMA	P19988 leucophaea	324	11	47.8	9	1	LITR_PHYRO	P08946 phyllomedus
252	11	47.8	8	1	LCK7_LEUMA	P19989 leucophaea	325	11	47.8	9	1	LMIP_LOCOMI	P31799 locusta mig
253	11	47.8	8	1	LCK8_LEUMA	P19990 leucophaea	326	11	47.8	9	1	NEF_HV128	P12481 human immu
254	11	47.8	8	1	NGIF_RAT	P82598 rattus norv	327	11	47.8	9	1	PTSP_BOMMO	P82003 bombyx mori
255	11	47.8	8	1	PK1_PERAM	P82685 periplaneta	328	11	47.8	9	2	O95953	O95953 homo sapien
256	11	47.8	8	1	PK2_PERAM	P82686 periplaneta	329	11	47.8	9	2	Q16386	Q16386 homo sapien
257	11	47.8	8	1	PK3_PERAM	P82687 periplaneta	330	11	47.8	9	2	Q6LDB5	Q6LDB5 homo sapien
258	11	47.8	8	1	PK4_PERAM	P82688 periplaneta	331	11	47.8	9	2	Q6QF45	Q6QF45 homo sapien
259	11	47.8	8	1	PK5_PERAM	P82689 periplaneta	332	11	47.8	9	2	Q71EB9	Q71EB9 homo sapien
260	11	47.8	8	1	PLP_BRANA	P81707 brassica na	333	11	47.8	9	2	Q71E39	Q71E39 homo sapien
261	11	47.8	8	1	RT34_BOVIN	P82929 bos taurus	334	11	47.8	9	2	Q7M4S2	Q7M4S2 homo sapien
262	11	47.8	8	1	VAM6_MOUSE	P83853 mus musculu	335	11	47.8	9	2	Q9H326	Q9H326 homo sapien
263	11	47.8	8	2	Q15888	Q15888 homo sapien	336	11	47.8	9	2	Q9H3Y3	Q9H3Y3 homo sapien
264	11	47.8	8	2	Q15890	Q15890 homo sapien	337	11	47.8	9	2	Q9UC36	Q9UC36 homo sapien
265	11	47.8	8	2	Q8IVK3	Q8IVK3 homo sapien	338	11	47.8	9	2	Q9UCQ9	Q9UCQ9 homo sapien
266	11	47.8	8	2	Q86SL0	Q86SL0 homo sapien	339	11	47.8	9	2	Q9UK44	Q9UK44 homo sapien
267	11	47.8	8	2	Q7M3S2	Q7M3S2 trypanosoma	340	11	47.8	9	2	Q9UMA0	Q9UMA0 homo sapien
268	11	47.8	8	2	Q7M3S3	Q7M3S3 trypanosoma	341	11	47.8	9	2	Q9UMF3	Q9UMF3 homo sapien
269	11	47.8	8	2	O02831	O02831 oryctolagus	342	11	47.8	9	2	Q9UQW0	Q9UQW0 homo sapien
270	11	47.8	8	2	Q95M23	Q95M23 sus scrofa	343	11	47.8	9	2	Q7M3N7	Q7M3N7 gryllus bim
271	11	47.8	8	2	Q9TRY3	Q9TRY3 sus sp. ins	344	11	47.8	9	2	Q7M3N8	Q7M3N8 gryllus bim
272	11	47.8	8	2	Q8W8G2	Q8W8G2 diadema sav	345	11	47.8	9	2	Q7M3N9	Q7M3N9 gryllus bim
273	11	47.8	8	2	Q8W8G3	Q8W8G3 diadema pau	346	11	47.8	9	2	Q7M4D5	Q7M4D5 diadema set
274	11	47.8	8	2	Q8W8G4	Q8W8G4 diadema mex	347	11	47.8	9	2	Q8SHF0	Q8SHF0 chamaeleo n
275	11	47.8	8	2	Q8W8G5	Q8W8G5 diadema ant	348	11	47.8	9	2	Q8W8W5	Q8W8W5 diadema set
276	11	47.8	8	2	Q8W8G6	Q8W8G6 diadema mex	349	11	47.8	9	2	Q8W8W6	Q8W8W6 diadema ant
277	11	47.8	8	2	Q8WGD7	Q8WGD7 lomix hirta	350	11	47.8	9	2	Q8W8X4	Q8W8X4 diadema mex
278	11	47.8	8	2	Q94PX5	Q94PX5 felis silve	351	11	47.8	9	2	Q8WFS4	Q8WFS4 diadema mex
279	11	47.8	8	2	Q94PX6	Q94PX6 felis libyc	352	11	47.8	9	2	Q94NA9	Q94NA9 daubentonia
280	11	47.8	8	2	Q94PX7	Q94PX7 felis silve	353	11	47.8	9	2	Q94NB0	Q94NB0 microcebus
281	11	47.8	8	2	Q94V82	Q94V82 varanus yuw	354	11	47.8	9	2	Q94NB1	Q94NB1 microcebus
282	11	47.8	8	2	Q94V88	Q94V88 varanus tri	355	11	47.8	9	2	Q94NB2	Q94NB2 microcebus
283	11	47.8	8	2	Q94V91	Q94V91 varanus tim	356	11	47.8	9	2	Q94VC6	Q94VC6 varanus pil
284	11	47.8	8	2	Q94VA7	Q94VA7 varanus sal	357	11	47.8	9	2	Q94VD8	Q94VD8 varanus nil
285	11	47.8	8	2	Q94VB2	Q94VB2 varanus sal	358	11	47.8	9	2	Q94VE1	Q94VE1 varanus mer
286	11	47.8	8	2	Q94VB5	Q94VB5 varanus sal	359	11	47.8	9	2	Q94VG2	Q94VG2 varanus ind
287	11	47.8	8	2	Q94VC1	Q94VC1 varanus rud	360	11	47.8	9	2	Q94VH4	Q94VH4 varanus gla
288	11	47.8	8	2	Q94VE4	Q94VE4 varanus mel	361	11	47.8	9	2	Q94VI0	Q94VI0 varanus gig
289	11	47.8	8	2	Q94VF6	Q94VF6 varanus job	362	11	47.8	9	2	Q94VI8	Q94VI8 varanus ere
290	11	47.8	8	2	Q94VF9	Q94VF9 varanus ind	363	11	47.8	9	2	Q94VJ1	Q94VJ1 varanus dor
291	11	47.8	8	2	Q94VJ4	Q94VJ4 varanus ben	364	11	47.8	9	2	Q94XE6	Q94XE6 tectocoris
292	11	47.8	8	2	Q70Y57	Q70Y57 fuerstia af	365	11	47.8	9	2	Q691D6	Q691D6 anolis sagr
293	11	47.8	8	2	Q70Y84	Q70Y84 plectranthu	366	11	47.8	9	2	Q71DX2	Q71DX2 urostrophus
294	11	47.8	8	2	Q715L5	Q715L5 varanus dum	367	11	47.8	9	2	Q85DB0	Q85DB0 lepitemur s
295	11	47.8	8	2	Q9T4Y2	Q9T4Y2 asterina pe	368	11	47.8	9	2	Q85DB8	Q85DB8 lepitemur e
296	11	47.8	8	2	Q9TD02	Q9TD02 terranatos	369	11	47.8	9	2	Q9T688	Q9T688 gecko gecko
297	11	47.8	8	2	Q6ZZ01	Q6ZZ01 silene con	370	11	47.8	9	2	Q38366	Q38366 bacterioph
298	11	47.8	8	2	Q6ZZ02	Q6ZZ02 lychnis cor	371	11	47.8	9	2	Q6A1H7	Q6A1H7 hordeum vul
299	11	47.8	8	2	Q85406	Q85406 coxiella bu	372	11	47.8	9	2	Q6ZZ00	Q6ZZ00 silene rotu
300	11	47.8	8	2	Q6LDP8	Q6LDP8 pseudomonas	373	11	47.8	9	2	Q47410	Q47410 escherichia
301	11	47.8	8	2	Q7M0L0	Q7M0L0 clostridium	374	11	47.8	9	2	Q6VCX0	Q6VCX0 streptomyce
302	11	47.8	8	2	Q7M124	Q7M124 kluyvera ci	375	11	47.8	9	2	Q8GL26	Q8GL26 borrelia bu
303	11	47.8	8	2	Q8G940	Q8G940 borrelia bu	376	11	47.8	9	2	Q8GL31	Q8GL31 borrelia bu
304	11	47.8	8	2	Q8GL21	Q8GL21 borrelia bu	377	11	47.8	9	2	Q9R5M1	Q9R5M1 staphylococ
305	11	47.8	8	2	Q35835	Q35835 rattus sp.	378	11	47.8	9	2	Q9R635	Q9R635 chlamydia t
306	11	47.8	8	2	P70243	P70243 mus musculu	379	11	47.8	9	2	Q9R9C4	Q9R9C4 borrelia bu
307	11	47.8	8	2	Q99MN0	Q99MN0 mus musculu	380	11	47.8	9	2	Q6LAQ1	Q6LAQ1 rattus norv
308	11	47.8	8	2	Q62721	Q62721 rattus norv	381	11	47.8	9	2	Q7M078	Q7M078 rattus norv
309	11	47.8	8	2	Q9ET16	Q9ET16 mesocricetu	382	11	47.8	9	2	Q80X07	Q80X07 mus sp. thr
310	11	47.8	8	2	Q9ET17	Q9ET17 mus caroli	383	11	47.8	9	2	Q90350	Q90350 gb virus c/
311	11	47.8	8	2	Q9ET18	Q9ET18 mus spretus	384	11	47.8	9	2	Q65711	Q65711 berne virus
312	11	47.8	8	2	Q64971	Q64971 alfalfa mos	385	11	47.8	9	2	Q69100	Q69100 human herpe
313	11	47.8	8	2	P79940	P79940 xenopus lae	386	11	47.8	9	2	Q89491	Q89491 murine minu
314	11	47.8	8	2	Q98TU5	Q98TU5 xenopus lae	387	11	47.8	9	2	Q673W5	Q673W5 tyrannus me
315	11	47.8	8	2	Q68LF1	Q68LF1 myrmotherul	388	11	47.8	9	2	Q673W6	Q673W6 terpsiphone
316	11	47.8	8	2	Q68LG3	Q68LG3 sakesphorus	389	11	47.8	9	2	Q673W7	Q673W7 telophorus
317	11	47.8	8	2	Q6R7U6	Q6R7U6 gnypetoscin	390	11	47.8	9	2	Q673W8	Q673W8 tchagra sen
318	11	47.8	8	2	Q7LZ27	Q7LZ27 naja oxiانا	391	11	47.8	9	2	Q673W9	Q673W9 tchagra aus
319	11	47.8	9	1	CAER_PHYSA	Q71ZC4 phyllomedus	392	11	47.8	9	2	Q673X0	Q673X0 rhodophoneu
320	11	47.8	9	1	COW_CONVE	P83047 conus ventr	393	11	47.8	9	2	Q673X1	Q673X1 rhipidura a
321	11	47.8	9	1	D1_NEPNO	P24816 nephrops no	394	11	47.8	9	2	Q673X2	Q673X2 pseudobias
322	11	47.8	9	1	DSIP_RABIT	P01158 oryctolagus	395	11	47.8	9	2	Q673X3	Q673X3 prionops sc
323	11	47.8	9	1	LITO_LITAU	P08945 litoria aur	396	11	47.8	9	2	Q673X4	Q673X4 prionops re

397	11	47.8	9	2	Q673X5	Q673x5 platysteira	470	11	47.8	10	2	Q9TR47	Q9tr47 bos taurus
398	11	47.8	9	2	Q673X6	Q673x6 oriolus xan	471	11	47.8	10	2	Q9TS43	Q9ts43 sus scrofa
399	11	47.8	9	2	Q673X7	Q673x7 nilaus afer	472	11	47.8	10	2	Q9TU33	Q9tu33 canis famil
400	11	47.8	9	2	Q673X8	Q673x8 bias flamm	473	11	47.8	10	2	Q79888	Q79888 basiliscus
401	11	47.8	9	2	Q673X9	Q673x9 malaconotus	474	11	47.8	10	2	Q79891	Q79891 crotophytus
402	11	47.8	9	2	Q673Y0	Q673y0 lanius coll	475	11	47.8	10	2	Q79894	Q79894 gambelia wi
403	11	47.8	9	2	Q673Y1	Q673y1 lanioturdus	476	11	47.8	10	2	Q79900	Q79900 liolaemus p
404	11	47.8	9	2	Q673Y2	Q673y2 laniarius l	477	11	47.8	10	2	Q79909	Q79909 sauromalus
405	11	47.8	9	2	Q673Y3	Q673y3 laniarius f	478	11	47.8	10	2	Q79912	Q79912 chamaeleo f
406	11	47.8	9	2	Q673Y4	Q673y4 laniarius b	479	11	47.8	10	2	Q79915	Q79915 leirolepis b
407	11	47.8	9	2	Q673Y5	Q673y5 laniarius a	480	11	47.8	10	2	Q79924	Q79924 elgaria pan
408	11	47.8	9	2	Q673Y6	Q673y6 platysteira	481	11	47.8	10	2	P92616	P92616 aspidosceli
409	11	47.8	9	2	Q673Y7	Q673y7 dryoscopus	482	11	47.8	10	2	P92632	P92632 eremias gra
410	11	47.8	9	2	Q673Y8	Q673y8 dryoscopus	483	11	47.8	10	2	P92648	P92648 lialis jica
411	11	47.8	9	2	Q673Y9	Q673y9 dicrurus pa	484	11	47.8	10	2	P92654	P92654 euprepis au
412	11	47.8	9	2	Q673Z0	Q673z0 cyanolanius	485	11	47.8	10	2	P92733	P92733 fejevaraya
413	11	47.8	9	2	Q673Z1	Q673z1 corvus coro	486	11	47.8	10	2	P92758	P92758 teratoscinc
414	11	47.8	9	2	Q673Z2	Q673z2 coracina me	487	11	47.8	10	2	P92762	P92762 uromastyx a
415	11	47.8	9	2	Q673Z3	Q673z3 telophorus	488	11	47.8	10	2	P92766	P92766 varanus gri
416	11	47.8	9	2	Q673Z4	Q673z4 telophorus	489	11	47.8	10	2	P92771	P92771 xenosaurus
417	11	47.8	9	2	Q673Z5	Q673z5 telophorus	490	11	47.8	10	2	P92774	P92774 xantusia vi
418	11	47.8	9	2	Q673Z6	Q673z6 campephaga	491	11	47.8	10	2	Q8SH83	Q8sh83 brookesia t
419	11	47.8	9	2	Q673Z7	Q673z7 tchagra min	492	11	47.8	10	2	Q8SH85	Q8sh85 brookesia t
420	11	47.8	9	2	Q673Z8	Q673z8 bias musicu	493	11	47.8	10	2	Q8SH88	Q8sh88 brookesia t
421	11	47.8	9	2	Q673Z9	Q673z9 batis poens	494	11	47.8	10	2	Q8SH90	Q8sh90 brookesia s
422	11	47.8	9	2	Q78DU2	Q78du2 gallus gall	495	11	47.8	10	2	Q8SH93	Q8sh93 brookesia p
423	11	47.8	9	2	Q7LZ66	Q7lz66 meleagris g	496	11	47.8	10	2	Q8SH96	Q8sh96 brookesia p
424	11	47.8	9	2	Q801K0	Q801k0 ilicura mil	497	11	47.8	10	2	Q8SH99	Q8sh99 brookesia n
425	11	47.8	9	2	Q801K1	Q801k1 chiroxiphia	498	11	47.8	10	2	Q8SHA2	Q8sha2 brookesia b
426	11	47.8	9	2	Q801K2	Q801k2 antilophia	499	11	47.8	10	2	Q8SHA5	Q8sha5 brookesia a
427	11	47.8	9	2	Q9PRJ4	Q9prj4 lepisosteus	500	11	47.8	10	2	Q8SHA8	Q8sha8 rhampholeon
428	11	47.8	9	2	Q85723	Q85723 simian sarc	501	11	47.8	10	2	Q8SHB1	Q8shb1 rhampholeon
429	11	47.8	10	1	A EGL_AGRAB	P83465 agrocyybe ae	502	11	47.8	10	2	Q8SHB4	Q8shb4 furcifer ve
430	11	47.8	10	1	A PE_CAPI	P80474 capnocytoph	503	11	47.8	10	2	Q8SHB7	Q8shb7 furcifer ou
431	11	47.8	10	1	BPP2_BOTIN	P30422 bothrops in	504	11	47.8	10	2	Q8SHC0	Q8shc0 furcifer la
432	11	47.8	10	1	BPP2_BOTJA	P01022 bothrops ja	505	11	47.8	10	2	Q8SHC3	Q8shc3 furcifer la
433	11	47.8	10	1	BPP8_BOTIN	P30426 bothrops in	506	11	47.8	10	2	Q8SHC6	Q8shc6 furcifer be
434	11	47.8	10	1	BPP_VIPAS	P31351 vipera aspi	507	11	47.8	10	2	Q8SHC9	Q8shc9 furcifer ba
435	11	47.8	10	1	BRK_ONCMY	Q9prz1 oncorhynch	508	11	47.8	10	2	Q8SHD2	Q8shd2 chamaeleo w
436	11	47.8	10	1	CA12_LITCI	P62540 litoria cit	509	11	47.8	10	2	Q8SHD5	Q8shd5 chamaeleo s
437	11	47.8	10	1	CA12_LITSP	P62541 litoria spl	510	11	47.8	10	2	Q8SHD8	Q8shd8 chamaeleo r
438	11	47.8	10	1	CAER_LITXA	P56264 litoria xan	511	11	47.8	10	2	Q8SHE1	Q8shel chamaeleo q
439	11	47.8	10	1	GON1_ALLMI	P37041 alligator m	512	11	47.8	10	2	Q8SHE4	Q8she4 chamaeleo q
440	11	47.8	10	1	GON1_CHEPR	P80677 chelyosoma	513	11	47.8	10	2	Q8SHE7	Q8she7 chamaeleo p
441	11	47.8	10	1	GON1_CLUPA	P81749 clupea pall	514	11	47.8	10	2	Q8SHF3	Q8shf3 chamaeleo m
442	11	47.8	10	1	GON2_ALUMI	P68073 alligator m	515	11	47.8	10	2	Q8SHF6	Q8shf6 chamaeleo m
443	11	47.8	10	1	GON2_CHEPR	P80678 chelyosoma	516	11	47.8	10	2	Q8SHF9	Q8shf9 chamaeleo j
444	11	47.8	10	1	GON2_CHICK	P68072 galius gall	517	11	47.8	10	2	Q8SHG2	Q8shg2 chamaeleo j
445	11	47.8	10	1	GON2_CLUPA	P68075 clupea pall	518	11	47.8	10	2	Q8SHG5	Q8shg5 chamaeleo h
446	11	47.8	10	1	GON2_HYDCO	P68076 hydrolagus	519	11	47.8	10	2	Q8SHG8	Q8shg8 chamaeleo g
447	11	47.8	10	1	GON2_SQUAC	P68074 squalus aca	520	11	47.8	10	2	Q8SHH1	Q8shh1 chamaeleo f
448	11	47.8	10	1	GON3_ONCKE	P20367 oncorhynch	521	11	47.8	10	2	Q8SHH4	Q8shh4 chamaeleo f
449	11	47.8	10	1	GON3_PETMA	P30948 petromyzon	522	11	47.8	10	2	Q8SHH7	Q8shh7 chamaeleo e
450	11	47.8	10	1	GONL_LITSP	P27429 squalus aca	523	11	47.8	10	2	Q8SHI0	Q8shi0 chamaeleo d
451	11	47.8	10	1	GRP_RANRI	P23260 rana ridibu	524	11	47.8	10	2	Q8SHI3	Q8shi3 chamaeleo c
452	11	47.8	10	1	LABA_JATMU	P13270 jatroph	525	11	47.8	10	2	Q8SHI6	Q8shi6 chamaeleo c
453	11	47.8	10	1	MP2_MICOC	P81533 microplitis	526	11	47.8	10	2	Q8SHI9	Q8shi9 chamaeleo c
454	11	47.8	10	1	NO40_TOBAC	P55962 nicotiana t	527	11	47.8	10	2	Q8SHJ2	Q8shj2 chamaeleo a
455	11	47.8	10	1	PNAL_PRUDU	P81899 prunus dulc	528	11	47.8	10	2	Q8SHJ5	Q8shj5 calumma par
456	11	47.8	10	1	TPIS_NICPL	P19118 nicotiana p	529	11	47.8	10	2	Q8SHJ8	Q8shj8 calumma osh
457	11	47.8	10	2	Q7M530	Q7m530 pyrococcus	530	11	47.8	10	2	Q8SHK1	Q8shk1 calumma nas
458	11	47.8	10	2	Q7M4X1	Q7m4x1 basidiobolu	531	11	47.8	10	2	Q8SHK4	Q8shk4 calumma hil
459	11	47.8	10	2	Q7SA62	Q7sa62 neurospora	532	11	47.8	10	2	Q8SHK7	Q8shk7 calumma glo
460	11	47.8	10	2	Q15342	Q15342 homo sapien	533	11	47.8	10	2	Q8SHL0	Q8shl0 calumma gas
461	11	47.8	10	2	Q8WTT4	Q8wt44 homo sapien	534	11	47.8	10	2	Q8SHL3	Q8shl3 calumma fur
462	11	47.8	10	2	Q96QA7	Q96qa7 homo sapien	535	11	47.8	10	2	Q8SHL6	Q8shl6 calumma cuc
463	11	47.8	10	2	Q6LA62	Q6la62 homo sapien	536	11	47.8	10	2	Q8SHL9	Q8shl9 calumma bre
464	11	47.8	10	2	Q25355	Q25355 locusta mig	537	11	47.8	10	2	Q8SHM2	Q8shm2 calumma boe
465	11	47.8	10	2	Q25356	Q25356 locusta mig	538	11	47.8	10	2	Q8SHM5	Q8shm5 bradypodion
466	11	47.8	10	2	Q7RRV6	Q7rrv6 plasmodium	539	11	47.8	10	2	Q8SHM8	Q8shm8 bradypodion
467	11	47.8	10	2	Q7M2Z8	Q7m2z8 bos taurus	540	11	47.8	10	2	Q8SHN1	Q8shn1 bradypodion
468	11	47.8	10	2	Q7M3E8	Q7m3e8 sus scrofa	541	11	47.8	10	2	Q8SHN4	Q8shn4 bradypodion
469	11	47.8	10	2	Q9N1X1	Q9n1x1 equus cabal	542	11	47.8	10	2	Q8SHN7	Q8shn7 bradypodion



543	11	47.8	10	2	Q8SHPO	Q8shp0 bradypodion	616	11	47.8	10	2	Q6WBL6	Q6wbl6 sceloporos
544	11	47.8	10	2	Q8SIT8	Q8sit8 xantusia ar	617	11	47.8	10	2	Q6WBL9	Q6wbl9 sceloporos
545	11	47.8	10	2	Q8SIU1	Q8siu1 xantusia be	618	11	47.8	10	2	Q6WBM2	Q6wbm2 sceloporos
546	11	47.8	10	2	Q8SIU4	Q8siu4 xantusia he	619	11	47.8	10	2	Q6WBM5	Q6wbm5 sceloporos
547	11	47.8	10	2	Q8W916	Q8w916 liolaemus m	620	11	47.8	10	2	Q6WBM8	Q6wbm8 sceloporos
548	11	47.8	10	2	Q8WDG8	Q8wdg8 anolis line	621	11	47.8	10	2	Q6WBN1	Q6wbn1 sceloporos
549	11	47.8	10	2	Q8WDI0	Q8wdi0 anolis sagr	622	11	47.8	10	2	Q6WBN4	Q6wbn4 sceloporos
550	11	47.8	10	2	Q8WFT5	Q8wft5 diadema ant	623	11	47.8	10	2	Q6WBP0	Q6wbp0 sceloporos
551	11	47.8	10	2	Q8WFT6	Q8wft6 diadema ant	624	11	47.8	10	2	Q6WBP3	Q6wbp3 sceloporos
552	11	47.8	10	2	Q94NH4	Q94nh4 rana muscos	625	11	47.8	10	2	Q6WBP6	Q6wbp6 sceloporos
553	11	47.8	10	2	Q94PD8	Q94pd8 varanus sca	626	11	47.8	10	2	Q6WBP9	Q6wbp9 sceloporos
554	11	47.8	10	2	Q94V85	Q94v85 varanus var	627	11	47.8	10	2	Q6WBQ2	Q6wbq2 sceloporos
555	11	47.8	10	2	Q94V97	Q94v97 varanus spe	628	11	47.8	10	2	Q6WBQ5	Q6wbq5 sceloporos
556	11	47.8	10	2	Q94VC9	Q94vc9 varanus pan	629	11	47.8	10	2	Q6WBQ8	Q6wbq8 sceloporos
557	11	47.8	10	2	Q94VD2	Q94vd2 varanus pan	630	11	47.8	10	2	Q6WBR7	Q6wbr7 sceloporos
558	11	47.8	10	2	Q94VD5	Q94vd5 varanus oli	631	11	47.8	10	2	Q6WBS0	Q6wbs0 sceloporos
559	11	47.8	10	2	Q94VF0	Q94vf0 varanus kin	632	11	47.8	10	2	Q6WBS6	Q6wbs6 sceloporos
560	11	47.8	10	2	Q94VG5	Q94vg5 varanus gri	633	11	47.8	10	2	Q6WBS9	Q6wbs9 sceloporos
561	11	47.8	10	2	Q94VH1	Q94vh1 varanus gle	634	11	47.8	10	2	Q6WBT2	Q6wbt2 sceloporos
562	11	47.8	10	2	Q958J8	Q958j8 rana muscos	635	11	47.8	10	2	Q6WBT5	Q6wbt5 sceloporos
563	11	47.8	10	2	Q958K0	Q958k0 rana cascad	636	11	47.8	10	2	Q6WBU7	Q6wbu7 urosaurus o
564	11	47.8	10	2	Q958K3	Q958k3 rana aurora	637	11	47.8	10	2	Q6WBV0	Q6wbv0 callisaurus
565	11	47.8	10	2	Q958K6	Q958k6 rana pretio	638	11	47.8	10	2	Q6WBV3	Q6wbv3 holbrookia
566	11	47.8	10	2	Q958K9	Q958k9 rana boylli	639	11	47.8	10	2	Q6WBV6	Q6wbv6 holbrookia
567	11	47.8	10	2	Q958L2	Q958l2 rana tempor	640	11	47.8	10	2	Q6WBV9	Q6wbv9 cophosaurus
568	11	47.8	10	2	Q958L5	Q958l5 rana sylvat	641	11	47.8	10	2	Q6X0E4	Q6x0e4 anolis stra
569	11	47.8	10	2	Q958L8	Q958l8 rana catesb	642	11	47.8	10	2	Q71DS1	Q71ds1 microlophus
570	11	47.8	10	2	Q6UJG7	Q6ujg7 heteronotia	643	11	47.8	10	2	Q71DV1	Q71dv1 sceloporos
571	11	47.8	10	2	Q6UJH0	Q6ujh0 gehyra vari	644	11	47.8	10	2	Q71DV4	Q71dv4 sceloporos
572	11	47.8	10	2	Q6UJH3	Q6ujh3 lialis jica	645	11	47.8	10	2	Q71DV7	Q71dv7 sceloporos
573	11	47.8	10	2	Q6UJH6	Q6ujh6 pseudotheca	646	11	47.8	10	2	Q71E02	Q71e02 anolis dist
574	11	47.8	10	2	Q6UJH9	Q6ujh9 phyllurus c	647	11	47.8	10	2	Q71E05	Q71e05 anolis cris
575	11	47.8	10	2	Q6UJ12	Q6uj12 nephurus m	648	11	47.8	10	2	Q71E14	Q71e14 brachylophu
576	11	47.8	10	2	Q6UJ15	Q6uj15 nephurus w	649	11	47.8	10	2	Q71E26	Q71e26 corytophane
577	11	47.8	10	2	Q6UJ18	Q6uj18 nephurus l	650	11	47.8	10	2	Q71E29	Q71e29 laemactus
578	11	47.8	10	2	Q6UJ11	Q6uj11 nephurus v	651	11	47.8	10	2	Q71E32	Q71e32 basiliscus
579	11	47.8	10	2	Q6UJ14	Q6uj14 nephurus l	652	11	47.8	10	2	Q71G22	Q71gz2 andrena lim
580	11	47.8	10	2	Q6UJ17	Q6uj17 carphodactyl	653	11	47.8	10	2	Q71SB8	Q71sb8 liolaemus r
581	11	47.8	10	2	Q6UJ10	Q6uj10 orenadactyl	654	11	47.8	10	2	Q71SC1	Q71sc1 liolaemus f
582	11	47.8	10	2	Q6UJ13	Q6uj13 oedura marm	655	11	47.8	10	2	Q71SC4	Q71sc4 liolaemus a
583	11	47.8	10	2	Q6UJ16	Q6uj16 rhynchoedur	656	11	47.8	10	2	Q71SC7	Q71sc7 liolaemus s
584	11	47.8	10	2	Q6UJ19	Q6uj19 diplodactyl	657	11	47.8	10	2	Q71SD6	Q71sd6 liolaemus a
585	11	47.8	10	2	Q6UJ18	Q6uj18 strophurus	658	11	47.8	10	2	Q71SD9	Q71sd9 liolaemus a
586	11	47.8	10	2	Q6UJ11	Q6uj11 strophurus	659	11	47.8	10	2	Q71SE2	Q71se2 phymaturus
587	11	47.8	10	2	Q6UJ14	Q6uj14 diplodactyl	660	11	47.8	10	2	Q71SE5	Q71se5 phymaturus
588	11	47.8	10	2	Q6UJ17	Q6uj17 strophurus	661	11	47.8	10	2	Q71SE8	Q71se8 ctenoblepha
589	11	47.8	10	2	Q6UJ10	Q6uj10 diplodactyl	662	11	47.8	10	2	Q76MK5	Q76mk5 eurypharynx
590	11	47.8	10	2	Q6UJ13	Q6uj13 diplodactyl	663	11	47.8	10	2	Q76ML6	Q76ml6 eurypharynx
591	11	47.8	10	2	Q6UJ16	Q6uj16 diplodactyl	664	11	47.8	10	2	Q76MM1	Q76mm1 eurypharynx
592	11	47.8	10	2	Q6UJ19	Q6uj19 diplodactyl	665	11	47.8	10	2	Q7J5U5	Q7j5u5 ovis aries
593	11	47.8	10	2	Q6UJ12	Q6uj12 diplodactyl	666	11	47.8	10	2	Q85J75	Q85j75 varanus bre
594	11	47.8	10	2	Q6UJ15	Q6uj15 diplodactyl	667	11	47.8	10	2	Q9B0Z6	Q9b0z6 salamandra
595	11	47.8	10	2	Q6UJ18	Q6uj18 diplodactyl	668	11	47.8	10	2	Q9B1W9	Q9b1w9 mertensiell
596	11	47.8	10	2	Q6UJ11	Q6uj11 diplodactyl	669	11	47.8	10	2	Q9B1X0	Q9b1x0 mertensiell
597	11	47.8	10	2	Q6UJ14	Q6uj14 strophurus	670	11	47.8	10	2	Q9B4S0	Q9b4s0 mertensiell
598	11	47.8	10	2	Q6UJ17	Q6uj17 strophurus	671	11	47.8	10	2	Q9B4S5	Q9b4s5 mertensiell
599	11	47.8	10	2	Q6UJ10	Q6uj10 strophurus	672	11	47.8	10	2	Q9B4S8	Q9b4s8 mertensiell
600	11	47.8	10	2	Q6WBG8	Q6wbg8 liolaemus c	673	11	47.8	10	2	Q9B4T1	Q9b4t1 mertensiell
601	11	47.8	10	2	Q6WBH1	Q6wbh1 liolaemus x	674	11	47.8	10	2	Q9B4U2	Q9b4u2 mertensiell
602	11	47.8	10	2	Q6WBH4	Q6wbh4 liolaemus r	675	11	47.8	10	2	Q9B4U5	Q9b4u5 mertensiell
603	11	47.8	10	2	Q6WBH7	Q6wbh7 liolaemus h	676	11	47.8	10	2	Q9B4U8	Q9b4u8 salamandra
604	11	47.8	10	2	Q6WBI0	Q6wbi0 liolaemus s	677	11	47.8	10	2	Q9B4V5	Q9b4v5 mertensiell
605	11	47.8	10	2	Q6WBI3	Q6wbi3 liolaemus p	678	11	47.8	10	2	Q9B4V8	Q9b4v8 chioglossa
606	11	47.8	10	2	Q6WBI6	Q6wbi6 liolaemus k	679	11	47.8	10	2	Q9B4W1	Q9b4w1 triturus vu
607	11	47.8	10	2	Q6WBI9	Q6wbi9 liolaemus h	680	11	47.8	10	2	Q9B4W4	Q9b4w4 pachytriton
608	11	47.8	10	2	Q6WBJ2	Q6wbj2 liolaemus p	681	11	47.8	10	2	Q9B4W7	Q9b4w7 tylototrito
609	11	47.8	10	2	Q6WBJ5	Q6wbj5 liolaemus g	682	11	47.8	10	2	Q9B4X0	Q9b4x0 notophthalm
610	11	47.8	10	2	Q6WBJ8	Q6wbj8 liolaemus n	683	11	47.8	10	2	Q9G362	Q9g362 acanthosaur
611	11	47.8	10	2	Q6WBK1	Q6wbk1 sceloporos	684	11	47.8	10	2	Q9G694	Q9g694 leirolepis g
612	11	47.8	10	2	Q6WBK4	Q6wbk4 sceloporos	685	11	47.8	10	2	Q9G697	Q9g697 chamaeleo d
613	11	47.8	10	2	Q6WBK7	Q6wbk7 sceloporos	686	11	47.8	10	2	Q9MJQ5	Q9mjq5 podospora c
614	11	47.8	10	2	Q6WBL0	Q6wbl0 sceloporos	687	11	47.8	10	2	Q9T4P9	Q9t4p9 liolaemus d
615	11	47.8	10	2	Q6WBL3	Q6wbl3 sceloporos	688	11	47.8	10	2	Q9T8F5	Q9t8f5 liolaemus b

689	11	47.8	10	2	Q9T8G0	Q9t8g0	liolaemus l	762	11	47.8	10	2	Q9TG74	Q9tg74	wetmorena h
690	11	47.8	10	2	Q9T8G5	Q9t8g5	liolaemus o	763	11	47.8	10	2	Q9TG77	Q9tg77	sauresia ag
691	11	47.8	10	2	Q9T8G8	Q9t8g8	liolaemus c	764	11	47.8	10	2	Q9TG80	Q9tg80	ophiodes st
692	11	47.8	10	2	Q9T8H1	Q9t8h1	liolaemus u	765	11	47.8	10	2	Q9TG83	Q9tg83	diploglossu
693	11	47.8	10	2	Q9T8H4	Q9t8h4	liolaemus i	766	11	47.8	10	2	Q9TG86	Q9tg86	diploglossu
694	11	47.8	10	2	Q9T8H7	Q9t8h7	liolaemus a	767	11	47.8	10	2	Q9TG89	Q9tg89	celestus en
695	11	47.8	10	2	Q9T8I0	Q9t8i0	liolaemus o	768	11	47.8	10	2	Q9TG92	Q9tg92	anniella pu
696	11	47.8	10	2	Q9T8I3	Q9t8i3	liolaemus q	769	11	47.8	10	2	Q9TG95	Q9tg95	anniella ge
697	11	47.8	10	2	Q9T8I6	Q9t8i6	liolaemus k	770	11	47.8	10	2	Q9TG98	Q9tg98	shinisaurus
698	11	47.8	10	2	Q9T8I9	Q9t8i9	liolaemus a	771	11	47.8	10	2	Q9TGA1	Q9tga1	heloderma s
699	11	47.8	10	2	Q9T8J2	Q9t8j2	liolaemus r	772	11	47.8	10	2	Q9XMB4	Q9xmb4	aegilops ta
700	11	47.8	10	2	Q9T8J5	Q9t8j5	liolaemus m	773	11	47.8	10	2	Q9ZYS9	Q9zys9	phymaturus
701	11	47.8	10	2	Q9T8J8	Q9t8j8	liolaemus w	774	11	47.8	10	2	Q9ZYT5	Q9zyt5	uta stansbu
702	11	47.8	10	2	Q9T8K1	Q9t8k1	liolaemus s	775	11	47.8	10	2	Q9ZYT8	Q9zyt8	urosaurus g
703	11	47.8	10	2	Q9T8K4	Q9t8k4	liolaemus s	776	11	47.8	10	2	Q9ZYU1	Q9zyu1	uma scopari
704	11	47.8	10	2	Q9T8K7	Q9t8k7	liolaemus m	777	11	47.8	10	2	Q9ZYU4	Q9zyu4	sceloporus
705	11	47.8	10	2	Q9T8L0	Q9t8l0	liolaemus o	778	11	47.8	10	2	Q9ZYU7	Q9zyu7	sator angus
706	11	47.8	10	2	Q9T8L3	Q9t8l3	liolaemus l	779	11	47.8	10	2	Q9ZVVO	Q9zyv0	petrosaurus
707	11	47.8	10	2	Q9T8L6	Q9t8l6	liolaemus p	780	11	47.8	10	2	Q9ZVY3	Q9zyv3	dipsosaurus
708	11	47.8	10	2	Q9T8L9	Q9t8l9	liolaemus f	781	11	47.8	10	2	P82443	P82443	nicotiana t
709	11	47.8	10	2	Q9T8M2	Q9t8m2	liolaemus c	782	11	47.8	10	2	Q99213	Q99213	aegilops ta
710	11	47.8	10	2	Q9T8M5	Q9t8m5	liolaemus a	783	11	47.8	10	2	Q6TS30	Q6ts30	lycopersico
711	11	47.8	10	2	Q9T8M8	Q9t8m8	liolaemus m	784	11	47.8	10	2	Q8GZC8	Q8gzc8	hordeum vul
712	11	47.8	10	2	Q9T8N1	Q9t8n1	liolaemus p	785	11	47.8	10	2	Q8KHN9	Q8khn9	clostridium
713	11	47.8	10	2	Q9T8N4	Q9t8n4	liolaemus d	786	11	47.8	10	2	Q93LX4	Q93lx4	vibrio chol
714	11	47.8	10	2	Q9T8N7	Q9t8n7	liolaemus o	787	11	47.8	10	2	Q93T35	Q93t35	acinetobact
715	11	47.8	10	2	Q9T8P0	Q9t8p0	liolaemus f	788	11	47.8	10	2	Q47561	Q47561	escherichia
716	11	47.8	10	2	Q9T8P3	Q9t8p3	liolaemus a	789	11	47.8	10	2	Q6JL97	Q6jl97	neisseria g
717	11	47.8	10	2	Q9T8P6	Q9t8p6	liolaemus r	790	11	47.8	10	2	Q6R101	Q6r101	clostridium
718	11	47.8	10	2	Q9T8P9	Q9t8p9	liolaemus m	791	11	47.8	10	2	Q79AV7	Q79av7	klebsiella
719	11	47.8	10	2	Q9T8Q2	Q9t8q2	liolaemus s	792	11	47.8	10	2	Q8G8W5	Q8g8w5	borrelia bu
720	11	47.8	10	2	Q9T8Q5	Q9t8q5	liolaemus l	793	11	47.8	10	2	Q9F9H5	Q9f9h5	helicobacte
721	11	47.8	10	2	Q9T8Q8	Q9t8q8	liolaemus e	794	11	47.8	10	2	Q9R5N2	Q9r5n2	clostridium
722	11	47.8	10	2	Q9T8R1	Q9t8r1	liolaemus a	795	11	47.8	10	2	O70580	O70580	mus musculu
723	11	47.8	10	2	Q9T8R4	Q9t8r4	liolaemus p	796	11	47.8	10	2	Q6LBT3	Q6lbt3	mus musculu
724	11	47.8	10	2	Q9T8R7	Q9t8r7	liolaemus c	797	11	47.8	10	2	Q8CJE0	Q8cje0	rattus norv
725	11	47.8	10	2	Q9T8R9	Q9t8r9	liolaemus b	798	11	47.8	10	2	Q9ESU5	Q9esu5	mus musculu
726	11	47.8	10	2	Q9T8S1	Q9t8s1	liolaemus l	799	11	47.8	10	2	O42355	O42355	brachydanio
727	11	47.8	10	2	Q9T8S4	Q9t8s4	liolaemus c	800	11	47.8	10	2	Q8JFE7	Q8jfe7	ficedula al
728	11	47.8	10	2	Q9T8S7	Q9t8s7	liolaemus n	801	11	47.8	10	2	Q8J33	Q8jj33	ficedula hy
729	11	47.8	10	2	Q9T8T0	Q9t8t0	liolaemus f	802	11	47.8	10	2	Q7LZC5	Q7lzc5	kassina mac
730	11	47.8	10	2	Q9T8T3	Q9t8t3	liolaemus n	803	11	47.8	10	2	Q9PRU9	Q9pru9	sparus aura
731	11	47.8	10	2	Q9T8T6	Q9t8t6	liolaemus m	804	11	47.8	10	2	Q8UT83	Q8ut83	human immun
732	11	47.8	10	2	Q9T8T9	Q9t8t9	liolaemus l	805	11	47.8	11	1	CEP1_ACHF	P22790	achatina fu
733	11	47.8	10	2	Q9T8U2	Q9t8u2	liolaemus t	806	11	47.8	11	1	CX5A_CONAL	P58848	conus aulic
734	11	47.8	10	2	Q9T8U5	Q9t8u5	liolaemus z	807	11	47.8	11	1	CX5B_CONAL	P58849	conus aulic
735	11	47.8	10	2	Q9T8V0	Q9t8v0	liolaemus c	808	11	47.8	11	1	LPW_THETH	P05624	thermus the
736	11	47.8	10	2	Q9T8V3	Q9t8v3	liolaemus c	809	11	47.8	11	1	MLG_THETS	P41989	theromyzon
737	11	47.8	10	2	Q9T8V6	Q9t8v6	liolaemus b	810	11	47.8	11	1	OAIF_SARBU	P83518	sarcophaga
738	11	47.8	10	2	Q9T8V9	Q9t8v9	liolaemus g	811	11	47.8	11	1	RANC_RANPI	P08951	rana pipien
739	11	47.8	10	2	Q9T8W2	Q9t8w2	liolaemus b	812	11	47.8	11	1	RR2_CONAM	P42341	conopholis
740	11	47.8	10	2	Q9T8W5	Q9t8w5	liolaemus r	813	11	47.8	11	2	Q9C1R7	Q9c1r7	saccharomyc
741	11	47.8	10	2	Q9T8W8	Q9t8w8	liolaemus b	814	11	47.8	11	2	Q8TDA8	Q8tda8	homo sapien
742	11	47.8	10	2	Q9T8X4	Q9t8x4	liolaemus c	815	11	47.8	11	2	Q9UCR1	Q9ucr1	homo sapien
743	11	47.8	10	2	Q9T8X7	Q9t8x7	phymaturus	816	11	47.8	11	2	Q9UE69	Q9ue69	homo sapien
744	11	47.8	10	2	Q9TFU6	Q9tfu6	teratoscinc	817	11	47.8	11	2	Q9UEL0	Q9uel0	homo sapien
745	11	47.8	10	2	Q9TFU9	Q9tfu9	teratoscinc	818	11	47.8	11	2	Q6UZ55	Q6uz55	littorina s
746	11	47.8	10	2	Q9TFV2	Q9tfv2	teratoscinc	819	11	47.8	11	2	Q7RH63	Q7rh63	plasmodium
747	11	47.8	10	2	Q9TFV5	Q9tfv5	eublepharus	820	11	47.8	11	2	Q6DW13	Q6dw13	bos taurus
748	11	47.8	10	2	Q9TG32	Q9tg32	ophisaurus	821	11	47.8	11	2	Q9GL48	Q9gl48	sus scrofa
749	11	47.8	10	2	Q9TG35	Q9tg35	ophisaurus	822	11	47.8	11	2	Q77884	Q77884	oreochromis
750	11	47.8	10	2	Q9TG38	Q9tg38	ophisaurus	823	11	47.8	11	2	Q77885	Q77885	oreochromis
751	11	47.8	10	2	Q9TG41	Q9tg41	ophisaurus	824	11	47.8	11	2	Q77892	Q77892	oreochromis
752	11	47.8	10	2	Q9TG44	Q9tg44	anguis frag	825	11	47.8	11	2	Q77893	Q77893	oreochromis
753	11	47.8	10	2	Q9TG47	Q9tg47	ophisaurus	826	11	47.8	11	2	Q77894	Q77894	oreochromis
754	11	47.8	10	2	Q9TG50	Q9tg50	elgaria mul	827	11	47.8	11	2	Q77895	Q77895	oreochromis
755	11	47.8	10	2	Q9TG53	Q9tg53	elgaria pau	828	11	47.8	11	2	Q77896	Q77896	oreochromis
756	11	47.8	10	2	Q9TG56	Q9tg56	elgaria kin	829	11	47.8	11	2	Q77898	Q77898	oreochromis
757	11	47.8	10	2	Q9TG59	Q9tg59	elgaria coe	830	11	47.8	11	2	Q77906	Q77906	oreochromis
758	11	47.8	10	2	Q9TG62	Q9tg62	mesaspis mo	831	11	47.8	11	2	Q77908	Q77908	oreochromis
759	11	47.8	10	2	Q9TG65	Q9tg65	abronia oax	832	11	47.8	11	2	Q77913	Q77913	oreochromis
760	11	47.8	10	2	Q9TG68	Q9tg68	gerrhonotus	833	11	47.8	11	2	Q77914	Q77914	oreochromis
761	11	47.8	10	2	Q9TG71	Q9tg71	barisia imb	834	11	47.8	11	2	Q77918	Q77918	pseudotroph

835	11	47.8	11	2	078118	078118 oreochromis
836	11	47.8	11	2	078120	078120 oreochromis
837	11	47.8	11	2	09UEX7	09UEX7 homo sapien
838	11	47.8	11	2	079636	079636 laudakia hi
839	11	47.8	11	2	079639	079639 laudakia le
840	11	47.8	11	2	079642	079642 laudakia mi
841	11	47.8	11	2	079918	079918 physignathu
842	11	47.8	11	2	079921	079921 phrynoceph
843	11	47.8	11	2	079985	079985 laudakia ca
844	11	47.8	11	2	079986	079986 laudakia er
845	11	47.8	11	2	08MAZ1	08MAZ1 maripa pani
846	11	47.8	11	2	08MAZ3	08MAZ3 maripa repe
847	11	47.8	11	2	08MB39	08MB39 wilsonia hu
848	11	47.8	11	2	08MB58	08MB58 seddera hir
849	11	47.8	11	2	08MB77	08MB77 odonellia h
850	11	47.8	11	2	08MB79	08MB79 aniseia arg
851	11	47.8	11	2	08MB97	08MB97 merremia pe
852	11	47.8	11	2	08MBE1	08MBE1 ipomoea alb
853	11	47.8	11	2	08SKN0	08SKN0 ctenophorus
854	11	47.8	11	2	08SKN3	08SKN3 ctenophorus
855	11	47.8	11	2	08SKN6	08SKN6 ctenophorus
856	11	47.8	11	2	08SKN9	08SKN9 ctenophorus
857	11	47.8	11	2	08SKP2	08SKP2 ctenophorus
858	11	47.8	11	2	08SKP5	08SKP5 ctenophorus
859	11	47.8	11	2	08SKP8	08SKP8 ctenophorus
860	11	47.8	11	2	08SKQ1	08SKQ1 ctenophorus
861	11	47.8	11	2	08SKQ4	08SKQ4 ctenophorus
862	11	47.8	11	2	08SKQ7	08SKQ7 ctenophorus
863	11	47.8	11	2	08SKR0	08SKR0 rankinia di
864	11	47.8	11	2	08WC29	08WC29 ctenophorus
865	11	47.8	11	2	08WD02	08WD02 ctenophorus
866	11	47.8	11	2	08WD05	08WD05 ctenophorus
867	11	47.8	11	2	08WD08	08WD08 ctenophorus
868	11	47.8	11	2	08WD11	08WD11 ctenophorus
869	11	47.8	11	2	08WD14	08WD14 ctenophorus
870	11	47.8	11	2	08WD17	08WD17 ctenophorus
871	11	47.8	11	2	08WD20	08WD20 ctenophorus
872	11	47.8	11	2	08WD23	08WD23 ctenophorus
873	11	47.8	11	2	08WD26	08WD26 ctenophorus
874	11	47.8	11	2	08WD29	08WD29 ctenophorus
875	11	47.8	11	2	08WD50	08WD50 ceratophora
876	11	47.8	11	2	08WER4	08WER4 ceratophora
877	11	47.8	11	2	08WER7	08WER7 ceratophora
878	11	47.8	11	2	094V74	094V74 lanthanotus
879	11	47.8	11	2	094V77	094V77 heloderma s
880	11	47.8	11	2	094V94	094V94 varanus sto
881	11	47.8	11	2	094VB8	094VB8 varanus sal
882	11	47.8	11	2	094VE7	094VE7 varanus kom
883	11	47.8	11	2	094VG8	094VG8 varanus gou
884	11	47.8	11	2	094VH7	094VH7 varanus gil
885	11	47.8	11	2	094VI5	094VI5 varanus exa
886	11	47.8	11	2	094VK1	094VK1 varanus aca
887	11	47.8	11	2	06E5N1	06E5N1 ptyctolaemu
888	11	47.8	11	2	06WR61	06WR61 nandayus ne
889	11	47.8	11	2	06WR64	06WR64 neophema el
890	11	47.8	11	2	07M2E6	07M2E6 solanum tub
891	11	47.8	11	2	07M2F2	07M2F2 lycopersico
892	11	47.8	11	2	07Y9B6	07Y9B6 amphiboluru
893	11	47.8	11	2	07Y9B9	07Y9B9 tympanocryp
894	11	47.8	11	2	07Y9C2	07Y9C2 tympanocryp
895	11	47.8	11	2	07Y9C5	07Y9C5 tympanocryp
896	11	47.8	11	2	07Y9C8	07Y9C8 tympanocryp
897	11	47.8	11	2	07Y9D1	07Y9D1 tympanocryp
898	11	47.8	11	2	07Y9D4	07Y9D4 pogona vitt
899	11	47.8	11	2	07Y9D7	07Y9D7 pogona null
900	11	47.8	11	2	07Y9E0	07Y9E0 pogona mitc
901	11	47.8	11	2	07Y9E3	07Y9E3 pogona mino
902	11	47.8	11	2	07Y9E6	07Y9E6 pogona mini
903	11	47.8	11	2	07Y9E9	07Y9E9 pogona henr
904	11	47.8	11	2	07Y9F2	07Y9F2 pogona brev
905	11	47.8	11	2	07Y9F5	07Y9F5 lophognathu
906	11	47.8	11	2	07Y9F8	07Y9F8 hypsilurus
907	11	47.8	11	2	07Y9G1	07Y9G1 hypsilurus

908	11	47.8	11	2	Q7Y9G4	Q7Y9G4 hypsilurus
909	11	47.8	11	2	Q7Y9G7	Q7Y9G7 hypsilurus
910	11	47.8	11	2	Q7Y9H0	Q7Y9H0 hypsilurus
911	11	47.8	11	2	Q7Y9H3	Q7Y9H3 hypsilurus
912	11	47.8	11	2	Q7Y9H6	Q7Y9H6 hypsilurus
913	11	47.8	11	2	Q7Y9H9	Q7Y9H9 diporiphora
914	11	47.8	11	2	Q7Y9I2	Q7Y9I2 diporiphora
915	11	47.8	11	2	Q7Y9I5	Q7Y9I5 diporiphora
916	11	47.8	11	2	Q7Y9I8	Q7Y9I8 diporiphora
917	11	47.8	11	2	Q7Y9J1	Q7Y9J1 diporiphora
918	11	47.8	11	2	Q7Y9J4	Q7Y9J4 diporiphora
919	11	47.8	11	2	Q7Y9J7	Q7Y9J7 diporiphora
920	11	47.8	11	2	Q7Y9K0	Q7Y9K0 diporiphora
921	11	47.8	11	2	Q7Y9K3	Q7Y9K3 diporiphora
922	11	47.8	11	2	Q7Y9K6	Q7Y9K6 diporiphora
923	11	47.8	11	2	Q7Y9K9	Q7Y9K9 amphiboluru
924	11	47.8	11	2	Q7Y9L3	Q7Y9L3 amphiboluru
925	11	47.8	11	2	Q7Y9L5	Q7Y9L5 amphiboluru
926	11	47.8	11	2	Q9G2N4	Q9G2N4 chlamydsau
927	11	47.8	11	2	Q9G350	Q9G350 laudakia sa
928	11	47.8	11	2	Q9G353	Q9G353 trapelus sa
929	11	47.8	11	2	Q9G356	Q9G356 agama atra
930	11	47.8	11	2	Q9G371	Q9G371 pogona barb
931	11	47.8	11	2	Q9G374	Q9G374 moloch horr
932	11	47.8	11	2	Q9G5V0	Q9G5V0 laudakia st
933	11	47.8	11	2	Q9G5V3	Q9G5V3 phrynoceph
934	11	47.8	11	2	Q9G5V6	Q9G5V6 phrynoceph
935	11	47.8	11	2	Q9G5V9	Q9G5V9 laudakia st
936	11	47.8	11	2	Q9G5W2	Q9G5W2 laudakia tu
937	11	47.8	11	2	Q9G5W5	Q9G5W5 laudakia nu
938	11	47.8	11	2	Q9G5W8	Q9G5W8 trapelus sa
939	11	47.8	11	2	Q9G5X1	Q9G5X1 trapelus pe
940	11	47.8	11	2	Q9G5X4	Q9G5X4 trapelus ag
941	11	47.8	11	2	Q9G5X7	Q9G5X7 trapelus ru
942	11	47.8	11	2	Q9G5Y0	Q9G5Y0 pseudotrape
943	11	47.8	11	2	Q9G5Y3	Q9G5Y3 agama impal
944	11	47.8	11	2	Q9G5Y6	Q9G5Y6 agama agama
945	11	47.8	11	2	Q9G5Z5	Q9G5Z5 japalura sp
946	11	47.8	11	2	Q9G5Z8	Q9G5Z8 acanthosaur
947	11	47.8	11	2	Q9G604	Q9G604 gonoccephalu
948	11	47.8	11	2	Q9G610	Q9G610 lyriocephal
949	11	47.8	11	2	Q9G613	Q9G613 cophotis ce
950	11	47.8	11	2	Q9G616	Q9G616 ceratophora
951	11	47.8	11	2	Q9G619	Q9G619 ceratophora
952	11	47.8	11	2	Q9G622	Q9G622 salea horsf
953	11	47.8	11	2	Q9G637	Q9G637 calotes lio
954	11	47.8	11	2	Q9G652	Q9G652 japalura va
955	11	47.8	11	2	Q9G655	Q9G655 japalura tr
956	11	47.8	11	2	Q9G658	Q9G658 hydrosaurus
957	11	47.8	11	2	Q9G661	Q9G661 tympanocryp
958	11	47.8	11	2	Q9G664	Q9G664 diporiphora
959	11	47.8	11	2	Q9G667	Q9G667 caimanops a
960	11	47.8	11	2	Q9G670	Q9G670 rankinia ad
961	11	47.8	11	2	Q9G673	Q9G673 ctenophorus
962	11	47.8	11	2	Q9G676	Q9G676 amphiboluru
963	11	47.8	11	2	Q9G679	Q9G679 hypsilurus
964	11	47.8	11	2	Q9G682	Q9G682 chelosania
965	11	47.8	11	2	Q9G685	Q9G685 arua modest
966	11	47.8	11	2	Q9G688	Q9G688 physignathu
967	11	47.8	11	2	Q9G691	Q9G691 lophognathu
968	11	47.8	11	2	Q9GD68	Q9GD68 elaeis guin
969	11	47.8	11	2	Q94IR5	Q94IR5 pinus radia
970	11	47.8	11	2	Q6T302	Q6T302 chlamydomon
971	11	47.8	11	2	Q7M1U2	Q7M1U2 oryza sativ
972	11	47.8	11	2	Q7M1W2	Q7M1W2 canavalia e
973	11	47.8	11	2	Q47602	Q47602 escherichia
974	11	47.8	11	2	Q56413	Q56413 escherichia
975	11	47.8	11	2	Q700S6	Q700S6 mycoplasma
976	11	47.8	11	2	Q798K4	Q798K4 bacillus su
977	11	47.8	11	2	Q8GL19	Q8GL19 borrelia bu
978	11	47.8	11	2	Q8GL24	Q8GL24 borrelia bu
979	11	47.8	11	2	Q8K432	Q8K432 spalax juda
980	11	47.8	11	2	Q8K433	Q8K433 spalax gall

981 11 47.8 11 2 Q99J33 Q99j33 rattus sp.  
982 11 47.8 11 2 Q6LD68 Q6ld68 mus sp. acu  
983 11 47.8 11 2 Q80W11 Q80wil mus sp. nt-  
984 11 47.8 11 2 Q8CGW6 Q8cgw6 rattus norv  
985 11 47.8 11 2 Q9QVH3 Q9qvh3 rattus sp.  
986 11 47.8 11 2 Q80GP0 Q80gp0 tomato leaf  
987 11 47.8 11 2 Q65CG7 Q65cg7 sinloa tom  
988 11 47.8 11 2 Q90735 Q90735 gallus gall  
989 11 47.8 11 2 Q7LZ10 Q7lzi0 gadus sp. a  
990 11 47.8 11 2 Q83410 Q83410 mouse mamma  
991 11 47.8 11 2 Q8ADI8 Q8adi8 human immun  
992 11 47.8 11 2 Q9D232 Q9dz32 human immun  
993 11 47.8 12 1 LICA\_BACSU P83878 bacillus su  
994 11 47.8 12 1 NO40\_LOTJA O22426 lotus japon  
995 11 47.8 12 1 NO40\_SESRO O24369 sesbania ro  
996 11 47.8 12 1 NO40\_SOYBN P55960 glycine max  
997 11 47.8 12 1 RF1\_CONSP P58805 conus spuri  
998 11 47.8 12 1 UP0I\_CAEEL P55954 caenorhabdi  
999 11 47.8 12 1 UR2A\_CATCO P04558 catostomus  
1000 11 47.8 12 2 Q90XU4 Q90xu4 phalacrocor

ALIGNMENTS

RESULT 1  
AKH\_HELZE STANDARD; PRT; 9 AA.  
AC P67787; P08901; AC  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 25-OCT-2004 (Rel. 45, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Adipokinetic hormone (Hex-AKH)  
OS Heliothis zea (Corn earworm) (Bollworm).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;  
OC Noctuidae; Heliothinae; Helicoverpa.  
OX NCBI\_TaxID=7113;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=86186794; PubMed=3964263;  
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Holman G.M.,  
RA Wagner R.M., Ridgway R.L., Hayes D.K.;  
RT "Isolation and primary structure of a peptide from the corpora  
cardiaca of Heliothis zea with adipokinetic activity.";  
RL Biochem. Biophys. Res. Commun. 135:622-628(1986).  
CC -1- FUNCTION: This hormone, released from cells in the corpora  
cardiaca after the beginning of flight, causes release of  
diglycerides from the fat body and then stimulates the flight  
muscles to use these diglycerides as an energy source.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.  
DR PIR; A24244; A24244.  
DR InterPro; IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
KW Amidation; Direct protein sequencing; Flight; Neuropeptide;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 Pyrrolidone carboxylic acid.  
FT MOD\_RES 9 9 Glycine amide.  
SQ SEQUENCE 9 AA; 1026 MW; 403665A5A1A9D1A7 CRC64;

Query Match 73.9%; Score 17; DB 1; Length 9;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
| |  
Db 4 FTSSW 8

RESULT 2  
Q9XLI2 PRELIMINARY; PRT; 13 AA.  
, ID Q9XLI2

AC Q9XLI2;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome oxidase I (Fragment).  
OS Bemisia tabaci (Sweetpotato whitefly).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aleyrodiformes;  
OC Aleyrodidae; Aleyrodidae; Aleyrodinae; Bemisia.  
OX NCBI\_TaxID=7038;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=10583831;  
RA Frohlich D.R., Torres-Jerez I., Bedford I.D., Markham P.G.,  
RA Brown J.K.;  
RT "A phylogeographical analysis of the Bemisia tabaci species complex  
based on mitochondrial DNA markers.";  
RL Mol. Ecol. 8:1683-1691(1999).  
DR EMBL; AF110703; AAD28415.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 1 1  
SQ SEQUENCE 13 AA; 1639 MW; 8DD68729F5744365 CRC64;

Query Match 73.9%; Score 17; DB 2; Length 13;  
Best Local Similarity 40.0%; Pred. No. 2.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
| |  
Db 3 FTSSW 7

RESULT 3  
AKHG\_GRYBI STANDARD; PRT; 8 AA.  
ID AKHG GRYBI  
AC P67785; P14086;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Adipokinetic hormone G (AKH-G).  
OS Gryllus bimaculatus (Two-spotted cricket).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;  
OC Gryllus.  
OX NCBI\_TaxID=6999;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Corpora cardiaca;  
RX MEDLINE=88106553; PubMed=3426616;  
RA Gaede G., Rinehart K.L. Jr.;  
RT "Primary sequence analysis by fast atom bombardment mass spectrometry  
of a peptide with adipokinetic activity from the corpora cardiaca of  
the cricket Gryllus bimaculatus.";  
RL Biochem. Biophys. Res. Commun. 149:908-914(1987).  
CC -1- FUNCTION: This hormone, released from cells in the corpora  
cardiaca after the beginning of flight, causes release of  
diglycerides from the fat body and then stimulates the flight  
muscles to use these diglycerides as an energy source.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.  
DR PIR; A28004; A28004.  
DR InterPro; IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
KW Amidation; Direct protein sequencing; Flight; Neuropeptide;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 Pyrrolidone carboxylic acid.  
FT MOD\_RES 8 8 Tryptophan amide.  
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 69.6%; Score 16; DB 1; Length 8;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5  
|  
4 FSTGW 8

Db

RESULT 4  
AKH ROMMI STANDARD; PRT; 8 AA.  
AC P6786; P14086;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Adipokinetic hormone (AKH) (RO II).  
OS Romalea microptera (Lubber grasshopper).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Romaleidae; Romalea.  
OX NCBI\_TaxID=7007;  
RN [1]  
RP SEQUENCE.

RC TISSUE=Corpora cardiaca;  
RX MEDLINE=89145002; PubMed=3226948; DOI=10.1016/0196-9781(88)90107-6;  
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;  
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from  
the lubber grasshopper; Romalea microptera.";  
RL Peptides 9:681-688(1988).  
CC -!- FUNCTION: This hormone, released from cells in the corpora  
cardiaca after the beginning of flight, causes release of  
diglycerides from the fat body and then stimulates the flight  
muscles to use these diglycerides as an energy source.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.  
DR InterPro; IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
KW Amidation; Direct protein sequencing; Flight; Neuropeptide;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 Pyrrolidone carboxylic acid.  
FT MOD\_RES 8 8 Tryptophan amide.  
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 69.6%; Score 16; DB 1; Length 8;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5  
|  
4 FSTGW 8

Db

RESULT 5  
HTF\_HELZE STANDARD; PRT; 10 AA.  
AC P16353;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Hypertrehalosaemic hormone (HeZ-HRTH).  
OS Heliothis zea (Corn earworm) (Bollworm).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;  
OC Noctuidae; Heliothinae; Helicoverpa.  
OX NCBI\_TaxID=7113;  
RN [1]  
RP SEQUENCE.

RC TISSUE=Corpora cardiaca;  
RX MEDLINE=88326324; PubMed=3415690;  
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Bird T.G., Tseng C.M.,  
RA Zhang Y.S., Hayes D.K.;  
RT "Isolation and primary structure of a neuropeptide hormone from  
Heliothis zea with hypertrehalosemic and adipokinetic activities.";  
RL Biochem. Biophys. Res. Commun. 155:344-350(1988).

CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that  
elevate the level of trehalose in the hemolymph (trehalose is the  
major carbohydrate in the hemolymph of insects).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.  
DR PIR; A31571; A31571.  
DR InterPro; IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
KW Amidation; Direct protein sequencing; Neuropeptide;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 Pyrrolidone carboxylic acid.  
FT MOD\_RES 10 10 Asparagine amide.  
SQ SEQUENCE 10 AA; 1096 MW; 8E70367865A5B9D1 CRC64;

Query Match 69.6%; Score 16; DB 1; Length 10;  
Best Local Similarity 40.0%; Pred. No. 3.8e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5  
|  
4 FSSGW 8

Db

RESULT 6  
Q6ESN4 PRELIMINARY; PRT; 11 AA.  
AC Q6ESN4;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN Name=COI;  
OS Mantheyus phuwanensis.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;  
OC Mantheyus.  
OX NCBI\_TaxID=282162;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Schulte J.A. II, Vindum J.V., Win H., Thin T., Lwin K.S., Shein A.K.,  
RA Tun H.;  
RT "Phylogenetic relationships of the genus Ptyctolaemus (Squamata:  
Agamidae), with a description of a new species from the Chin Hills of  
Western Myanmar.";  
RL Proceedings Calif. Acad. Sci. 55:222-247(2004).  
DR EMBL; AY555836; AAT74867.1; -;  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1343 MW; 932D371E336411B1 CRC64;

Query Match 69.6%; Score 16; DB 2; Length 11;  
Best Local Similarity 40.0%; Pred. No. 4.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5  
|  
3 FTTRW 7

Db

RESULT 7  
Q9G649 PRELIMINARY; PRT; 11 AA.  
AC Q9G649;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN Name=COI;  
OS Otopharyngus wiegmanni.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;  
OC Otokryptis.  
OX NCBI\_TaxID=118220;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;  
RA Macey J.R., Schulte J.A. II, Larson A.;  
RT "Evolution and phylogenetic information content of mitochondrial  
RT genomic structural features illustrated with acrodont lizards.";  
RL Syst. Biol. 49:257-277(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;  
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
RT "Evaluating trans-tethys migration: an example using acrodont lizard  
RT phylogenetics.";  
RL Syst. Biol. 49:233-256(2000).  
DR EMBL; AF128480; AAG00677.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 11 11  
SQ SEQUENCE 11 AA; 1347 MW; 932D3710D3640DC1 CRC64;  
  
Query Match 69.6%; Score 16; DB 2; Length 11;  
Best Local Similarity 40.0%; Pred. No. 4.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 FXXXW 5  
Db 3 FTARW 7  
  
RESULT 8  
O15276 PRELIMINARY; PRT; 17 AA.  
ID O15276  
AC O15276;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Mitochondrial translation elongation factor EF-Tu (Fragment).  
GN Name=TUFM;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Jacobs H.T., Smurthwaite L., Koshy R.;  
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Y11797; CAA72493.1; -.  
DR GO; GO:0003746; F:translation elongation factor activity; IEA.  
KW Elongation factor.  
FT NON TER 1 1  
FT NON TER 17 17  
SQ SEQUENCE 17 AA; 2019 MW; BF737D12D2AB0A7E CRC64;  
  
Query Match 69.6%; Score 16; DB 2; Length 17;  
Best Local Similarity 40.0%; Pred. No. 5.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 FXXXW 5  
Db 1 FSLTW 5  
  
RESULT 9  
Q7Y1X8 PRELIMINARY; PRT; 17 AA.  
ID Q7Y1X8  
AC Q7Y1X8;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Male gametic cell-specific (Fragment).  
GN Name=LGC1;  
OS Lilium longiflorum (Trumpet lily).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Lilium.  
OX NCBI\_TaxID=4690;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22615576; PubMed=12729896; DOI=10.1016/S0014-5793(03)00335-1;  
RA Singh M., Bhalla P.L., Xu H., Singh M.B.;  
RT "Isolation and characterization of a flowering plant male gametic  
RT cell-specific promoter(1).";  
RL FEBS Lett. 542:47-52(2003).  
DR EMBL; AY207012; AAP37155.1; -.  
FT NON TER 17 17  
SQ SEQUENCE 17 AA; 1880 MW; 661B63484969679F CRC64;  
  
Query Match 69.6%; Score 16; DB 2; Length 17;  
Best Local Similarity 40.0%; Pred. No. 5.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 FXXXW 5  
Db 11 FSSVW 15  
  
RESULT 10  
O91329 PRELIMINARY; PRT; 19 AA.  
ID O91329  
AC O91329;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN Name=env;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98285741; PubMed=9621043;  
RA Belec L., Si Mohamed A., Muller-Trutwin M.C., Gilquin J., Gutmann L.,  
RA Safar M., Barre-Sinoussi F., Kazatchkine M.D.;  
RT "Genetically related human immunodeficiency virus type 1 in three  
RT adults of a family with no identified risk factor for intrafamilial  
RT transmission.";  
RL J. Virol. 72:5831-5839(1998).  
DR EMBL; U87220; AAC32980.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.  
FT NON TER 1 1  
SQ SEQUENCE 19 AA; 2324 MW; 379CB14A9E073911 CRC64;  
  
Query Match 69.6%; Score 16; DB 2; Length 19;  
Best Local Similarity 40.0%; Pred. No. 6.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 FXXXW 5  
Db 10 FNSTW 14  
  
RESULT 11  
Q9WJB1 PRELIMINARY; PRT; 19 AA.  
ID Q9WJB1  
AC Q9WJB1;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)



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DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98285741; PubMed=9621043;
RA Belec L., Si Mohamed A., Muller-Trutwin M.C., Gilquin J., Gutmann L.,
SAfar M., Barre-Sinoussi F., Kazatchkine M.D.;
RT "Genetically related human immunodeficiency virus type 1 in three
RT adults of a family with no identified risk factor for intrafamilial
RT transmission.";
RL J. Virol. 72:5831-5839(1998).
DR EMBL; U87216; AAC32976.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 19 AA; 2294 MW; 3781714A9E073911 CRC64;

Query Match 69.6%; Score 16; DB 2; Length 19;
Best Local Similarity 40.0%; Pred. No. 6.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 10 FNSTW 14

RESULT 12
Q6LD18
ID Q6LD18 PRELIMINARY; PRT; 20 AA.
AC Q6LD18;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Interferon alpha/beta receptor (Fragment).
GN Name=IFNAR;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95047447; PubMed=7958966; DOI=10.1016/0378-1119(94)90710-2;
RA Lutfalla G., Uze G.;
RT "Structure of the murine interferon alpha/beta receptor-encoding gene:
RT high-frequency rearrangements in the interferon-resistant L1210 cell
RT line.";
RL Gene 148:343-346(1994).
DR EMBL; U06242; AAC5007.1; -.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
KW Receptor.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2204 MW; 9B9C1DF0C12EBC43 CRC64;

Query Match 69.6%; Score 16; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 2 FSTIW 6
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RESULT 13
AKH_LIBAU
ID AKH_LIBAU STANDARD; PRT; 8 AA.
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Adipokinetic hormone (AKH).
OS Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
OX NCBI_TaxID=6966;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90359055; PubMed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokinetic/red-pigment-
RT concentrating hormone family isolated and sequenced from a
RT dragonfly.";
RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC -!- FUNCTION: This hormone, released from cells in the corpora
CC cardiaca after the beginning of flight, causes release of
CC diglycerides from the fat body and then stimulates the flight
CC muscles to use these diglycerides as an energy source.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; S10596; S10596.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Amidation; Direct protein sequencing; Flight; Neuropeptide;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT MOD_RES 8 8 Tryptophan amide.
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 65.2%; Score 15; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 4 FTPSW 8

RESULT 14
Q7M3N6
ID Q7M3N6 PRELIMINARY; PRT; 9 AA.
AC Q7M3N6;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Neuropeptide Grb-AST B4.
OS Gryllus bimaculatus (Two-spotted cricket).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllinae;
OC Gryllus.
OX NCBI_TaxID=6999;
RN [1]
RP SEQUENCE.
RX MEDLINE=95403341; PubMed=7673141; DOI=10.1074/jbc.270.36.21103;
RA Lorenz M.W., Kellner R., Hoffmann K.H.;
RT "A family of neuropeptides that inhibit juvenile hormone biosynthesis
RT in the cricket, Gryllus bimaculatus.";
RL J. Biol. Chem. 270:21103-21108(1995).
DR PIR; D57444; D57444.
SQ SEQUENCE 9 AA; 1175 MW; 3860B871E9D40B03 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
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Db 5 FHGSW 9 | |

RESULT 15

Q8WGE6 PRELIMINARY; PRT; 9 AA.

ID Q8WGE6

AC Q8WGE6;

DT 01-MAR-2002 (TReMBLrel. 20, Created)

DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)

DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)

DE Cytochrome oxidase subunit 1 (Fragment).

OS Procambarius clarkii (Red swamp crayfish).

OG Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;

OC Astacoidea; Cambaridae; Procambarius.

OX NCBI\_TaxID=6728;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21884466; PubMed=11886621; DOI=10.1098/rspb.2001.1886;

RA Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,

RA Cunningham C.W.;

RT "Mitochondrial gene rearrangements confirm the parallel evolution of

RT the crab-like form.";

RL Proc. R. Soc. Lond., B, Biol. Sci. 269:345-350(2002).

DR EMBL; AF436024; AAL31599.1; -.

DR GO; GO:0005739; C:mitochondrion; IEA.

KW Mitochondrion.

FT NON\_TER 1 1

FT NON\_TER 9 9

SQ SEQUENCE 9 AA; 1185 MW; 936BB9C733640321 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 9;

Best Local Similarity 40.0%; Pred. No. 1.6e+06;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db 1 FTKRW 5

RESULT 16

AKHX\_LOCM1 STANDARD; PRT; 10 AA.

ID AKHX LOCM1

AC P81626;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Peptide hormone.

OS Locusta migratoria (Migratory locust).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;

OC Acridoidea; Acrididae; Oedipodinae; Locusta.

OX NCBI\_TaxID=7004;

RN [1]

RP SEQUENCE.

RC TISSUE=Corpora cardiaca;

RA Siebert K.J.;

RL Submitted (DEC-1998) to Swiss-Prot.

CC -!- FUNCTION: Probably involved in the regulation of locust

CC intermediary metabolism, behavior and/or development.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.

DR InterPro; IPR02047; AKH.

DR PROSITE; PS00256; AKH; 1.

KW Amidation; Direct protein sequencing; Neuropeptide;

FT MOD\_RES 1 1 Pyrrolidone carboxylic acid.

FT MOD\_RES 10 10 Proline amide.

SQ SEQUENCE 10 AA; 1222 MW; 81BFF67AB415B9D1 CRC64;

Query Match 65.2%; Score 15; DB 1; Length 10;

Best Local Similarity 40.0%; Pred. No. 6.5e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db 4 FSRDW 8

RESULT 17

Q7M465 PRELIMINARY; PRT; 10 AA.

ID Q7M465

AC Q7M465;

DT 01-MAR-2004 (TReMBLrel. 26, Created)

DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)

DE Neuropeptide Pec-HrTH.

OS Platyleura capensis.

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Cicadoidea; Cicadidae;

OC Cicadinae; Platyleurini; Platyleura.

OX NCBI\_TaxID=70904;

RN [1]

RP SEQUENCE.

RA Gaede G., Janssens M.P.E.;

RT "Cicadas contain novel members of the AKH/RPCH family peptides with

RT hypertrehalosaemic activity.";

RL Biol. Chem. Hoppe-Seyler 375:803-809(1994).

DR PIR; S53789; S53789.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0005179; F:hormone activity; IEA.

DR InterPro; IPR002047; AKH.

DR PROSITE; PS00256; AKH; 1.

SQ SEQUENCE 10 AA; 1135 MW; 10823665A775B9C4 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 10;

Best Local Similarity 40.0%; Pred. No. 6.5e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db 4 FSPSW 8

RESULT 18

Q70F01 PRELIMINARY; PRT; 10 AA.

ID Q70F01

AC Q70F01;

DT 05-JUL-2004 (TReMBLrel. 27, Created)

DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)

DE Calpastatin type 2 (Fragment).

GN Name=CAST;

OS Sus scrofa (pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI\_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21531263; PubMed=11673859; DOI=10.1006/abbi.2001.2546;

RA Parr T., Sensky P.L., Bardsley R.G., Buttery P.J.;

RT "Calpastatin expression in porcine cardiac and skeletal muscle and

RT partial gene structure.";

RL Arch. Biochem. Biophys. 395:1-13(2001).

RN [2]

RP SEQUENCE FROM N.A.

RA Parr T.;

RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ583410; CAE47431.1; -.

FT NON\_TER 10 10

SQ SEQUENCE 10 AA; 1291 MW; CFF912436365BDD9 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 10;

Best Local Similarity 40.0%; Pred. No. 6.5e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5  
Db 3 FASW 7

RESULT 19  
O79897 PRELIMINARY; PRT; 10 AA.  
AC O79897;  
DT 01-NOV-1998 (TReMBLrel. 08, Created)  
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN Name=COI;  
OS Hoplocercus spinosus (Club-tail iguana).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Iguanidae; Hoplocercinae;  
OC Hoplocercus.  
OX NCBI\_TaxID=52193;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97315309; PubMed=9169559;  
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;  
RT "Evolutionary shifts in three major structural features of the  
RT mitochondrial genome among iguanian lizards.";  
RL J. Mol. Evol. 44:660-674(1997).  
DR EMBL; U82683; AAC62284.1; -.  
DR PIR; T17063; T17063.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 10 10  
SQ SEQUENCE 10 AA; 1288 MW; 0A3480C7336415B0 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 6.5e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5  
Db 2 FISRW 6

RESULT 20  
P92707 PRELIMINARY; PRT; 10 AA.  
AC P92707;  
DT 01-MAY-1997 (TReMBLrel. 03, Created)  
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN Name=COI;  
OS Platysaurus capensis.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;  
OC Cordylidae; Platysaurus.  
OX NCBI\_TaxID=52175;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97153826; PubMed=9000757;  
RA Macey J.R., Larson A., Ananjeva N.B., Fang Z., Papenfuss T.J.;  
RT "Two novel gene orders and the role of light-strand replication in  
RT rearrangement of the vertebrate mitochondrial genome.";  
RL Mol. Biol. Evol. 14:91-104(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97153820; PubMed=9000751;  
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;  
RT "Replication slippage may cause parallel evolution in the secondary  
RT structures of mitochondrial transfer RNAs.";

RL Mol. Biol. Evol. 14:30-39(1997).  
DR EMBL; U71329; AAB48286.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 10 10  
SQ SEQUENCE 10 AA; 1322 MW; 0A3480C9D36415B0 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 6.5e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5  
Db 2 FISRW 6

RESULT 21  
Q6UJL5 PRELIMINARY; PRT; 10 AA.  
AC Q6UJL5;  
DT 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN Name=COI;  
OS Strophurus pulcher.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Gekkota; Gekkonidae; Strophurus.  
OX NCBI\_TaxID=255186;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Melville J., Schulte J.A. II, Larson A.;  
RT "A Molecular Study of Phylogenetic Relationships and Evolution of  
RT Antipredator Strategies in Australian Diplodactylus Geckos, Subgenus  
RT Strophurus";  
RL Biol. J. Linn. Soc. Lond. 82:123-138(2004).  
DR EMBL; AY369011; AAR18865.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 10 10  
SQ SEQUENCE 10 AA; 1288 MW; 0A3480C7336415B0 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 6.5e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5  
Db 2 FISRW 6

RESULT 22  
Q6WBU4 PRELIMINARY; PRT; 10 AA.  
AC Q6WBU4;  
DT 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
DE Cytochrome oxidase subunit I (Fragment).  
GN Name=COI;  
OS Sceloporus siniferus.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;  
OC Sceloporus.  
OX NCBI\_TaxID=59719;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22801591; PubMed=12920297; DOI=10.1126/science.1084786;  
RA Harmon L.J., Schulte J.A., Larson A., Losos J.B.;  
RT "Tempo and mode of evolutionary radiation in iguanian lizards.";  
RL Science 301:961-964(2003).

DR EMBL; AY297494; AAP84453.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 10  
SQ SEQUENCE 10 AA; 1303 MW; 933480C733640451 CRC64;  
Query Match 65.2%; Score 15; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 6.5e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 FXXXW 5  
Db 2 FTNRW 6  
RESULT 23  
Q6X0E7 PRELIMINARY; PRT; 10 AA.  
ID Q6X0E7  
AC Q6X0E7;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Cytochrome oxidase subunit I (Fragment).  
GN Name=COI;  
OS Anolis marcanoi.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.  
OX NCBI\_TaxID=75264;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22990428; PubMed=14628926;  
RA Glor R.E., Kolbe J.J., Powell R., Larson A., Losos J.B.;  
RT "Phylogenetic analysis of ecological and morphological diversification  
in Hispaniolan trunk-ground anoles (Anolis cybotes group).";  
RL Evolution 57:2383-2397(2003).  
DR EMBL; AY263006; AAP94301.1; -.  
DR EMBL; AY263005; AAP94298.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 10  
SQ SEQUENCE 10 AA; 1370 MW; C93480C9D36411A9 CRC64;  
Query Match 65.2%; Score 15; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 6.5e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 FXXXW 5  
Db 2 FFTRW 6  
RESULT 24  
Q71DW3 PRELIMINARY; PRT; 10 AA.  
ID Q71DW3;  
AC Q71DW3;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN Name=COI;  
OS Polychrus marmoratus.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Polychrus.  
OX NCBI\_TaxID=38934;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Schulte J.A. II, Valladares J.P., Larson A.;  
RT "Phylogenetic relationships within Iguanidae inferred using molecular  
and morphological data and a phylogenetic taxonomy of iguanian  
lizards.";  
RL Herpetologica 59:399-419(2003).  
QY 1 FXXXW 5  
Db 2 FFTRW 6

RN [2]  
RP SEQUENCE FROM N.A.  
RA Schulte J.A., Valladares J.P., Larson A.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF528738; AAQ09176.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 10  
SQ SEQUENCE 10 AA; 1302 MW; 0A3480C7336411A0 CRC64;  
Query Match 65.2%; Score 15; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 6.5e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 FXXXW 5  
Db 2 FITRW 6  
RESULT 25  
Q71DW6 PRELIMINARY; PRT; 10 AA.  
ID Q71DW6  
AC Q71DW6;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN Name=COI;  
OS Polychrus acutirostris (Iguanid lizard).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Polychrus.  
OX NCBI\_TaxID=161137;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Schulte J.A. II, Valladares J.P., Larson A.;  
RT "Phylogenetic relationships within Iguanidae inferred using molecular  
and morphological data and a phylogenetic taxonomy of iguanian  
lizards.";  
RL Herpetologica 59:399-419(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Schulte J.A., Valladares J.P., Larson A.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF528737; AAQ09173.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 10  
SQ SEQUENCE 10 AA; 1302 MW; 0A3480C7336411A0 CRC64;  
Query Match 65.2%; Score 15; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 6.5e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 FXXXW 5  
Db 2 FITRW 6  
RESULT 26  
Q71DW9 PRELIMINARY; PRT; 10 AA.  
ID Q71DW9  
AC Q71DW9;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN Name=COI;  
OS Anisolepis longicauda.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anisolepis.  
OX NCBI\_TaxID=161142;

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RN [1]
RP SEQUENCE FROM N.A.
RA Schulte J.A. II, Valladares J.P., Larson A.;
RT "Phylogenetic relationships within Iguanidae inferred using molecular
and morphological data and a phylogenetic taxonomy of iguanian
lizards.";
RL Herpetologica 59:399-419(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Schulte J.A., Valladares J.P., Larson A.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF528736; AAQ09170.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 10
SQ SEQUENCE 10 AA; 1288 MW; 0A3480C7336415B0 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 2 FISRW 6

RESULT 27
Q71E17
ID Q71E17 PRELIMINARY; PRT; 10 AA.
AC Q71E17;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Morunasaurus annularis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Hoplacercinae;
OC Morunasaurus.
OX NCBI_TaxID=211988;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte J.A. II, Valladares J.P., Larson A.;
RT "Phylogenetic relationships within Iguanidae inferred using molecular
and morphological data and a phylogenetic taxonomy of iguanian
lizards.";
RL Herpetologica 59:399-419(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Schulte J.A., Valladares J.P., Larson A.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF528720; AAQ09122.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 10
SQ SEQUENCE 10 AA; 1288 MW; 0A3480C7336415B0 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 2 FISRW 6

RESULT 28
Q71E20
ID Q71E20 PRELIMINARY; PRT; 10 AA.
AC Q71E20;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Enyalioides laticeps (Amazon wood lizard).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Hoplacercinae;
OC Enyalioides.
OX NCBI_TaxID=51206;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte J.A. II, Valladares J.P., Larson A.;
RT "Phylogenetic relationships within Iguanidae inferred using molecular
and morphological data and a phylogenetic taxonomy of iguanian
lizards.";
RL Herpetologica 59:399-419(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Schulte J.A., Valladares J.P., Larson A.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF528719; AAQ09119.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 10
SQ SEQUENCE 10 AA; 1288 MW; 0A3480C7336415B0 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 2 FISRW 6

RESULT 29
Q9ZYT2
ID Q9ZYT2 PRELIMINARY; PRT; 10 AA.
AC Q9ZYT2;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Leiocephalus carinatus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Tropidurinae;
OC Leiocephalus.
OX NCBI_TaxID=81825;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99162288; PubMed=10051389; DOI=10.1006/mpev.1998.0541;
RA Schulte J.A., Macey J.R., Larson A., Papenfuss T.J.;
RT "Molecular tests of phylogenetic taxonomies: a general procedure and
example using four subfamilies of the lizard family Iguanidae.";
RL Mol. Phylogenet. Evol. 10:367-376(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Schulte J.A. II, Macey J.R., Larson A., Papenfuss T.J.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF049864; AAD02535.1; -.
DR PIR; T12325; T12325.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 10
SQ SEQUENCE 10 AA; 1302 MW; 0A3480C7336411A0 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
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Db          | 2 FITRW 6
RESULT 30
Q8WES0
ID Q8WES0      PRELIMINARY;      PRT;      11 AA.
AC Q8WES0;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Ceratophora karu.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Ceratophora.
OX NCBI_TaxID=118086;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and phylogenetic information content of mitochondrial
genomic structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21655505; PubMed=11796034; DOI=10.1006/mpev.2001.1041;
RA Schulte J.A. II, Macey J.R., Pethiyagoda R., Larson A.;
RT "Rostral horn evolution among agamid lizards of the genus Ceratophora
endemic to Sri Lanka.";
RL Mol. Phylogenet. Evol. 22:111-117(2002).
DR EMBL; AF128520; AAL67604.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match      65.2%; Score 15; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 3 FLTRW 7

RESULT 31
Q9G365
ID Q9G365      PRELIMINARY;      PRT;      11 AA.
AC Q9G365;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Calotes emma.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Calotes.
OX NCBI_TaxID=52214;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97153820; PubMed=9000751;
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT "Replication slippage may cause parallel evolution in the secondary
structures of mitochondrial transfer RNAs.";
RL Mol. Biol. Evol. 14:30-39(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and phylogenetic information content of mitochondrial
genomic structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating trans-tethys migration: an example using acrodont lizard
phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128477; AAG00668.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1341 MW; 4B2D371E336415B7 CRC64;

Query Match      65.2%; Score 15; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and phylogenetic information content of mitochondrial
genomic structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating trans-tethys migration: an example using acrodont lizard
phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128487; AAG00698.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match      65.2%; Score 15; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 3 FLTRW 7

RESULT 32
Q9G368
ID Q9G368      PRELIMINARY;      PRT;      11 AA.
AC Q9G368;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Draco blanfordii.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Draco.
OX NCBI_TaxID=89021;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97153820; PubMed=9000751;
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT "Replication slippage may cause parallel evolution in the secondary
structures of mitochondrial transfer RNAs.";
RL Mol. Biol. Evol. 14:30-39(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and phylogenetic information content of mitochondrial
genomic structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating trans-tethys migration: an example using acrodont lizard
phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128477; AAG00668.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1341 MW; 4B2D371E336415B7 CRC64;

Query Match      65.2%; Score 15; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY      1 FXXXW 5
Db      3 FLSRW 7

RESULT 33
Q9G5Y9 ID Q9G5Y9 PRELIMINARY; PRT; 11 AA.
AC Q9G5Y9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Pseudocalotes flavigula.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Pseudocalotes.
OX NCBI_TaxID=118227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and phylogenetic information content of mitochondrial
RL genomic structural features illustrated with acrodont lizards."
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating trans-tethys migration: an example using acrodont lizard
RT phylogenetics."
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128503; AAG00746.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 11
SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
Db      3 FLTRW 7

RESULT 34
Q9G5Z2 ID Q9G5Z2 PRELIMINARY; PRT; 11 AA.
AC Q9G5Z2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Pseudocalotes brevipes.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Pseudocalotes.
OX NCBI_TaxID=118226;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and phylogenetic information content of mitochondrial
RL genomic structural features illustrated with acrodont lizards."
RL Syst. Biol. 49:257-277(2000).

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[2]
RN SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating trans-tethys migration: an example using acrodont lizard
RT phylogenetics."
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128502; AAG00743.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 11
SQ SEQUENCE 11 AA; 1389 MW; C92D371E336411A9 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
Db      3 FFTRW 7

RESULT 35
Q9G601 ID Q9G601 PRELIMINARY; PRT; 11 AA.
AC Q9G601;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Bronchocela cristatella (Green crested lizard).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Bronchocela.
OX NCBI_TaxID=118090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and phylogenetic information content of mitochondrial
RT genomic structural features illustrated with acrodont lizards."
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating trans-tethys migration: an example using acrodont lizard
RT phylogenetics."
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128497; AAG00728.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 11
SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match 65.2%; Score 15; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
Db      3 FLTRW 7

RESULT 36
Q9G625 ID Q9G625 PRELIMINARY; PRT; 11 AA.
AC Q9G625;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)

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DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN Name=COI;  
OS Calotes versicolor.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;  
OC Calotes.  
OX NCBI\_TaxID=48253;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;  
RA Macey J.R., Schulte J.A. II, Larson A.;  
RA "Evolution and phylogenetic information content of mitochondrial  
RT genomic structural features illustrated with acrodont lizards.";  
RL Syst. Biol. 49:257-277(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;  
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
RA "Evaluating trans-tethys migration: an example using acrodont lizard  
RT phylogenetics";  
RL Syst. Biol. 49:233-256(2000).  
DR EMBL; AF128489; AAG00704.1; --  
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DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN Name=COI;  
OS Calotes mystaceus.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;  
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OX NCBI\_TaxID=118097;  
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RX MEDLINE=22114082; PubMed=12118408; DOI=10.1080/10635159950173843;  
RA Macey J.R., Schulte J.A. II, Larson A.;  
RA "Evolution and phylogenetic information content of mitochondrial  
RT genomic structural features illustrated with acrodont lizards.";  
RL Syst. Biol. 49:257-277(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22114081; PubMed=12118407; DOI=10.1080/10635159950173834;  
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,  
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
RA "Evaluating trans-tethys migration: an example using acrodont lizard  
RT phylogenetics";  
RL Syst. Biol. 49:233-256(2000).  
DR EMBL; AF128488; AAG00701.1; --  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.

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DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
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RA Macey J.R., Schulte J.A. II, Larson A.;  
RA "Evolution and phylogenetic information content of mitochondrial  
RT genomic structural features illustrated with acrodont lizards.";  
RL Syst. Biol. 49:257-277(2000).  
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RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;  
RA "Evaluating trans-tethys migration: an example using acrodont lizard  
RT phylogenetics";  
RL Syst. Biol. 49:233-256(2000).  
DR EMBL; AF128486; AAG00695.1; --  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
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DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
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RT	"Evolution and phylogenetic information content of mitochondrial
RT	genomic structural features illustrated with acrodont lizards.";
RL	Syst. Biol. 49:257-277(2000).
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RA	Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
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RT	"Evaluating trans-tethys migration: an example using acrodont lizard
RT	phylogenetics.";
RL	Syst. Biol. 49:233-256(2000).
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DR	GO; GO:0005739; C:mitochondrion; IEA.
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DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
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OG	Mitochondrion.
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RT	"Evolution and phylogenetic information content of mitochondrial
RT	genomic structural features illustrated with acrodont lizards.";
RL	Syst. Biol. 49:257-277(2000).
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RA	Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT	"Evaluating trans-tethys migration: an example using acrodont lizard
RT	phylogenetics.";
RL	Syst. Biol. 49:233-256(2000).
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:58:45 ; Search time 102.588 Seconds  
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32.505 Million cell updates/sec

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Scoring table: BLOSUM62  
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Searched: 1860064 seqs, 416830855 residues

Total number of hits satisfying chosen parameters: 377382

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Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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4	17	73.9	8	18	US-10-818-036-30
5	17	73.9	9	14	US-10-072-419-3
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7	17	73.9	9	16	US-10-869-768-3
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9	17	73.9	9	18	US-10-818-036-14
10	17	73.9	9	18	US-10-818-036-15
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					Sequence 8, Appli
					Sequence 14, Appl
					Sequence 15, Appl
					Sequence 23, Appl

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86	16	69.6	10	15	US-10-436-782-6	Sequence 6, Appli	159	16	69.6	16	14	US-10-251-385-285	Sequence 285, App
87	16	69.6	10	15	US-10-239-656-14	Sequence 14, Appl	160	16	69.6	16	14	US-10-062-831-88	Sequence 88, Appl
88	16	69.6	10	16	US-10-128-520-367	Sequence 367, App	161	16	69.6	16	14	US-10-224-356-36	Sequence 36, Appl
89	16	69.6	10	16	US-10-468-250A-109	Sequence 109, App	162	16	69.6	16	14	US-10-062-599-88	Sequence 88, Appl
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91	16	69.6	10	16	US-10-869-768-36	Sequence 36, Appl	164	16	69.6	17	14	US-10-059-271-20	Sequence 20, Appl
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99	16	69.6	10	17	US-10-726-332-72	Sequence 72, Appl	172	16	69.6	18	10	US-09-963-693-283	Sequence 283, App
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102	16	69.6	10	17	US-10-726-332-107	Sequence 107, App	175	16	69.6	18	11	US-09-833-245-1959	Sequence 1959, Ap
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104	16	69.6	10	17	US-10-867-506-55	Sequence 55, Appl	177	16	69.6	19	9	US-09-864-761-41546	Sequence 41546, A
105	16	69.6	10	18	US-10-981-738-17	Sequence 17, Appl	178	16	69.6	20	9	US-09-812-528-19	Sequence 19, Appl
106	16	69.6	10	18	US-10-727-737-20	Sequence 20, Appl	179	16	69.6	20	9	US-09-884-441-411	Sequence 411, App
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126	16	69.6	12	17	US-10-235-043-391	Sequence 391, App	199	16	69.6	20	17	US-10-860-790-618	Sequence 618, App
127	16	69.6	12	17	US-10-926-893-36	Sequence 36, Appl	200	15	65.2	5	10	US-09-894-594-11	Sequence 11, Appl
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136	16	69.6	13	15	US-10-371-069-52	Sequence 52, Appl	209	15	65.2	6	15	US-10-651-723-130	Sequence 130, App
137	16	69.6	13	15	US-10-371-645-52	Sequence 52, Appl	210	15	65.2	6	15	US-10-645-761-130	Sequence 130, App
138	16	69.6	13	15	US-10-371-260-52	Sequence 52, Appl	211	15	65.2	6	15	US-10-666-696-130	Sequence 130, App
139	16	69.6	13	16	US-10-441-779C-33	Sequence 33, Appl	212	15	65.2	6	15	US-10-653-048-130	Sequence 130, App
140	16	69.6	13	16	US-10-643-954A-18	Sequence 18, Appl	213	15	65.2	6	18	US-10-645-784-130	Sequence 130, App
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151	16	69.6	15	9	US-09-205-658-284	Sequence 284, App	224	15	65.2	7	14	US-10-190-082-128	Sequence 128, App
152	16	69.6	15	10	US-09-963-693-284	Sequence 284, App	225	15	65.2	7	14	US-10-190-082-179	Sequence 179, App
153	16	69.6	15	14	US-10-216-122-22	Sequence 22, Appl	226	15	65.2	7	14	US-10-197-927-5	Sequence 5, Appli
154	16	69.6	15	15	US-10-442-456-1	Sequence 1, Appli	227	15	65.2	7	14	US-10-190-162-36	Sequence 36, Appl
155	16	69.6	15	18	US-10-946-647-790	Sequence 790, App	228	15	65.2	7	18	US-10-953-901-680	Sequence 680, App
156	16	69.6	15	18	US-10-946-647-957	Sequence 957, App	229	15	65.2	8	8	US-08-424-550B-252	Sequence 252, App
157	16	69.6	15	18	US-10-705-165-9	Sequence 9, Appli	230	15	65.2	8	9	US-09-214-371-12	Sequence 12, Appl

231	15	65.2	8	9	US-09-214-371-13	Sequence 13, Appl	304	15	65.2	8	18	US-10-927-262A-22	Sequence 22, Appl
232	15	65.2	8	9	US-09-214-371-21	Sequence 21, Appl	305	15	65.2	8	18	US-10-927-262A-46	Sequence 46, Appl
233	15	65.2	8	9	US-09-214-371-22	Sequence 22, Appl	306	15	65.2	8	18	US-10-927-262A-47	Sequence 47, Appl
234	15	65.2	8	9	US-09-214-371-46	Sequence 46, Appl	307	15	65.2	8	18	US-10-927-262A-48	Sequence 48, Appl
235	15	65.2	8	9	US-09-214-371-47	Sequence 47, Appl	308	15	65.2	8	18	US-10-927-262A-49	Sequence 49, Appl
236	15	65.2	8	9	US-09-214-371-48	Sequence 48, Appl	309	15	65.2	8	18	US-10-927-262A-52	Sequence 52, Appl
237	15	65.2	8	9	US-09-214-371-49	Sequence 49, Appl	310	15	65.2	8	18	US-10-946-647-346	Sequence 346, App
238	15	65.2	8	9	US-09-214-371-52	Sequence 52, Appl	311	15	65.2	8	18	US-10-946-647-621	Sequence 621, App
239	15	65.2	8	9	US-09-908-322-83	Sequence 83, Appl	312	15	65.2	8	18	US-10-776-521B-338	Sequence 338, App
240	15	65.2	8	10	US-09-783-931-83	Sequence 83, Appl	313	15	65.2	8	18	US-10-820-067A-848	Sequence 848, App
241	15	65.2	8	14	US-10-209-372-31	Sequence 31, Appl	314	15	65.2	8	20	US-11-051-411-203	Sequence 203, App
242	15	65.2	8	14	US-10-190-082-265	Sequence 265, App	315	15	65.2	8	20	US-11-051-411-345	Sequence 345, App
243	15	65.2	8	14	US-10-072-419-16	Sequence 16, Appl	316	15	65.2	8	20	US-11-051-411-475	Sequence 475, App
244	15	65.2	8	14	US-10-072-419-17	Sequence 17, Appl	317	15	65.2	8	20	US-11-051-411-690	Sequence 690, App
245	15	65.2	8	15	US-10-325-810-154	Sequence 154, App	318	15	65.2	8	20	US-11-051-411-902	Sequence 902, App
246	15	65.2	8	15	US-10-387-957-36	Sequence 36, Appl	319	15	65.2	8	20	US-11-051-411-1052	Sequence 1052, Ap
247	15	65.2	8	15	US-10-387-957-37	Sequence 37, Appl	320	15	65.2	8	20	US-11-013-537-39	Sequence 39, Appl
248	15	65.2	8	15	US-10-387-957-38	Sequence 38, Appl	321	15	65.2	9	8	US-08-821-739A-49	Sequence 49, Appl
249	15	65.2	8	15	US-10-387-957-39	Sequence 39, Appl	322	15	65.2	9	8	US-08-821-739A-53	Sequence 53, Appl
250	15	65.2	8	15	US-10-387-934-36	Sequence 36, Appl	323	15	65.2	9	9	US-09-214-371-37	Sequence 37, Appl
251	15	65.2	8	15	US-10-387-934-37	Sequence 37, Appl	324	15	65.2	9	9	US-09-214-371-38	Sequence 38, Appl
252	15	65.2	8	15	US-10-387-934-38	Sequence 38, Appl	325	15	65.2	9	9	US-09-764-304-12	Sequence 12, Appl
253	15	65.2	8	15	US-10-387-934-39	Sequence 39, Appl	326	15	65.2	9	9	US-09-862-260A-13	Sequence 13, Appl
254	15	65.2	8	16	US-10-340-179-2	Sequence 2, Appli	327	15	65.2	9	9	US-09-780-053-130	Sequence 130, App
255	15	65.2	8	16	US-10-340-179-3	Sequence 3, Appli	328	15	65.2	9	9	US-09-771-415-16	Sequence 16, Appl
256	15	65.2	8	16	US-10-387-955-36	Sequence 36, Appl	329	15	65.2	9	10	US-09-884-456-5	Sequence 5, Appli
257	15	65.2	8	16	US-10-387-955-37	Sequence 37, Appl	330	15	65.2	9	10	US-09-884-456-8	Sequence 8, Appli
258	15	65.2	8	16	US-10-387-955-38	Sequence 38, Appl	331	15	65.2	9	10	US-09-884-456-11	Sequence 11, Appl
259	15	65.2	8	16	US-10-387-955-39	Sequence 39, Appl	332	15	65.2	9	10	US-09-884-456-14	Sequence 14, Appl
260	15	65.2	8	16	US-10-869-768-16	Sequence 16, Appl	333	15	65.2	9	10	US-09-809-638-117	Sequence 117, App
261	15	65.2	8	16	US-10-869-768-17	Sequence 17, Appl	334	15	65.2	9	10	US-09-809-638-255	Sequence 255, App
262	15	65.2	8	16	US-10-877-124-154	Sequence 154, App	335	15	65.2	9	10	US-09-809-638-347	Sequence 347, App
263	15	65.2	8	16	US-10-877-022-154	Sequence 154, App	336	15	65.2	9	10	US-09-884-455-5	Sequence 5, Appli
264	15	65.2	8	16	US-10-488-219-36	Sequence 36, Appl	337	15	65.2	9	10	US-09-884-455-8	Sequence 8, Appli
265	15	65.2	8	16	US-10-488-219-37	Sequence 37, Appl	338	15	65.2	9	10	US-09-884-455-11	Sequence 11, Appl
266	15	65.2	8	16	US-10-488-219-38	Sequence 38, Appl	339	15	65.2	9	10	US-09-884-455-14	Sequence 14, Appl
267	15	65.2	8	16	US-10-488-219-39	Sequence 39, Appl	340	15	65.2	9	10	US-09-865-548A-186	Sequence 186, App
268	15	65.2	8	17	US-10-877-146-154	Sequence 154, App	341	15	65.2	9	11	US-09-920-480B-3	Sequence 3, Appli
269	15	65.2	8	17	US-10-480-954-49	Sequence 49, Appl	342	15	65.2	9	12	US-09-957-806A-62	Sequence 62, Appl
270	15	65.2	8	17	US-10-480-954-84	Sequence 84, Appl	343	15	65.2	9	12	US-09-957-806A-69	Sequence 69, Appl
271	15	65.2	8	17	US-10-480-954-86	Sequence 86, Appl	344	15	65.2	9	13	US-10-047-539-13	Sequence 13, Appl
272	15	65.2	8	17	US-10-480-954-88	Sequence 88, Appl	345	15	65.2	9	14	US-10-265-713-12	Sequence 12, Appl
273	15	65.2	8	17	US-10-480-954-90	Sequence 90, Appl	346	15	65.2	9	14	US-10-190-082-169	Sequence 169, App
274	15	65.2	8	17	US-10-480-954-92	Sequence 92, Appl	347	15	65.2	9	14	US-10-190-082-180	Sequence 180, App
275	15	65.2	8	17	US-10-480-954-94	Sequence 94, Appl	348	15	65.2	9	14	US-10-190-082-212	Sequence 212, App
276	15	65.2	8	17	US-10-480-954-96	Sequence 96, Appl	349	15	65.2	9	14	US-10-166-626-12	Sequence 12, Appl
277	15	65.2	8	17	US-10-480-954-98	Sequence 98, Appl	350	15	65.2	9	15	US-10-245-871-297	Sequence 297, App
278	15	65.2	8	17	US-10-480-954-113	Sequence 113, App	351	15	65.2	9	15	US-10-447-161-83	Sequence 83, Appl
279	15	65.2	8	17	US-10-480-954-115	Sequence 115, App	352	15	65.2	9	15	US-10-398-104-22	Sequence 22, Appl
280	15	65.2	8	17	US-10-480-954-117	Sequence 117, App	353	15	65.2	9	15	US-10-363-208-237	Sequence 237, App
281	15	65.2	8	17	US-10-480-954-119	Sequence 119, App	354	15	65.2	9	15	US-10-253-286-297	Sequence 297, App
282	15	65.2	8	17	US-10-480-954-121	Sequence 121, App	355	15	65.2	9	16	US-10-657-363-16	Sequence 16, Appl
283	15	65.2	8	17	US-10-480-954-123	Sequence 123, App	356	15	65.2	9	16	US-10-340-179-1	Sequence 1, Appli
284	15	65.2	8	17	US-10-480-954-125	Sequence 125, App	357	15	65.2	9	16	US-10-363-204-198	Sequence 198, App
285	15	65.2	8	17	US-10-480-954-143	Sequence 143, App	358	15	65.2	9	16	US-10-793-943-7	Sequence 7, Appli
286	15	65.2	8	17	US-10-480-954-145	Sequence 145, App	359	15	65.2	9	17	US-10-705-459-186	Sequence 186, App
287	15	65.2	8	17	US-10-480-954-147	Sequence 147, App	360	15	65.2	9	17	US-10-654-601-2374	Sequence 2374, Ap
288	15	65.2	8	17	US-10-480-954-149	Sequence 149, App	361	15	65.2	9	18	US-10-927-262A-37	Sequence 37, Appl
289	15	65.2	8	17	US-10-480-954-151	Sequence 151, App	362	15	65.2	9	18	US-10-927-262A-38	Sequence 38, Appl
290	15	65.2	8	17	US-10-480-954-153	Sequence 153, App	363	15	65.2	9	18	US-10-149-137A-540	Sequence 540, App
291	15	65.2	8	17	US-10-480-954-155	Sequence 155, App	364	15	65.2	9	18	US-10-953-901-690	Sequence 690, App
292	15	65.2	8	17	US-10-480-954-157	Sequence 157, App	365	15	65.2	9	18	US-10-510-523-33	Sequence 33, Appl
293	15	65.2	8	17	US-10-480-954-166	Sequence 166, App	366	15	65.2	9	18	US-10-510-523-34	Sequence 34, Appl
294	15	65.2	8	17	US-10-480-954-168	Sequence 168, App	367	15	65.2	9	20	US-11-051-411-73	Sequence 73, Appl
295	15	65.2	8	17	US-10-480-954-170	Sequence 170, App	368	15	65.2	9	20	US-11-051-411-281	Sequence 281, App
296	15	65.2	8	17	US-10-480-954-172	Sequence 172, App	369	15	65.2	9	20	US-11-051-411-346	Sequence 346, App
297	15	65.2	8	17	US-10-480-954-174	Sequence 174, App	370	15	65.2	9	20	US-11-051-411-473	Sequence 473, App
298	15	65.2	8	17	US-10-480-954-176	Sequence 176, App	371	15	65.2	9	20	US-11-051-411-607	Sequence 607, App
299	15	65.2	8	17	US-10-480-954-178	Sequence 178, App	372	15	65.2	9	20	US-11-051-411-1053	Sequence 1053, Ap
300	15	65.2	8	17	US-10-480-954-180	Sequence 180, App	373	15	65.2	10	9	US-09-214-371-35	Sequence 35, Appl
301	15	65.2	8	18	US-10-927-262A-12	Sequence 12, Appl	374	15	65.2	10	9	US-09-214-371-36	Sequence 36, Appl
302	15	65.2	8	18	US-10-927-262A-13	Sequence 13, Appl	375	15	65.2	10	9	US-09-767-460-53	Sequence 53, Appl
303	15	65.2	8	18	US-10-927-262A-21	Sequence 21, Appl	376	15	65.2	10	9	US-09-767-460-72	Sequence 72, Appl

377	15	65.2	10	9	US-09-780-053-175	Sequence 175, App	450	15	65.2	10	18	US-10-818-036-20	Sequence 20, Appl
378	15	65.2	10	9	US-09-826-290-390	Sequence 390, App	451	15	65.2	10	20	US-11-003-951-93	Sequence 93, Appl
379	15	65.2	10	10	US-09-809-638-187	Sequence 187, App	452	15	65.2	10	20	US-11-009-443-85	Sequence 85, Appl
380	15	65.2	10	10	US-09-809-638-273	Sequence 273, App	453	15	65.2	10	20	US-11-051-411-15	Sequence 15, Appl
381	15	65.2	10	10	US-09-995-529-26	Sequence 26, Appl	454	15	65.2	10	20	US-11-051-411-74	Sequence 74, Appl
382	15	65.2	10	10	US-09-995-529-43	Sequence 43, Appl	455	15	65.2	10	20	US-11-051-411-282	Sequence 282, App
383	15	65.2	10	10	US-09-995-529-44	Sequence 44, Appl	456	15	65.2	10	20	US-11-051-411-474	Sequence 474, App
384	15	65.2	10	10	US-09-995-529-45	Sequence 45, Appl	457	15	65.2	10	20	US-11-051-411-502	Sequence 502, App
385	15	65.2	10	10	US-09-995-529-46	Sequence 46, Appl	458	15	65.2	11	10	US-09-840-085-31	Sequence 31, Appl
386	15	65.2	10	10	US-09-995-529-47	Sequence 47, Appl	459	15	65.2	11	15	US-10-014-340-216	Sequence 216, App
387	15	65.2	10	10	US-09-795-798-10	Sequence 10, Appl	460	15	65.2	11	15	US-10-398-104-162	Sequence 162, App
388	15	65.2	10	11	US-09-995-529-26	Sequence 26, Appl	461	15	65.2	11	16	US-10-793-943-5	Sequence 5, Appl
389	15	65.2	10	11	US-09-995-529-43	Sequence 43, Appl	462	15	65.2	11	17	US-10-659-207-444	Sequence 444, App
390	15	65.2	10	11	US-09-995-529-44	Sequence 44, Appl	463	15	65.2	11	17	US-10-656-250-46	Sequence 46, Appl
391	15	65.2	10	11	US-09-995-529-45	Sequence 45, Appl	464	15	65.2	11	17	US-10-656-250-171	Sequence 171, App
392	15	65.2	10	11	US-09-995-529-46	Sequence 46, Appl	465	15	65.2	11	20	US-11-051-411-21	Sequence 21, Appl
393	15	65.2	10	11	US-09-995-529-47	Sequence 47, Appl	466	15	65.2	11	20	US-11-051-411-162	Sequence 162, App
394	15	65.2	10	14	US-10-094-401-172	Sequence 172, App	467	15	65.2	11	20	US-11-051-411-222	Sequence 222, App
395	15	65.2	10	14	US-10-190-082-167	Sequence 167, App	468	15	65.2	11	20	US-11-051-411-325	Sequence 325, App
396	15	65.2	10	14	US-10-190-082-170	Sequence 170, App	469	15	65.2	11	20	US-11-051-411-584	Sequence 584, App
397	15	65.2	10	14	US-10-190-082-171	Sequence 171, App	470	15	65.2	11	20	US-11-051-411-744	Sequence 744, App
398	15	65.2	10	14	US-10-190-082-178	Sequence 178, App	471	15	65.2	11	20	US-11-051-411-949	Sequence 949, App
399	15	65.2	10	14	US-10-190-082-276	Sequence 276, App	472	15	65.2	12	9	US-09-214-371-7	Sequence 7, Appl
400	15	65.2	10	14	US-10-190-082-290	Sequence 290, App	473	15	65.2	12	9	US-09-214-371-17	Sequence 17, Appl
401	15	65.2	10	14	US-10-160-506-29	Sequence 29, Appl	474	15	65.2	12	9	US-09-214-371-18	Sequence 18, Appl
402	15	65.2	10	14	US-10-072-419-32	Sequence 32, Appl	475	15	65.2	12	9	US-09-214-371-20	Sequence 20, Appl
403	15	65.2	10	14	US-10-031-874A-16	Sequence 16, Appl	476	15	65.2	12	9	US-09-214-371-24	Sequence 24, Appl
404	15	65.2	10	15	US-10-462-262-140	Sequence 140, App	477	15	65.2	12	9	US-09-214-371-25	Sequence 25, Appl
405	15	65.2	10	15	US-10-264-309-407	Sequence 407, App	478	15	65.2	12	9	US-09-214-371-26	Sequence 26, Appl
406	15	65.2	10	16	US-10-449-379-29	Sequence 29, Appl	479	15	65.2	12	9	US-09-214-371-31	Sequence 31, Appl
407	15	65.2	10	16	US-10-338-552-35	Sequence 35, Appl	480	15	65.2	12	9	US-09-214-371-64	Sequence 64, Appl
408	15	65.2	10	16	US-10-338-552-37	Sequence 37, Appl	481	15	65.2	12	10	US-09-820-053A-98	Sequence 98, Appl
409	15	65.2	10	16	US-10-338-552-39	Sequence 39, Appl	482	15	65.2	12	14	US-10-032-818-31	Sequence 31, Appl
410	15	65.2	10	16	US-10-338-552-41	Sequence 41, Appl	483	15	65.2	12	14	US-10-109-171-98	Sequence 98, Appl
411	15	65.2	10	16	US-10-338-627-35	Sequence 35, Appl	484	15	65.2	12	14	US-10-190-082-252	Sequence 252, App
412	15	65.2	10	16	US-10-338-627-37	Sequence 37, Appl	485	15	65.2	12	15	US-10-180-648-18	Sequence 18, Appl
413	15	65.2	10	16	US-10-338-627-39	Sequence 39, Appl	486	15	65.2	12	15	US-10-609-217-131	Sequence 131, App
414	15	65.2	10	16	US-10-338-627-41	Sequence 41, Appl	487	15	65.2	12	15	US-10-609-217-132	Sequence 132, App
415	15	65.2	10	16	US-10-688-015-29	Sequence 29, Appl	488	15	65.2	12	15	US-10-609-217-133	Sequence 133, App
416	15	65.2	10	16	US-10-450-036A-16	Sequence 16, Appl	489	15	65.2	12	15	US-10-609-217-134	Sequence 134, App
417	15	65.2	10	16	US-10-361-275-42	Sequence 42, Appl	490	15	65.2	12	15	US-10-609-217-137	Sequence 137, App
418	15	65.2	10	16	US-10-327-598-450	Sequence 450, App	491	15	65.2	12	15	US-10-609-217-143	Sequence 143, App
419	15	65.2	10	16	US-10-327-598-457	Sequence 457, App	492	15	65.2	12	15	US-10-609-217-144	Sequence 144, App
420	15	65.2	10	16	US-10-327-598-458	Sequence 458, App	493	15	65.2	12	15	US-10-609-217-145	Sequence 145, App
421	15	65.2	10	16	US-10-160-505-29	Sequence 29, Appl	494	15	65.2	12	15	US-10-609-217-146	Sequence 146, App
422	15	65.2	10	16	US-10-869-768-32	Sequence 32, Appl	495	15	65.2	12	15	US-10-632-388-131	Sequence 131, App
423	15	65.2	10	16	US-10-451-315A-8	Sequence 8, Appl	496	15	65.2	12	15	US-10-632-388-132	Sequence 132, App
424	15	65.2	10	17	US-10-823-253-1	Sequence 1, Appl	497	15	65.2	12	15	US-10-632-388-133	Sequence 133, App
425	15	65.2	10	17	US-10-823-253-11	Sequence 11, Appl	498	15	65.2	12	15	US-10-632-388-134	Sequence 134, App
426	15	65.2	10	17	US-10-823-253-19	Sequence 19, Appl	499	15	65.2	12	15	US-10-632-388-137	Sequence 137, App
427	15	65.2	10	17	US-10-823-253-26	Sequence 26, Appl	500	15	65.2	12	15	US-10-632-388-143	Sequence 143, App
428	15	65.2	10	17	US-10-769-308-29	Sequence 29, Appl	501	15	65.2	12	15	US-10-632-388-144	Sequence 144, App
429	15	65.2	10	17	US-10-725-962-61	Sequence 61, Appl	502	15	65.2	12	15	US-10-632-388-145	Sequence 145, App
430	15	65.2	10	17	US-10-777-829-53	Sequence 53, Appl	503	15	65.2	12	15	US-10-632-388-146	Sequence 146, App
431	15	65.2	10	17	US-10-777-829-72	Sequence 72, Appl	504	15	65.2	12	15	US-10-651-723-131	Sequence 131, App
432	15	65.2	10	17	US-10-879-994-67	Sequence 67, Appl	505	15	65.2	12	15	US-10-651-723-132	Sequence 132, App
433	15	65.2	10	17	US-10-726-332-128	Sequence 128, App	506	15	65.2	12	15	US-10-651-723-133	Sequence 133, App
434	15	65.2	10	17	US-10-769-074-29	Sequence 29, Appl	507	15	65.2	12	15	US-10-651-723-134	Sequence 134, App
435	15	65.2	10	17	US-10-818-067-53	Sequence 53, Appl	508	15	65.2	12	15	US-10-651-723-137	Sequence 137, App
436	15	65.2	10	17	US-10-818-067-72	Sequence 72, Appl	509	15	65.2	12	15	US-10-651-723-143	Sequence 143, App
437	15	65.2	10	18	US-10-996-316-138	Sequence 138, App	510	15	65.2	12	15	US-10-651-723-144	Sequence 144, App
438	15	65.2	10	18	US-10-996-316-147	Sequence 147, App	511	15	65.2	12	15	US-10-651-723-145	Sequence 145, App
439	15	65.2	10	18	US-10-996-316-148	Sequence 148, App	512	15	65.2	12	15	US-10-651-723-146	Sequence 146, App
440	15	65.2	10	18	US-10-927-262A-35	Sequence 35, Appl	513	15	65.2	12	15	US-10-645-761-131	Sequence 131, App
441	15	65.2	10	18	US-10-927-262A-36	Sequence 36, Appl	514	15	65.2	12	15	US-10-645-761-132	Sequence 132, App
442	15	65.2	10	18	US-10-823-810-1	Sequence 1, Appl	515	15	65.2	12	15	US-10-645-761-133	Sequence 133, App
443	15	65.2	10	18	US-10-823-810-11	Sequence 11, Appl	516	15	65.2	12	15	US-10-645-761-134	Sequence 134, App
444	15	65.2	10	18	US-10-823-810-19	Sequence 19, Appl	517	15	65.2	12	15	US-10-645-761-137	Sequence 137, App
445	15	65.2	10	18	US-10-823-810-26	Sequence 26, Appl	518	15	65.2	12	15	US-10-645-761-143	Sequence 143, App
446	15	65.2	10	18	US-10-727-737-19	Sequence 19, Appl	519	15	65.2	12	15	US-10-645-761-144	Sequence 144, App
447	15	65.2	10	18	US-10-727-737-21	Sequence 21, Appl	520	15	65.2	12	15	US-10-645-761-145	Sequence 145, App
448	15	65.2	10	18	US-10-727-737-22	Sequence 22, Appl	521	15	65.2	12	15	US-10-645-761-146	Sequence 146, App
449	15	65.2	10	18	US-10-264-309-407	Sequence 407, App	522	15	65.2	12	15	US-10-666-696-131	Sequence 131, App



523	15	65.2	12	15	US-10-666-696-132	Sequence 132, App	596	15	65.2	14	15	US-10-632-388-68	Sequence 68, Appl
524	15	65.2	12	15	US-10-666-696-133	Sequence 133, App	597	15	65.2	14	15	US-10-651-723-68	Sequence 68, Appl
525	15	65.2	12	15	US-10-666-696-134	Sequence 134, App	598	15	65.2	14	15	US-10-645-761-68	Sequence 68, Appl
526	15	65.2	12	15	US-10-666-696-137	Sequence 137, App	599	15	65.2	14	15	US-10-275-427A-13	Sequence 13, Appl
527	15	65.2	12	15	US-10-666-696-143	Sequence 143, App	600	15	65.2	14	15	US-10-666-696-68	Sequence 68, Appl
528	15	65.2	12	15	US-10-666-696-144	Sequence 144, App	601	15	65.2	14	15	US-10-653-048-68	Sequence 68, Appl
529	15	65.2	12	15	US-10-666-696-145	Sequence 145, App	602	15	65.2	14	16	US-10-387-955-61	Sequence 61, Appl
530	15	65.2	12	15	US-10-666-696-146	Sequence 146, App	603	15	65.2	14	16	US-10-712-447-158	Sequence 158, App
531	15	65.2	12	15	US-10-653-048-131	Sequence 131, App	604	15	65.2	14	16	US-10-712-447-159	Sequence 159, App
532	15	65.2	12	15	US-10-653-048-132	Sequence 132, App	605	15	65.2	14	16	US-10-712-447-160	Sequence 160, App
533	15	65.2	12	15	US-10-653-048-133	Sequence 133, App	606	15	65.2	14	16	US-10-712-447-194	Sequence 194, App
534	15	65.2	12	15	US-10-653-048-134	Sequence 134, App	607	15	65.2	14	16	US-10-712-447-195	Sequence 195, App
535	15	65.2	12	15	US-10-653-048-137	Sequence 137, App	608	15	65.2	14	16	US-10-712-447-196	Sequence 196, App
536	15	65.2	12	15	US-10-653-048-143	Sequence 143, App	609	15	65.2	14	16	US-10-712-447-204	Sequence 204, App
537	15	65.2	12	15	US-10-653-048-144	Sequence 144, App	610	15	65.2	14	16	US-10-865-478-854	Sequence 854, App
538	15	65.2	12	15	US-10-653-048-145	Sequence 145, App	611	15	65.2	14	17	US-10-808-187-1052	Sequence 1052, Ap
539	15	65.2	12	15	US-10-653-048-146	Sequence 146, App	612	15	65.2	14	18	US-10-645-784-68	Sequence 68, Appl
540	15	65.2	12	16	US-10-467-758-27	Sequence 27, Appl	613	15	65.2	14	18	US-10-853-973A-80	Sequence 80, Appl
541	15	65.2	12	16	US-10-467-758-31	Sequence 31, Appl	614	15	65.2	14	18	US-10-927-262A-33	Sequence 33, Appl
542	15	65.2	12	16	US-10-467-758-33	Sequence 33, Appl	615	15	65.2	14	18	US-10-927-262A-34	Sequence 34, Appl
543	15	65.2	12	16	US-10-467-758-36	Sequence 36, Appl	616	15	65.2	14	18	US-10-807-807-1052	Sequence 1052, Ap
544	15	65.2	12	16	US-10-363-204-228	Sequence 228, App	617	15	65.2	14	20	US-11-093-103-45	Sequence 45, Appl
545	15	65.2	12	16	US-10-649-873-61	Sequence 61, Appl	618	15	65.2	15	9	US-09-214-371-8	Sequence 8, Appli
546	15	65.2	12	16	US-10-839-525-98	Sequence 98, Appl	619	15	65.2	15	9	US-09-214-371-29	Sequence 29, Appl
547	15	65.2	12	17	US-10-873-848B-1	Sequence 1, Appli	620	15	65.2	15	9	US-09-214-371-30	Sequence 30, Appl
548	15	65.2	12	18	US-10-645-784-131	Sequence 131, App	621	15	65.2	15	9	US-09-214-371-66	Sequence 66, Appl
549	15	65.2	12	18	US-10-645-784-132	Sequence 132, App	622	15	65.2	15	9	US-09-829-549A-23	Sequence 23, Appl
550	15	65.2	12	18	US-10-645-784-133	Sequence 133, App	623	15	65.2	15	9	US-09-258-981-3	Sequence 3, Appli
551	15	65.2	12	18	US-10-645-784-134	Sequence 134, App	624	15	65.2	15	9	US-09-950-692-6	Sequence 6, Appli
552	15	65.2	12	18	US-10-645-784-137	Sequence 137, App	625	15	65.2	15	9	US-09-953-510-51	Sequence 51, Appl
553	15	65.2	12	18	US-10-645-784-143	Sequence 143, App	626	15	65.2	15	9	US-09-953-510-52	Sequence 52, Appl
554	15	65.2	12	18	US-10-645-784-144	Sequence 144, App	627	15	65.2	15	9	US-09-732-384-6	Sequence 6, Appli
555	15	65.2	12	18	US-10-645-784-145	Sequence 145, App	628	15	65.2	15	10	US-09-894-594-31	Sequence 31, Appl
556	15	65.2	12	18	US-10-645-784-146	Sequence 146, App	629	15	65.2	15	10	US-09-894-594-43	Sequence 43, Appl
557	15	65.2	12	18	US-10-927-262A-7	Sequence 7, Appli	630	15	65.2	15	10	US-09-952-680A-55	Sequence 55, Appl
558	15	65.2	12	18	US-10-927-262A-17	Sequence 17, Appl	631	15	65.2	15	10	US-09-840-085-33	Sequence 33, Appl
559	15	65.2	12	18	US-10-927-262A-18	Sequence 18, Appl	632	15	65.2	15	10	US-09-840-085-37	Sequence 37, Appl
560	15	65.2	12	18	US-10-927-262A-20	Sequence 20, Appl	633	15	65.2	15	11	US-09-953-413-51	Sequence 51, Appl
561	15	65.2	12	18	US-10-927-262A-24	Sequence 24, Appl	634	15	65.2	15	11	US-09-953-413-52	Sequence 52, Appl
562	15	65.2	12	18	US-10-927-262A-25	Sequence 25, Appl	635	15	65.2	15	14	US-10-067-649-90	Sequence 90, Appl
563	15	65.2	12	18	US-10-927-262A-26	Sequence 26, Appl	636	15	65.2	15	14	US-10-186-867-28	Sequence 28, Appl
564	15	65.2	12	18	US-10-927-262A-31	Sequence 31, Appl	637	15	65.2	15	14	US-10-186-867-29	Sequence 29, Appl
565	15	65.2	12	18	US-10-927-262A-64	Sequence 64, Appl	638	15	65.2	15	14	US-10-211-088-141	Sequence 141, App
566	15	65.2	12	18	US-10-312-637-1	Sequence 1, Appli	639	15	65.2	15	14	US-10-147-255-51	Sequence 51, Appl
567	15	65.2	12	20	US-11-136-186-98	Sequence 98, Appl	640	15	65.2	15	14	US-10-147-255-52	Sequence 52, Appl
568	15	65.2	13	14	US-10-058-053A-275	Sequence 275, App	641	15	65.2	15	14	US-10-239-313A-667	Sequence 667, App
569	15	65.2	13	14	US-10-300-694A-18	Sequence 18, Appl	642	15	65.2	15	14	US-10-080-608A-165	Sequence 165, App
570	15	65.2	13	14	US-10-113-512-1	Sequence 1, Appli	643	15	65.2	15	14	US-10-295-693-90	Sequence 90, Appl
571	15	65.2	13	16	US-10-838-226-275	Sequence 275, App	644	15	65.2	15	15	US-10-370-685-74	Sequence 74, Appl
572	15	65.2	13	16	US-10-468-496-692	Sequence 692, App	645	15	65.2	15	15	US-10-375-157-64	Sequence 64, Appl
573	15	65.2	13	16	US-10-468-496-693	Sequence 693, App	646	15	65.2	15	15	US-10-609-217-139	Sequence 139, App
574	15	65.2	13	16	US-10-468-496-694	Sequence 694, App	647	15	65.2	15	15	US-10-609-217-140	Sequence 140, App
575	15	65.2	13	16	US-10-468-496-695	Sequence 695, App	648	15	65.2	15	15	US-10-609-217-141	Sequence 141, App
576	15	65.2	13	16	US-10-468-496-1718	Sequence 1718, Ap	649	15	65.2	15	15	US-10-425-970-4	Sequence 4, Appli
577	15	65.2	13	16	US-10-468-496-1719	Sequence 1719, Ap	650	15	65.2	15	15	US-10-632-388-139	Sequence 139, App
578	15	65.2	13	16	US-10-468-496-1720	Sequence 1720, Ap	651	15	65.2	15	15	US-10-632-388-140	Sequence 140, App
579	15	65.2	13	16	US-10-468-496-1721	Sequence 1721, Ap	652	15	65.2	15	15	US-10-632-388-141	Sequence 141, App
580	15	65.2	13	16	US-10-495-146-185	Sequence 185, App	653	15	65.2	15	15	US-10-651-723-139	Sequence 139, App
581	15	65.2	13	16	US-10-495-146-186	Sequence 186, App	654	15	65.2	15	15	US-10-651-723-140	Sequence 140, App
582	15	65.2	13	16	US-10-495-146-187	Sequence 187, App	655	15	65.2	15	15	US-10-651-723-141	Sequence 141, App
583	15	65.2	13	16	US-10-495-146-188	Sequence 188, App	656	15	65.2	15	15	US-10-645-761-139	Sequence 139, App
584	15	65.2	13	16	US-10-793-943-4	Sequence 4, Appli	657	15	65.2	15	15	US-10-645-761-140	Sequence 140, App
585	15	65.2	13	18	US-10-948-707-1379	Sequence 1379, Ap	658	15	65.2	15	15	US-10-645-761-141	Sequence 141, App
586	15	65.2	13	20	US-11-093-103-7	Sequence 7, Appli	659	15	65.2	15	15	US-10-666-696-139	Sequence 139, App
587	15	65.2	14	9	US-09-214-371-33	Sequence 33, Appl	660	15	65.2	15	15	US-10-666-696-140	Sequence 140, App
588	15	65.2	14	9	US-09-214-371-34	Sequence 34, Appl	661	15	65.2	15	15	US-10-666-696-141	Sequence 141, App
589	15	65.2	14	14	US-10-186-867-7	Sequence 7, Appli	662	15	65.2	15	15	US-10-653-048-139	Sequence 139, App
590	15	65.2	14	14	US-10-083-768-33	Sequence 33, Appl	663	15	65.2	15	15	US-10-653-048-140	Sequence 140, App
591	15	65.2	14	14	US-10-083-768-213	Sequence 213, App	664	15	65.2	15	15	US-10-653-048-141	Sequence 141, App
592	15	65.2	14	15	US-10-435-766-80	Sequence 80, Appl	665	15	65.2	15	16	US-10-775-965-74	Sequence 74, Appl
593	15	65.2	14	15	US-10-436-715-430	Sequence 430, App	666	15	65.2	15	16	US-10-215-982-55	Sequence 55, Appl
594	15	65.2	14	15	US-10-436-715-442	Sequence 442, App	667	15	65.2	15	16	US-10-695-155-51	Sequence 51, Appl
595	15	65.2	14	15	US-10-609-217-68	Sequence 68, Appl	668	15	65.2	15	16	US-10-695-155-52	Sequence 52, Appl



669	15	65.2	15	US-10-695-155-110	Sequence 110, App	742	15	65.2	18	20	US-11-093-103-47	Sequence 47, Appl
670	15	65.2	15	US-10-695-155-111	Sequence 111, App	743	15	65.2	18	20	US-11-093-103-48	Sequence 48, Appl
671	15	65.2	15	US-10-495-146-23	Sequence 23, Appl	744	15	65.2	19	9	US-09-214-371-1	Sequence 1, Appli
672	15	65.2	15	US-10-495-146-24	Sequence 24, Appl	745	15	65.2	19	9	US-09-732-357A-9	Sequence 9, Appli
673	15	65.2	15	US-10-495-146-25	Sequence 25, Appl	746	15	65.2	19	9	US-09-732-384-7	Sequence 7, Appli
674	15	65.2	15	US-10-495-146-26	Sequence 26, Appl	747	15	65.2	19	10	US-09-774-639-342	Sequence 342, App
675	15	65.2	15	US-10-793-943-3	Sequence 3, Appli	748	15	65.2	19	10	US-09-229-173-45	Sequence 45, Appl
676	15	65.2	15	US-10-182-613A-6	Sequence 6, Appli	749	15	65.2	19	10	US-09-977-797A-116	Sequence 116, App
677	15	65.2	15	US-10-182-613A-7	Sequence 7, Appli	750	15	65.2	19	10	US-09-969-730-289	Sequence 289, App
678	15	65.2	15	US-10-645-784-139	Sequence 139, App	751	15	65.2	19	13	US-10-155-059-13	Sequence 13, Appl
679	15	65.2	15	US-10-645-784-140	Sequence 140, App	752	15	65.2	19	14	US-10-144-929-231	Sequence 231, App
680	15	65.2	15	US-10-645-784-141	Sequence 141, App	753	15	65.2	19	14	US-10-225-567A-1318	Sequence 1318, Ap
681	15	65.2	15	US-10-927-262A-8	Sequence 8, Appli	754	15	65.2	19	14	US-10-300-694A-42	Sequence 42, Appl
682	15	65.2	15	US-10-927-262A-29	Sequence 29, Appl	755	15	65.2	19	14	US-10-029-386-28258	Sequence 28258, A
683	15	65.2	15	US-10-927-262A-30	Sequence 30, Appl	756	15	65.2	19	14	US-10-029-386-33510	Sequence 33510, A
684	15	65.2	15	US-10-927-262A-66	Sequence 66, Appl	757	15	65.2	19	15	US-10-120-885A-45	Sequence 45, Appl
685	15	65.2	15	US-10-862-195-2239	Sequence 2239, Ap	758	15	65.2	19	15	US-10-144-929-231	Sequence 231, App
686	15	65.2	15	US-10-754-473-30	Sequence 30, Appl	759	15	65.2	19	15	US-10-621-363-289	Sequence 289, App
687	15	65.2	15	US-11-051-411-1069	Sequence 1069, Ap	760	15	65.2	19	15	US-10-616-279-9	Sequence 9, Appli
688	15	65.2	15	US-11-051-411-1109	Sequence 1109, Ap	761	15	65.2	19	15	US-10-257-864A-100	Sequence 100, App
689	15	65.2	15	US-11-051-411-1169	Sequence 1169, Ap	762	15	65.2	19	15	US-10-328-953-14	Sequence 14, Appl
690	15	65.2	16	US-09-214-371-39	Sequence 39, Appl	763	15	65.2	19	15	US-10-399-518-129	Sequence 129, App
691	15	65.2	16	US-09-214-371-40	Sequence 40, Appl	764	15	65.2	19	16	US-10-624-884-9	Sequence 9, Appli
692	15	65.2	16	US-09-214-371-41	Sequence 41, Appl	765	15	65.2	19	16	US-10-754-457-9	Sequence 9, Appli
693	15	65.2	16	US-09-019-679-3	Sequence 3, Appli	766	15	65.2	19	16	US-10-399-585-128	Sequence 128, App
694	15	65.2	16	US-09-962-805-13	Sequence 13, Appl	767	15	65.2	19	16	US-10-645-085A-100	Sequence 100, App
695	15	65.2	16	US-09-813-333-20	Sequence 20, Appl	768	15	65.2	19	17	US-10-895-183-9	Sequence 9, Appli
696	15	65.2	16	US-09-825-517A-56	Sequence 56, Appl	769	15	65.2	19	17	US-10-637-317-58	Sequence 58, Appl
697	15	65.2	16	US-09-825-517A-105	Sequence 105, App	770	15	65.2	19	17	US-10-866-831-231	Sequence 231, App
698	15	65.2	16	US-09-825-517A-130	Sequence 130, App	771	15	65.2	19	17	US-10-947-352-37	Sequence 37, Appl
699	15	65.2	16	US-09-825-517A-137	Sequence 137, App	772	15	65.2	19	18	US-10-927-262A-1	Sequence 1, Appli
700	15	65.2	16	US-10-044-703-20	Sequence 20, Appl	773	15	65.2	20	9	US-09-735-705-234	Sequence 234, App
701	15	65.2	16	US-10-223-047-19	Sequence 19, Appl	774	15	65.2	20	9	US-09-735-705-381	Sequence 381, App
702	15	65.2	16	US-10-094-401-220	Sequence 220, App	775	15	65.2	20	9	US-09-850-716A-234	Sequence 234, App
703	15	65.2	16	US-10-462-262-188	Sequence 188, App	776	15	65.2	20	9	US-09-850-716A-381	Sequence 381, App
704	15	65.2	16	US-10-239-103-20	Sequence 20, Appl	777	15	65.2	20	9	US-09-897-778-234	Sequence 234, App
705	15	65.2	16	US-10-467-758-14	Sequence 14, Appl	778	15	65.2	20	9	US-09-897-778-381	Sequence 381, App
706	15	65.2	16	US-10-927-262A-39	Sequence 39, Appl	779	15	65.2	20	10	US-09-764-891-4348	Sequence 4348, Ap
707	15	65.2	16	US-10-927-262A-40	Sequence 40, Appl	780	15	65.2	20	13	US-10-155-059-8	Sequence 8, Appli
708	15	65.2	16	US-10-927-262A-41	Sequence 41, Appl	781	15	65.2	20	13	US-10-155-059-10	Sequence 10, Appl
709	15	65.2	16	US-11-045-477-56	Sequence 56, Appl	782	15	65.2	20	13	US-10-155-059-11	Sequence 11, Appl
710	15	65.2	16	US-11-045-477-105	Sequence 105, App	783	15	65.2	20	13	US-10-155-059-14	Sequence 14, Appl
711	15	65.2	16	US-11-045-477-130	Sequence 130, App	784	15	65.2	20	13	US-10-155-059-15	Sequence 15, Appl
712	15	65.2	16	US-11-045-477-137	Sequence 137, App	785	15	65.2	20	13	US-10-155-059-16	Sequence 16, Appl
713	15	65.2	17	US-10-280-066-83	Sequence 83, Appl	786	15	65.2	20	13	US-10-155-059-19	Sequence 19, Appl
714	15	65.2	17	US-10-029-386-27504	Sequence 27504, A	787	15	65.2	20	13	US-10-155-059-20	Sequence 20, Appl
715	15	65.2	17	US-10-029-386-28133	Sequence 28133, A	788	15	65.2	20	14	US-10-007-700-234	Sequence 234, App
716	15	65.2	17	US-10-120-885A-44	Sequence 44, Appl	789	15	65.2	20	14	US-10-007-700-381	Sequence 381, App
717	15	65.2	17	US-10-258-144-248	Sequence 248, App	790	15	65.2	20	14	US-10-205-428-377	Sequence 377, App
718	15	65.2	17	US-10-258-144-258	Sequence 258, App	791	15	65.2	20	14	US-10-162-538-11	Sequence 11, Appl
719	15	65.2	17	US-10-258-144-442	Sequence 442, App	792	15	65.2	20	14	US-10-117-982-234	Sequence 234, App
720	15	65.2	17	US-10-695-155-155	Sequence 155, App	793	15	65.2	20	14	US-10-117-982-381	Sequence 381, App
721	15	65.2	17	US-10-661-156-93	Sequence 93, Appl	794	15	65.2	20	14	US-10-280-066-286	Sequence 286, App
722	15	65.2	17	US-10-946-647-66	Sequence 66, Appl	795	15	65.2	20	14	US-10-280-066-316	Sequence 316, App
723	15	65.2	18	US-09-214-371-74	Sequence 74, Appl	796	15	65.2	20	14	US-10-280-066-343	Sequence 343, App
724	15	65.2	18	US-09-896-841A-48	Sequence 48, Appl	797	15	65.2	20	14	US-10-029-386-33058	Sequence 33058, A
725	15	65.2	18	US-09-896-841A-49	Sequence 49, Appl	798	15	65.2	20	15	US-10-329-087-26	Sequence 26, Appl
726	15	65.2	18	US-10-225-567A-2147	Sequence 2147, Ap	799	15	65.2	20	15	US-10-329-087-31	Sequence 31, Appl
727	15	65.2	18	US-10-187-215-48	Sequence 48, Appl	800	15	65.2	20	15	US-10-313-986-234	Sequence 234, App
728	15	65.2	18	US-10-187-215-49	Sequence 49, Appl	801	15	65.2	20	15	US-10-313-986-381	Sequence 381, App
729	15	65.2	18	US-10-273-386-48	Sequence 48, Appl	802	15	65.2	20	15	US-10-644-703-14	Sequence 14, Appl
730	15	65.2	18	US-10-273-386-49	Sequence 49, Appl	803	15	65.2	20	16	US-10-666-480-5	Sequence 5, Appli
731	15	65.2	18	US-10-258-144-268	Sequence 268, App	804	15	65.2	20	16	US-10-467-758-8	Sequence 8, Appli
732	15	65.2	18	US-10-258-144-358	Sequence 358, App	805	15	65.2	20	16	US-10-467-758-9	Sequence 9, Appli
733	15	65.2	18	US-10-742-379-68	Sequence 68, Appl	806	15	65.2	20	16	US-10-467-758-10	Sequence 10, Appl
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ALIGNMENTS

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US-10-818-036-24  
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; Publication No. US2005022040A1  
; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice Z  
; APPLICANT: Schacter, Lee P.  
; APPLICANT: Zeldin, Michael H.  
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM  
; FILE REFERENCE: 303544.3000-100  
; CURRENT APPLICATION NUMBER: US/10/818,036  
; CURRENT FILING DATE: 2004-04-05  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-818-036-24

Query Match 73.9%; Score 17; DB 18; Length 8;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 4 FTASW 8

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; Publication No. US2005022040A1  
; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice Z  
; APPLICANT: Schacter, Lee P.  
; APPLICANT: Zeldin, Michael H.  
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM  
; FILE REFERENCE: 303544.3000-100  
; CURRENT APPLICATION NUMBER: US/10/818,036  
; CURRENT FILING DATE: 2004-04-05  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 27  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: MOD RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (8)..(8)  
; OTHER INFORMATION: AMIDATION  
US-10-818-036-27

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RESULT 3  
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; Sequence 28, Application US/10818036  
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; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice Z  
; APPLICANT: Schacter, Lee P.  
; APPLICANT: Zeldin, Michael H.  
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM  
; FILE REFERENCE: 303544.3000-100  
; CURRENT APPLICATION NUMBER: US/10/818,036  
; CURRENT FILING DATE: 2004-04-05  
; NUMBER OF SEQ ID NOS: 38  
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US-10-818-036-28

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RESULT 4  
US-10-818-036-30

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; Publication No. US20050222040A1
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; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
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RESULT 5
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; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
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; LENGTH: 9
; TYPE: PRT
; ORGANISM: Apis mellifera
US-10-072-419-3

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; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
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; LENGTH: 9
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; ORGANISM: Vanessa cardui
US-10-072-419-8

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Db      4 FTSSW 8

RESULT 7
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; Publication No. US20040224898A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/869,768
; CURRENT FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: US 10/072,419
; PRIOR FILING DATE: 2002-02-07
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; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Apis mellifera
US-10-869-768-3

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Db      4 FTSSW 8

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US-10-869-768-8
; Sequence 8, Application US/10869768
; Publication No. US20040224898A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/869,768
; CURRENT FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: US 10/072,419
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Vanessa cardui
US-10-869-768-8

Query Match      73.9%; Score 17; DB 16; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
      |
Db      4 FTSSW 8
```

```

RESULT 9
US-10-818-036-14
; Sequence 14, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-818-036-14

Query Match      73.9%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
Db      4 FTASW 8

RESULT 10
US-10-818-036-15
; Sequence 15, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-818-036-15

Query Match      73.9%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
Db      4 FTASW 8

RESULT 11
US-10-818-036-23
; Sequence 23, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Manduca sexta
US-10-818-036-23

Query Match      73.9%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
Db      4 FTASW 8

RESULT 12
US-10-818-036-25
; Sequence 25, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-818-036-25

Query Match      73.9%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
Db      4 FTASW 8

RESULT 13
US-10-818-036-26
; Sequence 26, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Manduca sexta
US-10-818-036-26
```

; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (9)..(9)  
; OTHER INFORMATION: AMIDATION  
US-10-818-036-26

Query Match 73.9%; Score 17; DB 18; Length 9;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 4 FTASW 8

RESULT 14  
US-10-818-036-29  
; Sequence 29, Application US/10818036  
; Publication No. US2005022040A1  
; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice Z  
; APPLICANT: Schacter, Lee P.  
; APPLICANT: Zeldin, Michael H.  
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM  
; FILE REFERENCE: 303544.3000-100  
; CURRENT APPLICATION NUMBER: US/10/818,036  
; CURRENT FILING DATE: 2004-04-05  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 29  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
; NAME/KEY: MOD\_RES  
; LOCATION: (9)..(9)  
; OTHER INFORMATION: AMIDATION  
US-10-818-036-29

Query Match 73.9%; Score 17; DB 18; Length 9;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 4 FTASW 8

RESULT 15  
US-09-842-776A-28  
; Sequence 28, Application US/09842776A  
; Publication No. US20040023316A1  
; GENERAL INFORMATION:  
; APPLICANT: CONNEX GMBH  
; TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS  
; TITLE OF INVENTION: IN THE STOOL  
; FILE REFERENCE: 41735  
; CURRENT APPLICATION NUMBER: US/09/842,776A  
; CURRENT FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: PCT/EP99/08212  
; PRIOR FILING DATE: 1999-10-29  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Complementarity determining region (CDR1) of an  
; OTHER INFORMATION: antibody heavy chain directed to a beta-urease  
; OTHER INFORMATION: epitope (alternative sequence)  
US-09-842-776A-28

Query Match 73.9%; Score 17; DB 11; Length 10;  
Best Local Similarity 40.0%; Pred. No. 6.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 4 FSTSW 8

RESULT 16  
US-10-996-316-139  
; Sequence 139, Application US/10996316  
; Publication No. US20050129690A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexion Pharmaceuticals, Inc.  
; APPLICANT: Bowdish, Katherine S.  
; APPLICANT: McWhirter, John  
; APPLICANT: Kretz-Rommel, Anke  
; TITLE OF INVENTION: POLYPEPTIDES AND ANTIBODIES DERIVED FROM CHRONIC LYMPHOCYTIC  
; TITLE OF INVENTION: LEUKEMIA CELLS AND USES THEREOF  
; FILE REFERENCE: 60 CIP IV (1087-43 CIP IV)  
; CURRENT APPLICATION NUMBER: US/10/996,316  
; CURRENT FILING DATE: 2004-11-23  
; PRIOR APPLICATION NUMBER: US 10/894,672  
; PRIOR FILING DATE: 2004-07-20  
; PRIOR APPLICATION NUMBER: US 10/736,188  
; PRIOR FILING DATE: 2003-12-15  
; PRIOR APPLICATION NUMBER: US 10/379,151  
; PRIOR FILING DATE: 2003-03-04  
; PRIOR APPLICATION NUMBER: PCT/US01/47931  
; PRIOR FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: US 60/254,113  
; PRIOR FILING DATE: 2000-12-08  
; NUMBER OF SEQ ID NOS: 211  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 139  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: murine  
US-10-996-316-139

Query Match 73.9%; Score 17; DB 18; Length 10;  
Best Local Similarity 40.0%; Pred. No. 6.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 4 FSAAW 8

RESULT 17  
US-10-072-419-37  
; Sequence 37, Application US/10072419  
; Publication No. US20030162717A1  
; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice  
; APPLICANT: Schacter, Lee  
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human  
; FILE REFERENCE: 10739-1  
; CURRENT APPLICATION NUMBER: US/10/072,419  
; CURRENT FILING DATE: 2002-02-07  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 37  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Vanessa cardui

US-10-072-419-37

Query Match 73.9%; Score 17; DB 14; Length 11;  
Best Local Similarity 40.0%; Pred. No. 6.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5  
|  
Db 4 FTSSW 8

RESULT 18

US-10-869-768-37  
; Sequence 37, Application US/10869768  
; Publication No. US20040224898A1  
; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice  
; APPLICANT: Schacter, Lee  
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human  
; FILE REFERENCE: 10739-1  
; CURRENT APPLICATION NUMBER: US/10/869,768  
; CURRENT FILING DATE: 2004-06-16  
; PRIOR APPLICATION NUMBER: US 10/072,419  
; PRIOR FILING DATE: 2002-02-07  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 37  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Vanessa cardui  
US-10-869-768-37

Query Match 73.9%; Score 17; DB 16; Length 11;  
Best Local Similarity 40.0%; Pred. No. 6.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5  
|  
Db 4 FTSSW 8

RESULT 19

US-10-354-240-87  
; Sequence 87, Application US/10354240  
; Publication No. US20030185847A1  
; GENERAL INFORMATION:  
; APPLICANT: Sone, Toshio  
; APPLICANT: Kume, Akinori  
; APPLICANT: Dairiki, Kazuo  
; APPLICANT: Iwama, Akiko  
; APPLICANT: Kino, Kohsuke  
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease  
; FILE REFERENCE: SPO-103D1  
; CURRENT APPLICATION NUMBER: US/10/354,240  
; CURRENT FILING DATE: 2003-01-29  
; PRIOR APPLICATION NUMBER: PCT/JP97/00740  
; PRIOR FILING DATE: 1997-03-10  
; PRIOR APPLICATION NUMBER: US 09/142,524  
; PRIOR FILING DATE: 1998-09-09  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 87  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Cryptomeria japonica  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(15)  
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 4  
US-10-354-240-87

Query Match 73.9%; Score 17; DB 14; Length 15;  
Best Local Similarity 40.0%; Pred. No. 8e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5  
|  
Db 9 FSTAW 13

RESULT 20

US-10-354-240-88  
; Sequence 88, Application US/10354240  
; Publication No. US20030185847A1  
; GENERAL INFORMATION:  
; APPLICANT: Sone, Toshio  
; APPLICANT: Kume, Akinori  
; APPLICANT: Dairiki, Kazuo  
; APPLICANT: Iwama, Akiko  
; APPLICANT: Kino, Kohsuke  
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease  
; FILE REFERENCE: SPO-103D1  
; CURRENT APPLICATION NUMBER: US/10/354,240  
; CURRENT FILING DATE: 2003-01-29  
; PRIOR APPLICATION NUMBER: PCT/JP97/00740  
; PRIOR FILING DATE: 1997-03-10  
; PRIOR APPLICATION NUMBER: US 09/142,524  
; PRIOR FILING DATE: 1998-09-09  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 88  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Cryptomeria japonica  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(15)  
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 5  
US-10-354-240-88

Query Match 73.9%; Score 17; DB 14; Length 15;  
Best Local Similarity 40.0%; Pred. No. 8e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5  
|  
Db 4 FSTAW 8

RESULT 21

US-09-963-339-10  
; Sequence 10, Application US/09963339  
; Publication No. US20030049700A1  
; GENERAL INFORMATION:  
; APPLICANT: Bandaru, Rajasekhar  
; TITLE OF INVENTION: 22108 AND 47916, NOVEL HUMAN THIOREDOXIN  
; TITLE OF INVENTION: FAMILY MEMBERS AND USES THEREOF  
; FILE REFERENCE: 10448-090001  
; CURRENT APPLICATION NUMBER: US/09/963,339  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 60/235,049  
; PRIOR FILING DATE: 2000-09-25  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-963-339-10

Query Match 73.9%; Score 17; DB 10; Length 19;  
Best Local Similarity 40.0%; Pred. No. 9.3e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5  
|



Db 4 FSATW 8

RESULT 22

US-10-145-596-59

; Sequence 59, Application US/10145586

; Publication No. US20030138890A1

; GENERAL INFORMATION:

; APPLICANT: Alexandra Glucksmann, Maria

; APPLICANT: Silos-Santiago, Immaculada

; APPLICANT: M. Galvin, Katherine

; APPLICANT: Weich, Nadine

; APPLICANT: Curtis, Rory A.J.

; APPLICANT: Bandaru, Rajasekhar

; APPLICANT: Kapeller-Libermann, Rosana

; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS,

; TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LEUCINE-RICH

; TITLE OF INVENTION: REPEAT FAMILY MEMBERS, AND HUMAN RINGFINGER FAMILY MEMBER

; FILE REFERENCE: 10448-188001

; CURRENT APPLICATION NUMBER: US/10/145,586

; CURRENT FILING DATE: 2002-05-14

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 95

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 59

; LENGTH: 19

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-145-586-59

Query Match 73.9%; Score 17; DB 14; Length 19;

Best Local Similarity 40.0%; Pred. No. 9.3e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db 4 FSATW 8

RESULT 23

US-10-931-260-265

; Sequence 265, Application US/10931260

; Publication No. US20050152927A1

; GENERAL INFORMATION:

; APPLICANT: Griffith, Irwin J.;

; Pollock, Joanne;

; Bond, Julian F.;

; Garman, Richard D.;

; Kuo, Mei-Chang;

; Powers, Stephen P.;

; Exley, Mark A.;

; Chen, Xian;

; Shaked, Ze'ev

; TITLE OF INVENTION: Allergenic Proteins And Peptides From

; Japanese Cedar Pollen

; NUMBER OF SEQUENCES: 283

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lahive & Cockfield, LLP

; STREET: 28 State St

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/931,260

; FILING DATE: 30-Aug-2004

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/240,203

FILING DATE: 29-Jan-1999

APPLICATION NUMBER: 08/467,023

FILING DATE: 1995-JUN-06

APPLICATION NUMBER: 08/350,225

FILING DATE: 1994-DEC-06

APPLICATION NUMBER: 08/226,248

FILING DATE: 1994-APR-08

APPLICATION NUMBER: PCT/US93/00139

FILING DATE: 1993-JAN-15

APPLICATION NUMBER: 07/938,990

FILING DATE: 1992-SEP-01

APPLICATION NUMBER: 07/730,452

FILING DATE: 1991-JUL-15

APPLICATION NUMBER: 07/729,134

FILING DATE: 1991-JUL-12

APPLICATION NUMBER: 07/975,179

FILING DATE: 1992-NOV-12

APPLICATION NUMBER: PCT/US92/05661

FILING DATE: 1992-JUL-10

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras, Esq.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IM1-028CD2CCPA2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 742-4214

INFORMATION FOR SEQ ID NO: 265:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 265:

US-10-931-260-265

Query Match 73.9%; Score 17; DB 18; Length 20;

Best Local Similarity 40.0%; Pred. No. 9.6e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db 12 FSTAW 16

RESULT 24

US-10-190-082-36

; Sequence 36, Application US/10190082

; Publication No. US20030148264A1

; GENERAL INFORMATION:

; APPLICANT: Lasky, Lawrence A.

; APPLICANT: Sidhu, Sachdev S.

; APPLICANT: Held, Heike A.

; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS

; FILE REFERENCE: P1905R1

; CURRENT APPLICATION NUMBER: US/10/190,082

; CURRENT FILING DATE: 2002-07-03

; PRIOR APPLICATION NUMBER: US 60/303,634

; PRIOR FILING DATE: 2001-07-06

; NUMBER OF SEQ ID NOS: 683

; SEQ ID NO 36

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Synthetic

US-10-190-082-36

Query Match 69.6%; Score 16; DB 14; Length 6;

Best Local Similarity 40.0%; Pred. No. 1.6e+06;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
QY      1 FXXW 5
      |  |
Db      1 FSDTW 5

RESULT 25
US-09-774-639-284
; Sequence 284, Application US/09774639
; Publication No. US2003000355A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P1
; CURRENT APPLICATION NUMBER: US/09/774,639
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 284
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-774-639-284

Query Match      69.6%; Score 16; DB 10; Length 7;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXW 5
      |  |
Db      2 FGTSW 6

RESULT 26
US-09-969-730-267
; Sequence 267, Application US/09969730
; Publication No. US2003005443A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P2
; CURRENT APPLICATION NUMBER: US/09/969,730
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,367
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,365
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,731
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,557
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,563
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/055,970

Query Match      69.6%; Score 16; DB 10; Length 7;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXW 5
      |  |
Db      2 FGTSW 6

RESULT 27
US-10-046-922-48
; Sequence 48, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGF-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 48
; LENGTH: 7
; TYPE: PRT
; ORGANISM: peptide
US-10-046-922-48

Query Match      69.6%; Score 16; DB 13; Length 7;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXW 5
      |  |
Db      3 FEAW 7
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RESULT 28
US-10-621-363-267
; Sequence 267, Application US/10621363
; Publication No. US20040023283A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P2C1
; CURRENT APPLICATION NUMBER: US/10/621,363
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,370
; PRIOR FILING DATE: 1997-08-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 267
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-621-363-267

Query Match      69.6%; Score 16; DB 15; Length 7;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 FXXXW 5
      |
Db      2 FGTSW 6

RESULT 29
US-10-072-419-4
; Sequence 4, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Schistocerca gregaria
US-10-072-419-4

Query Match      69.6%; Score 16; DB 14; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 FXXXW 5
      |
Db      2 FGTSW 6
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Db      4 FSTGW 8

RESULT 30
US-10-072-419-11
; Sequence 11, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Locusta migratoria
US-10-072-419-11

Query Match      69.6%; Score 16; DB 14; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 FXXXW 5
      |
Db      4 FSAGW 8

RESULT 31
US-10-072-419-15
; Sequence 15, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Phymateus leprosus
US-10-072-419-15

Query Match      69.6%; Score 16; DB 14; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 FXXXW 5
      |
Db      4 FSTGW 8

RESULT 32
US-10-072-419-24
; Sequence 24, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
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; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Gryllodes sigillatus  
US-10-072-419-24

Query Match 69.6%; Score 16; DB 14; Length 8;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 4 FSTGW 8

RESULT 33

US-10-072-419-25  
; Sequence 25, Application US/10072419  
; Publication No. US20030162717A1

; GENERAL INFORMATION:

; APPLICANT: Schacter, Bernice

; APPLICANT: Schacter, Lee

; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human

; FILE REFERENCE: 10739-1

; CURRENT APPLICATION NUMBER: US/10/072,419

; CURRENT FILING DATE: 2002-02-07

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 25

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Libanasidus vittatus

US-10-072-419-25

Query Match 69.6%; Score 16; DB 14; Length 8;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 4 FSTGW 8

RESULT 34

US-10-072-419-30

; Sequence 30, Application US/10072419

; Publication No. US20030162717A1

; GENERAL INFORMATION:

; APPLICANT: Schacter, Bernice

; APPLICANT: Schacter, Lee

; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human

; FILE REFERENCE: 10739-1

; CURRENT APPLICATION NUMBER: US/10/072,419

; CURRENT FILING DATE: 2002-02-07

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 30

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Onitis sp.

US-10-072-419-30

Query Match 69.6%; Score 16; DB 14; Length 8;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
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Db 4 FSTGW 8

RESULT 35

US-10-367-580-260

; Sequence 260, Application US/10367580

; Publication No. US20040071720A1  
; GENERAL INFORMATION:  
; APPLICANT: Rothman, James E.  
; APPLICANT: Hartl, F. Ulrich  
; APPLICANT: Hoe, Mee H.  
; APPLICANT: Houghton, Alan  
; APPLICANT: Takechi, Yoshizumi  
; APPLICANT: Mayhew, Mark  
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies  
; FILE REFERENCE: 11746/461061  
; CURRENT APPLICATION NUMBER: US/10/367,580  
; CURRENT FILING DATE: 2003-02-14  
; PRIOR APPLICATION NUMBER: US 09/794,832  
; PRIOR FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: US 09/011,645  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: PCT/US96/13363  
; PRIOR FILING DATE: 1996-08-16  
; PRIOR APPLICATION NUMBER: US 60/002,490  
; PRIOR FILING DATE: 1995-08-18  
; PRIOR APPLICATION NUMBER: US 60/002,479  
; PRIOR FILING DATE: 1995-08-18  
; NUMBER OF SEQ ID NOS: 349  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 260  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide  
US-10-367-580-260

Query Match 69.6%; Score 16; DB 15; Length 8;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 2 FLSSW 6

RESULT 36

US-10-367-580-264

; Sequence 264, Application US/10367580

; Publication No. US20040071720A1

; GENERAL INFORMATION:

; APPLICANT: Rothman, James E.

; APPLICANT: Hartl, F. Ulrich

; APPLICANT: Hoe, Mee H.

; APPLICANT: Houghton, Alan

; APPLICANT: Takechi, Yoshizumi

; APPLICANT: Mayhew, Mark

; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies

; FILE REFERENCE: 11746/461061

; CURRENT APPLICATION NUMBER: US/10/367,580

; CURRENT FILING DATE: 2003-02-14

; PRIOR APPLICATION NUMBER: US 09/794,832

; PRIOR FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: US 09/011,645

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: PCT/US96/13363

; PRIOR FILING DATE: 1996-08-16

; PRIOR APPLICATION NUMBER: US 60/002,490

; PRIOR FILING DATE: 1995-08-18

; PRIOR APPLICATION NUMBER: US 60/002,479

; PRIOR FILING DATE: 1995-08-18

; NUMBER OF SEQ ID NOS: 349

; SOFTWARE: WordPerfect 8.0 for Windows

; SEQ ID NO 264

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

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; OTHER INFORMATION: synthetic peptide
US-10-367-580-264

Query Match          69.6%; Score 16; DB 15; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 2 FLSSW 6

RESULT 37
US-10-367-593-260
; Sequence 260, Application US/10367593
; Publication No. US20040071721A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461012
; CURRENT APPLICATION NUMBER: US/10/367,593
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 260
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-593-260

Query Match          69.6%; Score 16; DB 15; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 2 FLSSW 6

RESULT 38
US-10-367-593-264
; Sequence 264, Application US/10367593
; Publication No. US20040071721A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461012
; CURRENT APPLICATION NUMBER: US/10/367,593
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
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; OTHER INFORMATION: synthetic peptide
US-10-367-593-264

Query Match          69.6%; Score 16; DB 15; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 2 FLSSW 6

RESULT 39
US-10-367-594-260
; Sequence 260, Application US/10367594
; Publication No. US20040071722A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461041
; CURRENT APPLICATION NUMBER: US/10/367,594
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/680,806
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 260
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-594-260

Query Match          69.6%; Score 16; DB 15; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5
Db 2 FLSSW 6

RESULT 40
US-10-367-594-264
; Sequence 264, Application US/10367594
; Publication No. US20040071722A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
```

APPLICANT: Hartl, F. Ulrich  
APPLICANT: Hoe, Mee H.  
APPLICANT: Houghton, Alan  
APPLICANT: Takechi, Yoshizumi  
APPLICANT: Mayhew, Mark  
TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies  
FILE REFERENCE: 11746/461041  
CURRENT APPLICATION NUMBER: US/10/367,594  
CURRENT FILING DATE: 2003-02-14  
PRIOR APPLICATION NUMBER: US 09/680,806  
PRIOR FILING DATE: 2000-10-05  
PRIOR APPLICATION NUMBER: US 09/011,645  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: PCT/US96/13363  
PRIOR FILING DATE: 1996-08-16  
PRIOR APPLICATION NUMBER: US 60/002,490  
PRIOR FILING DATE: 1995-08-18  
PRIOR APPLICATION NUMBER: US 60/002,479  
PRIOR FILING DATE: 1995-08-18  
NUMBER OF SEQ ID NOS: 349  
SOFTWARE: WordPerfect 8.0 for Windows  
SEQ ID NO 264  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic peptide  
US-10-367-594-264

Query Match 69.6%; Score 16; DB 15; Length 8;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
| |  
Db 2 FLSSW 6

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Job time : 110.588 secs

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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:46:49 ; Search time 27.7647 Seconds  
(without alignments)  
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Title: US-09-214-371-10  
Perfect score: 23  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 196327

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Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	17	73.9	13	3	US-09-085-072-7
2	17	73.9	15	4	US-09-142-524D-87
3	17	73.9	15	4	US-09-142-524D-88
4	16	69.6	6	1	US-07-920-519-10
5	16	69.6	6	1	US-08-086-410-7
6	16	69.6	6	1	US-08-314-586-10
7	16	69.6	7	4	US-09-774-639-284
8	16	69.6	9	4	US-09-702-114A-28
9	16	69.6	10	1	US-08-208-886C-87
10	16	69.6	10	1	US-08-704-744-89
11	16	69.6	10	1	US-08-469-557-68
12	16	69.6	10	2	US-08-290-793B-68
13	16	69.6	11	1	US-08-277-660A-16
14	16	69.6	11	1	US-08-277-660A-17
15	16	69.6	11	1	US-08-424-957-29
16	16	69.6	11	1	US-08-424-957-30
17	16	69.6	11	3	US-09-035-686-29
18	16	69.6	11	3	US-09-035-686-30
19	16	69.6	12	2	US-08-406-330-32
20	16	69.6	12	2	US-08-556-597-32
21	16	69.6	13	1	US-08-305-871A-23
22	16	69.6	13	3	US-08-912-560-11
23	16	69.6	13	4	US-08-788-822A-27
24	16	69.6	13	4	US-09-543-608A-27
25	16	69.6	13	4	US-09-556-818-65
26	16	69.6	13	6	5185431-25
27	16	69.6	13	6	5185431-25



101	15	65.2	9	1	US-08-638-911A-12	Sequence 12, Appl	174	15	65.2	11	3	US-09-035-686-42	Sequence 42, Appl
102	15	65.2	9	1	US-08-638-911A-15	Sequence 15, Appl	175	15	65.2	11	3	US-09-035-686-43	Sequence 43, Appl
103	15	65.2	9	1	US-08-638-911A-18	Sequence 18, Appl	176	15	65.2	11	3	US-09-035-686-44	Sequence 44, Appl
104	15	65.2	9	1	US-08-638-911A-21	Sequence 21, Appl	177	15	65.2	11	3	US-09-035-686-45	Sequence 45, Appl
105	15	65.2	9	2	US-08-709-177-5	Sequence 5, Appli	178	15	65.2	11	3	US-09-035-686-46	Sequence 46, Appl
106	15	65.2	9	2	US-08-709-177-8	Sequence 8, Appli	179	15	65.2	11	4	US-09-603-052-5	Sequence 5, Appli
107	15	65.2	9	2	US-08-709-177-11	Sequence 11, Appl	180	15	65.2	11	4	US-09-069-827A-46	Sequence 46, Appl
108	15	65.2	9	2	US-08-709-177-14	Sequence 14, Appl	181	15	65.2	11	4	US-09-069-827A-172	Sequence 172, App
109	15	65.2	9	3	US-08-396-385-7	Sequence 7, Appli	182	15	65.2	11	4	US-09-620-091-444	Sequence 444, App
110	15	65.2	9	3	US-09-249-272-3	Sequence 3, Appli	183	15	65.2	11	5	PCT-US96-09473-2	Sequence 2, Appli
111	15	65.2	9	3	US-09-287-221-7	Sequence 7, Appli	184	15	65.2	12	1	US-08-439-114-4	Sequence 4, Appli
112	15	65.2	9	4	US-09-225-322B-12	Sequence 12, Appl	185	15	65.2	12	1	US-08-200-011-5	Sequence 5, Appli
113	15	65.2	9	4	US-09-764-304-12	Sequence 12, Appl	186	15	65.2	12	3	US-08-665-643A-6	Sequence 6, Appli
114	15	65.2	9	4	US-08-634-332A-71	Sequence 71, Appl	187	15	65.2	12	4	US-08-634-332A-70	Sequence 70, Appl
115	15	65.2	9	4	US-09-555-790A-7	Sequence 7, Appli	188	15	65.2	12	4	US-09-428-082B-131	Sequence 131, App
116	15	65.2	9	4	US-09-555-790A-9	Sequence 9, Appli	189	15	65.2	12	4	US-09-428-082B-132	Sequence 132, App
117	15	65.2	9	4	US-09-771-415-16	Sequence 16, Appl	190	15	65.2	12	4	US-09-428-082B-133	Sequence 133, App
118	15	65.2	9	4	US-09-239-043D-2374	Sequence 2374, Ap	191	15	65.2	12	4	US-09-428-082B-134	Sequence 134, App
119	15	65.2	10	1	US-08-221-580-2	Sequence 2, Appli	192	15	65.2	12	4	US-09-428-082B-137	Sequence 137, App
120	15	65.2	10	1	US-08-208-886C-83	Sequence 83, Appl	193	15	65.2	12	4	US-09-428-082B-143	Sequence 143, App
121	15	65.2	10	1	US-08-277-660A-7	Sequence 7, Appli	194	15	65.2	12	4	US-09-428-082B-144	Sequence 144, App
122	15	65.2	10	1	US-08-277-660A-8	Sequence 8, Appli	195	15	65.2	12	4	US-09-428-082B-145	Sequence 145, App
123	15	65.2	10	1	US-08-704-744-85	Sequence 85, Appl	196	15	65.2	12	4	US-09-428-082B-146	Sequence 146, App
124	15	65.2	10	1	US-08-424-957-11	Sequence 11, Appl	197	15	65.2	13	1	US-08-463-115-102	Sequence 102, App
125	15	65.2	10	1	US-08-424-957-12	Sequence 12, Appl	198	15	65.2	13	1	US-08-465-388-102	Sequence 102, App
126	15	65.2	10	1	US-08-424-957-18	Sequence 18, Appl	199	15	65.2	13	2	US-08-480-190-26	Sequence 26, Appl
127	15	65.2	10	1	US-08-469-557-64	Sequence 64, Appl	200	15	65.2	13	2	US-08-488-379-26	Sequence 26, Appl
128	15	65.2	10	2	US-08-290-793B-64	Sequence 93, Appl	201	15	65.2	13	4	US-08-475-399A-26	Sequence 26, Appl
129	15	65.2	10	2	US-08-556-597-93	Sequence 4, Appli	202	15	65.2	13	4	US-08-077-255A-26	Sequence 26, Appl
130	15	65.2	10	2	US-08-713-636-4	Sequence 10, Appl	203	15	65.2	13	4	US-09-695-437A-19	Sequence 19, Appl
131	15	65.2	10	3	US-08-974-899-10	Sequence 10, Appl	204	15	65.2	13	4	US-09-695-437A-23	Sequence 23, Appl
132	15	65.2	10	3	US-09-035-686-11	Sequence 11, Appl	205	15	65.2	13	4	US-09-695-437A-42	Sequence 42, Appl
133	15	65.2	10	3	US-09-035-686-12	Sequence 12, Appl	206	15	65.2	13	5	PCT-US93-07545-26	Sequence 26, Appl
134	15	65.2	10	3	US-09-035-686-18	Sequence 18, Appl	207	15	65.2	14	2	US-08-764-640-33	Sequence 33, Appl
135	15	65.2	10	4	US-09-490-702B-53	Sequence 53, Appl	208	15	65.2	14	3	US-08-973-225-33	Sequence 33, Appl
136	15	65.2	10	4	US-09-490-702B-72	Sequence 72, Appl	209	15	65.2	14	3	US-09-244-298A-33	Sequence 213, App
137	15	65.2	10	4	US-09-795-798-10	Sequence 10, Appl	210	15	65.2	14	3	US-09-516-704-33	Sequence 33, Appl
138	15	65.2	10	5	PCT-US95-04018-64	Sequence 64, Appl	211	15	65.2	14	3	US-09-549-090-33	Sequence 33, Appl
139	15	65.2	11	1	US-08-277-660A-9	Sequence 9, Appli	212	15	65.2	14	4	US-09-549-090-33	Sequence 33, Appl
140	15	65.2	11	1	US-08-277-660A-10	Sequence 10, Appl	213	15	65.2	14	4	US-09-549-090-213	Sequence 213, App
141	15	65.2	11	1	US-08-277-660A-11	Sequence 11, Appl	214	15	65.2	14	4	US-09-832-230A-33	Sequence 33, Appl
142	15	65.2	11	1	US-08-277-660A-12	Sequence 12, Appl	215	15	65.2	14	4	US-09-428-082B-68	Sequence 68, Appl
143	15	65.2	11	1	US-08-277-660A-13	Sequence 13, Appl	216	15	65.2	14	4	US-09-695-437A-18	Sequence 18, Appl
144	15	65.2	11	1	US-08-277-660A-15	Sequence 15, Appl	217	15	65.2	14	4	US-09-695-437A-24	Sequence 24, Appl
145	15	65.2	11	1	US-08-277-660A-19	Sequence 19, Appl	218	15	65.2	14	4	US-09-695-437A-25	Sequence 25, Appl
146	15	65.2	11	1	US-08-277-660A-20	Sequence 20, Appl	219	15	65.2	14	4	US-09-695-437A-26	Sequence 26, Appl
147	15	65.2	11	1	US-08-424-957-17	Sequence 17, Appl	220	15	65.2	15	1	US-08-277-660A-1	Sequence 1, Appli
148	15	65.2	11	1	US-08-424-957-23	Sequence 23, Appl	221	15	65.2	15	1	US-08-277-660A-4	Sequence 4, Appli
149	15	65.2	11	1	US-08-424-957-24	Sequence 24, Appl	222	15	65.2	15	1	US-08-277-660A-5	Sequence 5, Appli
150	15	65.2	11	1	US-08-424-957-25	Sequence 25, Appl	223	15	65.2	15	1	US-08-277-660A-6	Sequence 6, Appli
151	15	65.2	11	1	US-08-424-957-26	Sequence 26, Appl	224	15	65.2	15	1	US-08-424-957-1	Sequence 1, Appli
152	15	65.2	11	1	US-08-424-957-28	Sequence 28, Appl	225	15	65.2	15	1	US-08-424-957-20	Sequence 20, Appl
153	15	65.2	11	1	US-08-424-957-32	Sequence 32, Appl	226	15	65.2	15	1	US-08-424-957-21	Sequence 21, Appl
154	15	65.2	11	1	US-08-424-957-33	Sequence 33, Appl	227	15	65.2	15	1	US-08-424-957-22	Sequence 22, Appl
155	15	65.2	11	1	US-08-424-957-34	Sequence 34, Appl	228	15	65.2	15	2	US-08-553-257A-52	Sequence 52, Appl
156	15	65.2	11	1	US-08-424-957-36	Sequence 36, Appl	229	15	65.2	15	3	US-09-280-047-6	Sequence 6, Appli
157	15	65.2	11	1	US-08-424-957-40	Sequence 40, Appl	230	15	65.2	15	3	US-09-165-042-16	Sequence 16, Appl
158	15	65.2	11	1	US-08-424-957-42	Sequence 42, Appl	231	15	65.2	15	3	US-09-035-686-1	Sequence 1, Appli
159	15	65.2	11	1	US-08-424-957-43	Sequence 43, Appl	232	15	65.2	15	3	US-09-035-686-20	Sequence 20, Appl
160	15	65.2	11	1	US-08-424-957-44	Sequence 44, Appl	233	15	65.2	15	3	US-09-035-686-21	Sequence 21, Appl
161	15	65.2	11	1	US-08-424-957-45	Sequence 45, Appl	234	15	65.2	15	3	US-09-035-686-22	Sequence 22, Appl
162	15	65.2	11	1	US-08-424-957-46	Sequence 46, Appl	235	15	65.2	15	3	US-08-208-573B-6	Sequence 6, Appli
163	15	65.2	11	3	US-09-035-686-17	Sequence 17, Appl	236	15	65.2	15	4	US-09-914-259-165	Sequence 165, App
164	15	65.2	11	3	US-09-035-686-23	Sequence 23, Appl	237	15	65.2	15	4	US-08-634-332A-65	Sequence 65, Appl
165	15	65.2	11	3	US-09-035-686-24	Sequence 24, Appl	238	15	65.2	15	4	US-08-634-332A-69	Sequence 69, Appl
166	15	65.2	11	3	US-09-035-686-25	Sequence 25, Appl	239	15	65.2	15	4	US-09-441-992-52	Sequence 52, Appl
167	15	65.2	11	3	US-09-035-686-26	Sequence 26, Appl	240	15	65.2	15	4	US-09-157-689-51	Sequence 51, Appl
168	15	65.2	11	3	US-09-035-686-28	Sequence 28, Appl	241	15	65.2	15	4	US-09-157-689-52	Sequence 52, Appl
169	15	65.2	11	3	US-09-035-686-32	Sequence 32, Appl	242	15	65.2	15	4	US-09-258-981-3	Sequence 3, Appli
170	15	65.2	11	3	US-09-035-686-33	Sequence 33, Appl	243	15	65.2	15	4	US-09-428-082B-139	Sequence 139, App
171	15	65.2	11	3	US-09-035-686-34	Sequence 34, Appl	244	15	65.2	15	4	US-09-428-082B-140	Sequence 140, App
172	15	65.2	11	3	US-09-035-686-36	Sequence 36, Appl	245	15	65.2	15	4	US-09-428-082B-141	Sequence 141, App
173	15	65.2	11	3	US-09-035-686-40	Sequence 40, Appl	246	15	65.2	15	4	US-09-511-204B-3	Sequence 3, Appli

247	15	65.2	15	4	US-09-950-692-6	Sequence 6, Appli	320	14	60.9	5	1	US-08-424-957-4	Sequence 4, Appli
248	15	65.2	15	4	US-09-955-437A-8	Sequence 8, Appli	321	14	60.9	5	1	US-08-424-957-5	Sequence 5, Appli
249	15	65.2	15	4	US-09-695-437A-11	Sequence 11, Appl	322	14	60.9	5	3	US-08-981-122-37	Sequence 37, Appl
250	15	65.2	15	4	US-09-695-437A-13	Sequence 13, Appl	323	14	60.9	5	3	US-09-035-686-4	Sequence 4, Appli
251	15	65.2	15	4	US-09-695-437A-14	Sequence 14, Appl	324	14	60.9	5	3	US-09-035-686-5	Sequence 5, Appli
252	15	65.2	15	4	US-09-695-437A-15	Sequence 15, Appl	325	14	60.9	5	3	US-09-099-053-3	Sequence 3, Appli
253	15	65.2	15	4	US-09-695-437A-16	Sequence 16, Appl	326	14	60.9	5	4	US-10-122-246A-100	Sequence 100, App
254	15	65.2	15	4	US-09-695-437A-17	Sequence 17, Appl	327	14	60.9	5	4	US-10-122-246A-101	Sequence 101, App
255	15	65.2	15	4	US-09-695-437A-20	Sequence 20, Appl	328	14	60.9	5	4	US-10-122-246A-102	Sequence 102, App
256	15	65.2	15	4	US-09-695-437A-21	Sequence 21, Appl	329	14	60.9	5	4	US-10-122-246A-103	Sequence 103, App
257	15	65.2	15	4	US-09-695-437A-22	Sequence 22, Appl	330	14	60.9	5	4	US-10-122-246A-104	Sequence 104, App
258	15	65.2	15	4	US-09-695-437A-32	Sequence 32, Appl	331	14	60.9	5	4	US-10-122-246A-105	Sequence 105, App
259	15	65.2	15	4	US-09-695-437A-33	Sequence 33, Appl	332	14	60.9	5	4	US-10-122-246A-106	Sequence 106, App
260	15	65.2	15	4	US-09-953-510-51	Sequence 51, Appl	333	14	60.9	5	4	US-10-337-105-3	Sequence 3, Appli
261	15	65.2	15	4	US-09-953-510-52	Sequence 52, Appl	334	14	60.9	5	4	US-10-337-105-4	Sequence 4, Appli
262	15	65.2	15	4	US-09-581-472B-4	Sequence 4, Appli	335	14	60.9	6	1	US-07-973-235A-29	Sequence 29, Appl
263	15	65.2	15	4	US-09-732-384-6	Sequence 6, Appli	336	14	60.9	6	1	US-08-269-257-7	Sequence 7, Appli
264	15	65.2	15	5	PCT-US95-02856-6	Sequence 6, Appli	337	14	60.9	6	1	US-08-269-257-36	Sequence 36, Appl
265	15	65.2	16	2	US-08-629-291A-19	Sequence 19, Appl	338	14	60.9	6	1	US-08-269-257-39	Sequence 39, Appl
266	15	65.2	16	2	US-08-658-335B-19	Sequence 19, Appl	339	14	60.9	6	1	US-08-269-257-61	Sequence 61, Appl
267	15	65.2	16	3	US-09-149-303-1	Sequence 1, Appli	340	14	60.9	6	1	US-08-180-209B-28	Sequence 28, Appl
268	15	65.2	16	3	US-09-171-705-32	Sequence 32, Appl	341	14	60.9	6	1	US-08-321-625-27	Sequence 27, Appl
269	15	65.2	16	4	US-09-406-640-19	Sequence 19, Appl	342	14	60.9	6	1	US-08-321-625-28	Sequence 28, Appl
270	15	65.2	16	4	US-09-541-345-56	Sequence 56, Appl	343	14	60.9	6	1	US-08-321-625-29	Sequence 29, Appl
271	15	65.2	16	4	US-09-541-345-105	Sequence 105, App	344	14	60.9	6	1	US-08-321-625-30	Sequence 30, Appl
272	15	65.2	16	6	5208144-11	Patent No. 5208144	345	14	60.9	6	1	US-08-476-000-30	Sequence 30, Appl
273	15	65.2	16	6	5208144-11	Patent No. 5208144	346	14	60.9	6	1	US-08-462-661A-41	Sequence 41, Appl
274	15	65.2	17	2	US-08-545-562A-64	Sequence 64, Appl	347	14	60.9	6	1	US-08-472-840-30	Sequence 30, Appl
275	15	65.2	17	2	US-08-637-759B-238	Sequence 238, App	348	14	60.9	6	1	US-08-424-957-16	Sequence 16, Appl
276	15	65.2	17	3	US-08-871-355A-238	Sequence 238, App	349	14	60.9	6	1	US-08-672-255-2	Sequence 2, Appli
277	15	65.2	17	3	US-09-201-945-238	Sequence 238, App	350	14	60.9	6	2	US-08-672-805-4	Sequence 4, Appli
278	15	65.2	18	2	US-08-248-839C-166	Sequence 166, App	351	14	60.9	6	2	US-08-672-805-5	Sequence 5, Appli
279	15	65.2	18	4	US-08-634-332A-8	Sequence 8, Appli	352	14	60.9	6	2	US-08-462-720-29	Sequence 29, Appl
280	15	65.2	18	4	US-08-634-332A-9	Sequence 9, Appli	353	14	60.9	6	2	US-08-476-976-30	Sequence 30, Appl
281	15	65.2	18	4	US-08-634-332A-10	Sequence 10, Appl	354	14	60.9	6	3	US-08-474-410-30	Sequence 30, Appl
282	15	65.2	18	4	US-08-634-332A-11	Sequence 11, Appl	355	14	60.9	6	3	US-09-035-686-16	Sequence 16, Appl
283	15	65.2	18	4	US-08-634-332A-24	Sequence 24, Appl	356	14	60.9	6	3	US-09-147-933-24	Sequence 24, Appl
284	15	65.2	18	4	US-08-634-332A-25	Sequence 25, Appl	357	14	60.9	6	3	US-09-196-934-17	Sequence 17, Appl
285	15	65.2	18	4	US-08-634-332A-62	Sequence 62, Appl	358	14	60.9	6	3	US-09-181-083-27	Sequence 27, Appl
286	15	65.2	18	4	US-08-634-332A-63	Sequence 63, Appl	359	14	60.9	6	3	US-09-181-083-28	Sequence 28, Appl
287	15	65.2	18	4	US-09-695-437A-63	Sequence 63, Appl	360	14	60.9	6	3	US-09-181-083-29	Sequence 29, Appl
288	15	65.2	18	4	US-09-695-437A-64	Sequence 64, Appl	361	14	60.9	6	3	US-09-181-083-30	Sequence 30, Appl
289	15	65.2	19	2	US-08-537-400-35	Sequence 35, Appl	362	14	60.9	6	3	US-08-486-673B-30	Sequence 30, Appl
290	15	65.2	19	4	US-09-081-975-13	Sequence 13, Appl	363	14	60.9	6	3	US-09-166-205B-28	Sequence 28, Appl
291	15	65.2	19	4	US-09-732-357B-9	Sequence 9, Appli	364	14	60.9	6	4	US-09-155-613A-84	Sequence 84, Appl
292	15	65.2	19	4	US-09-774-639-342	Sequence 342, App	365	14	60.9	6	4	US-08-757-425B-8	Sequence 2, Appli
293	15	65.2	19	4	US-09-732-384-7	Sequence 7, Appli	366	14	60.9	6	4	US-09-209-676-47	Sequence 47, Appl
294	15	65.2	20	2	US-08-637-759B-458	Sequence 458, App	367	14	60.9	6	4	US-09-750-754-27	Sequence 27, Appl
295	15	65.2	20	2	US-08-447-430A-26	Sequence 26, Appl	368	14	60.9	6	4	US-09-750-754-28	Sequence 28, Appl
296	15	65.2	20	2	US-08-447-430A-31	Sequence 31, Appl	369	14	60.9	6	4	US-09-750-754-29	Sequence 29, Appl
297	15	65.2	20	2	US-08-053-451B-114	Sequence 114, App	370	14	60.9	6	4	US-09-750-754-30	Sequence 30, Appl
298	15	65.2	20	3	US-08-504-538A-11	Sequence 11, Appl	371	14	60.9	6	4	US-09-692-945-10	Sequence 10, Appl
299	15	65.2	20	3	US-08-871-355A-458	Sequence 458, App	372	14	60.9	6	4	US-09-446-109A-20	Sequence 20, Appl
300	15	65.2	20	3	US-09-201-945-458	Sequence 458, App	373	14	60.9	6	4	US-09-446-109A-21	Sequence 21, Appl
301	15	65.2	20	3	US-08-630-052-11	Sequence 11, Appl	374	14	60.9	6	4	PCT-US94-02629-28	Sequence 28, Appl
302	15	65.2	20	4	US-09-643-597-234	Sequence 8, Appli	375	14	60.9	6	5	PCT-US95-04171-7	Sequence 7, Appli
303	15	65.2	20	4	US-09-081-975-8	Sequence 10, Appl	376	14	60.9	6	5	PCT-US95-04171-36	Sequence 36, Appl
304	15	65.2	20	4	US-09-081-975-10	Sequence 11, Appl	377	14	60.9	6	5	PCT-US95-04171-39	Sequence 39, Appl
305	15	65.2	20	4	US-09-081-975-11	Sequence 14, Appl	378	14	60.9	6	5	PCT-US95-04171-61	Sequence 61, Appl
306	15	65.2	20	4	US-09-081-975-14	Sequence 15, Appl	379	14	60.9	6	6	5318899-58	Patent No. 5318899
307	15	65.2	20	4	US-09-081-975-15	Sequence 16, Appl	380	14	60.9	6	6	5318899-58	Patent No. 5318899
308	15	65.2	20	4	US-09-081-975-16	Sequence 19, Appl	381	14	60.9	6	6	US-07-956-700B-71	Sequence 71, Appl
309	15	65.2	20	4	US-09-081-975-19	Sequence 20, Appl	382	14	60.9	6	7	US-08-321-625-26	Sequence 26, Appl
310	15	65.2	20	4	US-09-081-975-20	Sequence 234, App	383	14	60.9	7	1	US-08-321-625-70	Sequence 70, Appl
311	15	65.2	20	4	US-09-480-884A-234	Sequence 234, App	384	14	60.9	7	1	US-08-321-625-79	Sequence 79, Appl
312	15	65.2	20	4	US-09-542-615A-234	Sequence 234, App	385	14	60.9	7	1	US-08-484-184-4	Sequence 4, Appli
313	15	65.2	20	4	US-09-342-673-26	Sequence 26, Appl	386	14	60.9	7	1	US-08-087-219-4	Sequence 4, Appli
314	15	65.2	20	4	US-09-342-673-31	Sequence 31, Appl	387	14	60.9	7	1	US-08-476-537-71	Sequence 71, Appl
315	15	65.2	20	4	US-09-606-421B-234	Sequence 234, App	388	14	60.9	7	1	US-08-269-929-8	Sequence 8, Appli
316	15	65.2	20	4	US-09-476-496A-234	Sequence 234, App	389	14	60.9	7	1	US-08-485-607-71	Sequence 71, Appl
317	15	65.2	20	4	US-09-630-940B-234	Sequence 234, App	390	14	60.9	7	1		
318	15	65.2	20	4	US-09-471-276-1481	Sequence 1481, Ap	391	14	60.9	7	1		
319	15	65.2	20	5	PCT-US95-09307-11	Sequence 11, Appl	392	14	60.9	7	1		

393	14	60.9	7	2	US-08-475-879-71	Sequence 71, Appl	466	14	60.9	10	2	US-08-751-300-96	Sequence 96, Appl
394	14	60.9	7	3	US-09-258-754-402	Sequence 402, App	467	14	60.9	10	2	US-08-751-300-97	Sequence 97, Appl
395	14	60.9	7	3	US-09-181-083-26	Sequence 26, Appl	468	14	60.9	10	2	US-08-751-300-98	Sequence 98, Appl
396	14	60.9	7	3	US-09-181-083-70	Sequence 70, Appl	469	14	60.9	10	2	US-08-751-300-99	Sequence 99, Appl
397	14	60.9	7	3	US-09-181-083-79	Sequence 79, Appl	470	14	60.9	10	3	US-08-485-324-16	Sequence 16, Appl
398	14	60.9	7	3	US-09-042-107-402	Sequence 402, App	471	14	60.9	10	3	US-08-447-506-16	Sequence 16, Appl
399	14	60.9	7	3	US-09-099-053-7	Sequence 7, Appli	472	14	60.9	10	3	US-08-235-437-16	Sequence 16, Appl
400	14	60.9	7	3	US-09-433-043B-71	Sequence 71, Appl	473	14	60.9	10	3	US-08-447-515-16	Sequence 16, Appl
401	14	60.9	7	4	US-09-722-250D-402	Sequence 402, App	474	14	60.9	10	3	US-09-181-083-74	Sequence 74, Appl
402	14	60.9	7	4	US-09-750-754-26	Sequence 26, Appl	475	14	60.9	10	3	US-07-901-713A-4	Sequence 4, Appli
403	14	60.9	7	4	US-09-750-754-70	Sequence 70, Appl	476	14	60.9	10	3	US-09-268-347-2	Sequence 2, Appli
404	14	60.9	7	4	US-09-750-754-79	Sequence 79, Appl	477	14	60.9	10	3	US-09-261-182-2	Sequence 2, Appli
405	14	60.9	7	4	US-09-676-475A-402	Sequence 402, App	478	14	60.9	10	4	US-09-490-702B-40	Sequence 40, Appl
406	14	60.9	8	2	US-08-466-103A-9	Sequence 9, Appli	479	14	60.9	10	4	US-09-750-754-74	Sequence 74, Appl
407	14	60.9	8	2	US-08-669-284B-31	Sequence 31, Appl	480	14	60.9	10	4	US-09-428-082B-142	Sequence 142, App
408	14	60.9	8	3	US-09-063-893A-8	Sequence 8, Appli	481	14	60.9	10	4	US-09-239-043D-2392	Sequence 2392, Ap
409	14	60.9	8	3	US-08-444-818-323	Sequence 323, App	482	14	60.9	10	4	US-09-620-091-46	Sequence 46, Appl
410	14	60.9	8	3	US-08-444-818-346	Sequence 346, App	483	14	60.9	10	4	US-09-043-813-2	Sequence 2, Appli
411	14	60.9	8	3	US-08-444-818-347	Sequence 347, App	484	14	60.9	10	4	US-09-043-813-5	Sequence 5, Appli
412	14	60.9	8	3	US-08-444-818-348	Sequence 348, App	485	14	60.9	10	4	US-09-043-813-8	Sequence 8, Appli
413	14	60.9	8	3	US-08-444-818-384	Sequence 384, App	486	14	60.9	10	4	US-09-043-813-11	Sequence 11, Appl
414	14	60.9	8	3	US-08-444-818-385	Sequence 385, App	487	14	60.9	10	4	US-09-043-813-14	Sequence 14, Appl
415	14	60.9	8	3	US-08-444-818-386	Sequence 386, App	488	14	60.9	10	4	US-09-043-813-17	Sequence 17, Appl
416	14	60.9	8	3	US-09-314-242-4	Sequence 4, Appli	489	14	60.9	10	4	US-09-043-813-20	Sequence 20, Appl
417	14	60.9	8	4	US-09-402-641-3	Sequence 3, Appli	490	14	60.9	10	4	US-09-043-813-23	Sequence 23, Appl
418	14	60.9	8	4	US-09-601-729-168	Sequence 168, App	491	14	60.9	10	4	US-09-043-813-26	Sequence 26, Appl
419	14	60.9	8	4	US-09-620-091-484	Sequence 484, App	492	14	60.9	10	4	US-09-043-813-29	Sequence 29, Appl
420	14	60.9	9	1	US-08-318-970B-23	Sequence 23, Appl	493	14	60.9	10	4	US-09-043-813-32	Sequence 32, Appl
421	14	60.9	9	2	US-08-417-174-77	Sequence 77, Appl	494	14	60.9	10	4	US-09-043-813-35	Sequence 35, Appl
422	14	60.9	9	3	US-08-676-818-16	Sequence 16, Appl	495	14	60.9	10	4	US-09-043-813-38	Sequence 38, Appl
423	14	60.9	9	3	US-09-267-439-77	Sequence 77, Appl	496	14	60.9	10	4	US-09-043-813-41	Sequence 41, Appl
424	14	60.9	9	3	US-09-407-549-16	Sequence 16, Appl	497	14	60.9	10	4	US-09-043-813-44	Sequence 44, Appl
425	14	60.9	9	4	US-09-402-641-5	Sequence 5, Appli	498	14	60.9	10	4	US-09-043-813-57	Sequence 57, Appl
426	14	60.9	9	4	US-09-073-138-77	Sequence 77, Appl	499	14	60.9	10	4	US-09-043-813-59	Sequence 59, Appl
427	14	60.9	9	4	US-09-870-089B-3	Sequence 3, Appli	500	14	60.9	10	4	US-09-043-813-63	Sequence 63, Appl
428	14	60.9	9	4	US-09-870-089B-7	Sequence 7, Appli	501	14	60.9	10	4	US-09-043-813-65	Sequence 65, Appl
429	14	60.9	9	4	US-09-870-089B-9	Sequence 9, Appli	502	14	60.9	10	4	US-09-043-813-76	Sequence 76, Appl
430	14	60.9	10	1	US-08-321-625-74	Sequence 74, Appl	503	14	60.9	10	4	US-09-756-247-16	Sequence 16, Appl
431	14	60.9	10	1	US-08-242-678D-5	Sequence 5, Appli	504	14	60.9	10	4	US-09-756-247-36	Sequence 36, Appl
432	14	60.9	10	1	US-08-487-568-88	Sequence 88, Appl	505	14	60.9	11	1	US-08-318-970B-10	Sequence 10, Appl
433	14	60.9	10	2	US-08-370-909-16	Sequence 16, Appl	506	14	60.9	11	1	US-08-321-625-10	Sequence 10, Appl
434	14	60.9	10	2	US-08-370-909-17	Sequence 17, Appl	507	14	60.9	11	1	US-08-424-957-35	Sequence 35, Appl
435	14	60.9	10	2	US-08-556-597-120	Sequence 120, App	508	14	60.9	11	2	US-08-486-839-9	Sequence 9, Appli
436	14	60.9	10	2	US-08-902-623-37	Sequence 37, Appl	509	14	60.9	11	3	US-08-485-324-14	Sequence 14, Appl
437	14	60.9	10	2	US-08-902-623-40	Sequence 40, Appl	510	14	60.9	11	3	US-09-151-011-9	Sequence 9, Appli
438	14	60.9	10	2	US-08-902-623-72	Sequence 72, Appl	511	14	60.9	11	3	US-08-447-506-14	Sequence 14, Appl
439	14	60.9	10	2	US-08-747-137-122	Sequence 122, App	512	14	60.9	11	3	US-08-235-437-14	Sequence 14, Appl
440	14	60.9	10	2	US-08-751-300-2	Sequence 2, Appli	513	14	60.9	11	3	US-09-035-686-35	Sequence 35, Appl
441	14	60.9	10	2	US-08-751-300-5	Sequence 5, Appli	514	14	60.9	11	3	US-08-447-515-14	Sequence 14, Appl
442	14	60.9	10	2	US-08-751-300-8	Sequence 8, Appli	515	14	60.9	11	3	US-09-181-083-10	Sequence 10, Appl
443	14	60.9	10	2	US-08-751-300-11	Sequence 11, Appl	516	14	60.9	11	3	US-09-224-785-5	Sequence 5, Appli
444	14	60.9	10	2	US-08-751-300-14	Sequence 14, Appl	517	14	60.9	11	3	US-09-186-958-5	Sequence 5, Appli
445	14	60.9	10	2	US-08-751-300-17	Sequence 17, Appl	518	14	60.9	11	3	US-09-186-958-6	Sequence 6, Appli
446	14	60.9	10	2	US-08-751-300-20	Sequence 20, Appl	519	14	60.9	11	3	US-09-186-958-8	Sequence 8, Appli
447	14	60.9	10	2	US-08-751-300-23	Sequence 23, Appl	520	14	60.9	11	3	US-09-186-958-9	Sequence 9, Appli
448	14	60.9	10	2	US-08-751-300-26	Sequence 26, Appl	521	14	60.9	11	3	US-09-669-271A-5	Sequence 5, Appli
449	14	60.9	10	2	US-08-751-300-29	Sequence 29, Appl	522	14	60.9	11	3	US-09-669-271A-6	Sequence 6, Appli
450	14	60.9	10	2	US-08-751-300-32	Sequence 32, Appl	523	14	60.9	11	3	US-09-669-271A-8	Sequence 8, Appli
451	14	60.9	10	2	US-08-751-300-35	Sequence 35, Appl	524	14	60.9	11	3	US-09-669-271A-9	Sequence 9, Appli
452	14	60.9	10	2	US-08-751-300-38	Sequence 38, Appl	525	14	60.9	11	3	US-09-343-623-9	Sequence 9, Appli
453	14	60.9	10	2	US-08-751-300-41	Sequence 41, Appl	526	14	60.9	11	4	US-09-081-975-21	Sequence 21, Appl
454	14	60.9	10	2	US-08-751-300-44	Sequence 44, Appl	527	14	60.9	11	4	US-09-461-325-504	Sequence 504, App
455	14	60.9	10	2	US-08-751-300-57	Sequence 57, Appl	528	14	60.9	11	4	US-09-881-276-5	Sequence 5, Appli
456	14	60.9	10	2	US-08-751-300-59	Sequence 59, Appl	529	14	60.9	11	4	US-09-881-276-6	Sequence 6, Appli
457	14	60.9	10	2	US-08-751-300-65	Sequence 65, Appl	530	14	60.9	11	4	US-09-881-276-8	Sequence 8, Appli
458	14	60.9	10	2	US-08-751-300-63	Sequence 63, Appl	531	14	60.9	11	4	US-09-881-276-9	Sequence 9, Appli
459	14	60.9	10	2	US-08-751-300-77	Sequence 77, Appl	532	14	60.9	11	4	US-09-756-594-5	Sequence 5, Appli
460	14	60.9	10	2	US-08-751-300-90	Sequence 90, Appl	533	14	60.9	11	4	US-09-069-827A-43	Sequence 43, Appl
461	14	60.9	10	2	US-08-751-300-91	Sequence 91, Appl	534	14	60.9	11	4	US-09-069-827A-44	Sequence 44, Appl
462	14	60.9	10	2	US-08-751-300-92	Sequence 92, Appl	535	14	60.9	11	4	US-09-069-827A-47	Sequence 47, Appl
463	14	60.9	10	2	US-08-751-300-93	Sequence 93, Appl	536	14	60.9	11	4	US-10-012-542-504	Sequence 504, App
464	14	60.9	10	2	US-08-751-300-94	Sequence 94, Appl	537	14	60.9	11	4	US-09-750-754-10	Sequence 10, Appl
465	14	60.9	10	2	US-08-751-300-95	Sequence 95, Appl	538	14	60.9	11	4	US-09-428-082B-325	Sequence 325, App

539	14	60.9	11	4	US-10-115-123-504	Sequence 504, App	612	14	60.9	15	4	US-09-072-596-118	Sequence 118, App
540	14	60.9	12	1	US-08-487-568-113	Sequence 113, App	613	14	60.9	15	4	US-08-634-332A-64	Sequence 64, Appl
541	14	60.9	12	3	US-09-188-579-45	Sequence 45, Appl	614	14	60.9	15	4	US-09-441-992-50	Sequence 50, Appl
542	14	60.9	12	3	US-09-315-444-45	Sequence 45, Appl	615	14	60.9	15	4	US-09-441-992-51	Sequence 51, Appl
543	14	60.9	12	3	US-09-186-958-13	Sequence 13, Appl	616	14	60.9	15	4	US-09-574-749B-54	Sequence 54, Appl
544	14	60.9	12	3	US-09-669-271A-13	Sequence 13, Appl	617	14	60.9	15	4	US-09-644-442-7	Sequence 7, Appli
545	14	60.9	12	4	US-09-721-362-45	Sequence 45, Appl	618	14	60.9	15	4	US-09-072-967-57	Sequence 57, Appl
546	14	60.9	12	4	US-09-752-165-65	Sequence 65, Appl	619	14	60.9	15	4	US-09-072-967-123	Sequence 123, App
547	14	60.9	12	4	US-09-881-276-13	Sequence 13, Appl	620	14	60.9	15	4	US-09-428-082B-138	Sequence 138, App
548	14	60.9	12	4	US-09-716-129-87	Sequence 87, Appl	621	14	60.9	15	4	US-09-689-097-53	Sequence 53, Appl
549	14	60.9	12	4	US-09-440-772C-28	Sequence 28, Appl	622	14	60.9	15	5	PCT-US93-06751-28	Sequence 28, Appl
550	14	60.9	12	4	US-09-428-082B-135	Sequence 135, App	623	14	60.9	15	5	PCT-US94-02465-51	Sequence 51, Appl
551	14	60.9	12	4	US-09-428-082B-136	Sequence 136, App	624	14	60.9	15	5	PCT-US94-10356-2	Sequence 2, Appli
552	14	60.9	13	1	US-08-487-568-87	Sequence 87, Appl	625	14	60.9	15	5	PCT-US94-10356-3	Sequence 3, Appli
553	14	60.9	13	3	US-08-702-054B-35	Sequence 35, Appl	626	14	60.9	15	5	PCT-US94-10356-6	Sequence 6, Appli
554	14	60.9	13	3	US-09-236-415-5	Sequence 5, Appli	627	14	60.9	15	5	PCT-US94-10356-7	Sequence 7, Appli
555	14	60.9	13	4	US-09-081-975-9	Sequence 9, Appli	628	14	60.9	15	5	PCT-US94-10356-20	Sequence 20, Appl
556	14	60.9	13	4	US-09-700-993-26	Sequence 26, Appl	629	14	60.9	15	5	PCT-US94-10356-22	Sequence 22, Appl
557	14	60.9	13	5	PCT-US94-01234-47	Sequence 47, Appl	630	14	60.9	15	5	PCT-US95-00498-51	Sequence 51, Appl
558	14	60.9	14	1	US-08-534-975-10	Sequence 10, Appl	631	14	60.9	15	5	PCT-US95-00656-51	Sequence 51, Appl
559	14	60.9	14	2	US-08-449-933-11	Sequence 11, Appl	632	14	60.9	16	1	US-07-959-946-5	Sequence 5, Appli
560	14	60.9	14	2	US-08-392-816-12	Sequence 12, Appl	633	14	60.9	16	1	US-08-321-625-18	Sequence 18, Appl
561	14	60.9	14	2	US-08-954-470-10	Sequence 10, Appl	634	14	60.9	16	1	US-08-321-625-20	Sequence 20, Appl
562	14	60.9	14	2	US-08-750-359-3	Sequence 3, Appli	635	14	60.9	16	1	US-08-321-625-21	Sequence 21, Appl
563	14	60.9	14	2	US-08-750-359-4	Sequence 4, Appli	636	14	60.9	16	1	US-08-321-625-22	Sequence 22, Appl
564	14	60.9	14	3	US-08-564-225-10	Sequence 10, Appl	637	14	60.9	16	1	US-08-321-625-23	Sequence 23, Appl
565	14	60.9	14	3	US-09-129-855A-10	Sequence 10, Appl	638	14	60.9	16	1	US-08-321-625-24	Sequence 24, Appl
566	14	60.9	14	3	US-09-247-154-10	Sequence 10, Appl	639	14	60.9	16	1	US-08-321-625-25	Sequence 25, Appl
567	14	60.9	14	3	US-08-786-455B-4	Sequence 4, Appli	640	14	60.9	16	1	US-08-321-625-53	Sequence 53, Appl
568	14	60.9	14	3	US-07-966-049A-11	Sequence 11, Appl	641	14	60.9	16	1	US-08-321-625-63	Sequence 63, Appl
569	14	60.9	14	3	US-08-687-590-49	Sequence 49, Appl	642	14	60.9	16	1	US-08-321-625-64	Sequence 64, Appl
570	14	60.9	14	4	US-09-480-718-10	Sequence 10, Appl	643	14	60.9	16	1	US-08-321-625-65	Sequence 65, Appl
571	14	60.9	14	4	US-09-461-325-508	Sequence 508, App	644	14	60.9	16	1	US-08-321-625-68	Sequence 68, Appl
572	14	60.9	14	4	US-09-610-833-10	Sequence 10, Appl	645	14	60.9	16	1	US-08-321-625-80	Sequence 80, Appl
573	14	60.9	14	4	US-09-129-855A-10	Sequence 10, Appl	646	14	60.9	16	1	US-08-077-797A-43	Sequence 43, Appl
574	14	60.9	14	4	US-10-012-542-508	Sequence 508, App	647	14	60.9	16	1	US-08-473-344-51	Sequence 51, Appl
575	14	60.9	14	4	US-10-115-123-508	Sequence 508, App	648	14	60.9	16	1	US-08-333-577-5	Sequence 5, Appli
576	14	60.9	15	1	US-08-311-611A-51	Sequence 51, Appl	649	14	60.9	16	3	US-09-181-083-18	Sequence 18, Appl
577	14	60.9	15	1	US-08-372-783-51	Sequence 51, Appl	650	14	60.9	16	3	US-09-181-083-20	Sequence 20, Appl
578	14	60.9	15	1	US-08-372-105-51	Sequence 51, Appl	651	14	60.9	16	3	US-09-181-083-21	Sequence 21, Appl
579	14	60.9	15	1	US-08-148-160-2	Sequence 2, Appli	652	14	60.9	16	3	US-09-181-083-22	Sequence 22, Appl
580	14	60.9	15	1	US-08-306-473A-51	Sequence 51, Appl	653	14	60.9	16	3	US-09-181-083-23	Sequence 23, Appl
581	14	60.9	15	1	US-08-209-762-51	Sequence 51, Appl	654	14	60.9	16	3	US-09-181-083-24	Sequence 24, Appl
582	14	60.9	15	1	US-08-625-691-10	Sequence 10, Appl	655	14	60.9	16	3	US-09-181-083-25	Sequence 25, Appl
583	14	60.9	15	1	US-08-487-568-112	Sequence 112, App	656	14	60.9	16	3	US-09-181-083-53	Sequence 53, Appl
584	14	60.9	15	2	US-08-621-803-9	Sequence 9, Appli	657	14	60.9	16	3	US-09-181-083-63	Sequence 63, Appl
585	14	60.9	15	2	US-08-485-445A-51	Sequence 51, Appl	658	14	60.9	16	3	US-09-181-083-64	Sequence 64, Appl
586	14	60.9	15	2	US-08-553-257A-50	Sequence 50, Appl	659	14	60.9	16	3	US-09-181-083-65	Sequence 65, Appl
587	14	60.9	15	2	US-08-553-257A-51	Sequence 51, Appl	660	14	60.9	16	3	US-09-181-083-68	Sequence 68, Appl
588	14	60.9	15	3	US-09-119-263-51	Sequence 51, Appl	661	14	60.9	16	3	US-09-181-083-80	Sequence 80, Appl
589	14	60.9	15	3	US-08-657-162-51	Sequence 51, Appl	662	14	60.9	16	3	US-09-093-539-51	Sequence 51, Appl
590	14	60.9	15	3	US-09-224-480-51	Sequence 51, Appl	663	14	60.9	16	4	US-09-009-953-39	Sequence 39, Appl
591	14	60.9	15	3	US-09-217-352-9	Sequence 9, Appli	664	14	60.9	16	4	US-09-009-953-230	Sequence 230, App
592	14	60.9	15	3	US-08-818-112-57	Sequence 57, Appl	665	14	60.9	16	4	US-09-081-975-23	Sequence 23, Appl
593	14	60.9	15	3	US-08-818-112-123	Sequence 123, App	666	14	60.9	16	4	US-09-790-230-51	Sequence 51, Appl
594	14	60.9	15	3	US-08-818-111-57	Sequence 57, Appl	667	14	60.9	16	4	US-09-311-784A-308	Sequence 308, App
595	14	60.9	15	3	US-08-818-111-118	Sequence 118, App	668	14	60.9	16	4	US-09-546-013-72	Sequence 72, Appl
596	14	60.9	15	3	US-09-056-556-57	Sequence 57, Appl	669	14	60.9	16	4	US-09-750-754-18	Sequence 18, Appl
597	14	60.9	15	3	US-09-056-556-123	Sequence 123, App	670	14	60.9	16	4	US-09-750-754-20	Sequence 20, Appl
598	14	60.9	15	3	US-09-063-733A-28	Sequence 28, Appl	671	14	60.9	16	4	US-09-750-754-21	Sequence 21, Appl
599	14	60.9	15	4	US-09-009-953-247	Sequence 247, App	672	14	60.9	16	4	US-09-750-754-22	Sequence 22, Appl
600	14	60.9	15	4	US-08-487-795A-2	Sequence 2, Appli	673	14	60.9	16	4	US-09-750-754-23	Sequence 23, Appl
601	14	60.9	15	4	US-08-487-795A-3	Sequence 3, Appli	674	14	60.9	16	4	US-09-750-754-25	Sequence 24, Appl
602	14	60.9	15	4	US-08-487-795A-16	Sequence 16, Appl	675	14	60.9	16	4	US-09-750-754-25	Sequence 25, Appl
603	14	60.9	15	4	US-08-487-795A-17	Sequence 17, Appl	676	14	60.9	16	4	US-09-750-754-53	Sequence 53, Appl
604	14	60.9	15	4	US-08-487-795A-19	Sequence 19, Appl	677	14	60.9	16	4	US-09-750-754-63	Sequence 63, Appl
605	14	60.9	15	4	US-08-121-105B-2	Sequence 2, Appli	678	14	60.9	16	4	US-09-750-754-64	Sequence 64, Appl
606	14	60.9	15	4	US-08-121-105B-3	Sequence 3, Appli	679	14	60.9	16	4	US-09-750-754-65	Sequence 65, Appl
607	14	60.9	15	4	US-08-121-105B-16	Sequence 16, Appl	680	14	60.9	16	4	US-09-750-754-68	Sequence 68, Appl
608	14	60.9	15	4	US-08-121-105B-17	Sequence 17, Appl	681	14	60.9	16	4	US-09-750-754-80	Sequence 80, Appl
609	14	60.9	15	4	US-08-121-105B-19	Sequence 19, Appl	682	14	60.9	16	4	US-09-854-133-587	Sequence 587, App
610	14	60.9	15	4	US-09-081-975-24	Sequence 24, Appl	683	14	60.9	16	4	US-09-541-345-4	Sequence 4, Appli
611	14	60.9	15	4	US-09-072-596-57	Sequence 57, Appl	684	14	60.9	16	4	US-09-541-345-20	Sequence 20, Appl

685	14	60.9	16	4	US-09-541-345-35	Sequence 35, Appl	758	14	60.9	17	4	US-09-350-641C-814	Sequence 814, App
686	14	60.9	16	4	US-09-541-345-37	Sequence 37, Appl	759	14	60.9	17	4	US-09-428-082B-209	Sequence 209, App
687	14	60.9	16	4	US-09-541-345-38	Sequence 38, Appl	760	14	60.9	17	4	US-08-077-255A-123	Sequence 123, App
688	14	60.9	16	4	US-09-541-345-39	Sequence 39, Appl	761	14	60.9	17	4	US-09-490-070A-222	Sequence 222, App
689	14	60.9	16	4	US-09-541-345-40	Sequence 40, Appl	762	14	60.9	17	4	US-09-490-070A-228	Sequence 228, App
690	14	60.9	16	4	US-09-541-345-41	Sequence 41, Appl	763	14	60.9	17	4	US-09-490-070A-254	Sequence 254, App
691	14	60.9	16	4	US-09-541-345-42	Sequence 42, Appl	764	14	60.9	17	4	US-09-490-070A-262	Sequence 262, App
692	14	60.9	16	4	US-09-541-345-43	Sequence 43, Appl	765	14	60.9	17	4	US-09-490-153-222	Sequence 222, App
693	14	60.9	16	4	US-09-541-345-44	Sequence 44, Appl	766	14	60.9	17	4	US-09-490-153-228	Sequence 228, App
694	14	60.9	16	4	US-09-541-345-45	Sequence 45, Appl	767	14	60.9	17	4	US-09-490-153-254	Sequence 254, App
695	14	60.9	16	4	US-09-541-345-46	Sequence 46, Appl	768	14	60.9	17	4	US-09-490-153-262	Sequence 262, App
696	14	60.9	16	4	US-09-541-345-47	Sequence 47, Appl	769	14	60.9	17	4	US-09-350-841A-814	Sequence 814, App
697	14	60.9	16	4	US-09-541-345-48	Sequence 48, Appl	770	14	60.9	17	4	US-09-695-437A-40	Sequence 40, Appl
698	14	60.9	16	4	US-09-541-345-50	Sequence 50, Appl	771	14	60.9	17	4	US-09-490-324-222	Sequence 222, App
699	14	60.9	16	4	US-09-541-345-51	Sequence 51, Appl	772	14	60.9	17	4	US-09-490-324-228	Sequence 228, App
700	14	60.9	16	4	US-09-541-345-52	Sequence 52, Appl	773	14	60.9	17	4	US-09-490-324-254	Sequence 254, App
701	14	60.9	16	4	US-09-541-345-53	Sequence 53, Appl	774	14	60.9	17	4	US-09-490-324-262	Sequence 262, App
702	14	60.9	16	4	US-09-541-345-55	Sequence 55, Appl	775	14	60.9	17	5	PCT-US93-07545-123	Sequence 123, App
703	14	60.9	16	4	US-09-541-345-57	Sequence 57, Appl	776	14	60.9	17	5	PCT-US94-05684-7	Sequence 7, Appl
704	14	60.9	16	4	US-09-541-345-58	Sequence 58, Appl	777	14	60.9	17	5	PCT-US94-10356-19	Sequence 19, Appl
705	14	60.9	16	4	US-09-541-345-59	Sequence 59, Appl	778	14	60.9	17	5	PCT-US94-10356-21	Sequence 21, Appl
706	14	60.9	16	4	US-09-541-345-61	Sequence 61, Appl	779	14	60.9	18	1	US-08-218-025A-3	Sequence 3, Appl
707	14	60.9	16	4	US-09-541-345-62	Sequence 62, Appl	780	14	60.9	18	1	US-08-375-100-3	Sequence 3, Appl
708	14	60.9	16	4	US-09-541-345-63	Sequence 63, Appl	781	14	60.9	18	2	US-08-448-603A-24	Sequence 24, Appl
709	14	60.9	16	4	US-09-541-345-64	Sequence 64, Appl	782	14	60.9	18	2	US-08-484-905-36	Sequence 36, Appl
710	14	60.9	16	4	US-09-541-345-66	Sequence 66, Appl	783	14	60.9	18	3	US-08-940-095-199	Sequence 199, App
711	14	60.9	16	4	US-09-541-345-69	Sequence 69, Appl	784	14	60.9	18	3	US-08-940-095-224	Sequence 224, App
712	14	60.9	16	4	US-09-541-345-71	Sequence 71, Appl	785	14	60.9	18	3	US-08-481-985B-36	Sequence 36, Appl
713	14	60.9	16	4	US-09-541-345-73	Sequence 73, Appl	786	14	60.9	18	3	US-08-940-093-199	Sequence 199, App
714	14	60.9	16	4	US-09-541-345-74	Sequence 74, Appl	787	14	60.9	18	3	US-08-940-093-224	Sequence 224, App
715	14	60.9	16	4	US-09-541-345-75	Sequence 75, Appl	788	14	60.9	18	3	US-09-134-075-24	Sequence 24, Appl
716	14	60.9	16	4	US-09-541-345-76	Sequence 76, Appl	789	14	60.9	18	3	US-08-940-096-199	Sequence 199, App
717	14	60.9	16	4	US-09-541-345-77	Sequence 77, Appl	790	14	60.9	18	3	US-08-940-096-224	Sequence 224, App
718	14	60.9	16	4	US-09-541-345-79	Sequence 79, Appl	791	14	60.9	18	3	US-08-370-476-36	Sequence 36, Appl
719	14	60.9	16	4	US-09-541-345-81	Sequence 81, Appl	792	14	60.9	18	3	US-09-082-279B-1147	Sequence 1147, Ap
720	14	60.9	16	4	US-09-541-345-83	Sequence 83, Appl	793	14	60.9	18	3	US-09-465-719-199	Sequence 199, App
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722	14	60.9	16	4	US-09-541-345-85	Sequence 85, Appl	795	14	60.9	18	3	US-09-453-605-199	Sequence 199, App
723	14	60.9	16	4	US-09-541-345-86	Sequence 86, Appl	796	14	60.9	18	3	US-09-453-605-224	Sequence 224, App
724	14	60.9	16	4	US-09-541-345-89	Sequence 89, Appl	797	14	60.9	18	3	US-09-492-739-24	Sequence 24, Appl
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726	14	60.9	16	4	US-09-541-345-92	Sequence 92, Appl	799	14	60.9	18	3	US-09-315-304B-1147	Sequence 1147, Ap
727	14	60.9	16	4	US-09-541-345-96	Sequence 96, Appl	800	14	60.9	18	3	US-09-453-838-199	Sequence 199, App
728	14	60.9	16	4	US-09-541-345-98	Sequence 98, Appl	801	14	60.9	18	3	US-09-453-838-224	Sequence 224, App
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730	14	60.9	16	4	US-09-541-345-106	Sequence 106, App	803	14	60.9	18	4	US-08-940-136-199	Sequence 199, App
731	14	60.9	16	5	PCT-US92-08634-5	Sequence 5, Appl	804	14	60.9	18	4	US-08-940-136-224	Sequence 224, App
732	14	60.9	16	5	PCT-US94-01238-43	Sequence 43, Appl	805	14	60.9	18	4	US-08-634-332A-12	Sequence 12, Appl
733	14	60.9	17	1	US-08-321-625-35	Sequence 35, Appl	806	14	60.9	18	4	US-08-634-332A-13	Sequence 13, Appl
734	14	60.9	17	1	US-08-370-567-7	Sequence 7, Appl	807	14	60.9	18	4	US-09-834-784-1147	Sequence 1147, Ap
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746	14	60.9	17	3	US-09-315-304B-814	Sequence 814, App	819	14	60.9	18	4	US-09-453-840-199	Sequence 199, App
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750	14	60.9	17	4	US-08-121-105B-18	Sequence 18, Appl	823	14	60.9	18	4	US-09-350-841A-1147	Sequence 1147, Ap
751	14	60.9	17	4	US-08-475-399A-123	Sequence 123, App	824	14	60.9	18	4	US-09-453-834-199	Sequence 199, App
752	14	60.9	17	4	US-09-205-258-363	Sequence 363, App	825	14	60.9	18	4	US-09-453-834-224	Sequence 224, App
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755	14	60.9	17	4	US-09-477-135A-89	Sequence 89, Appl	828	14	60.9	19	4	US-09-489-847-359	Sequence 359, App
756	14	60.9	17	4	US-09-515-965A-814	Sequence 814, App	829	14	60.9	19	4	US-09-489-847-360	Sequence 360, App
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832	14	60.9	19	4	US-09-620-091-382	Sequence 382, App	905	14	60.9	20	3	US-09-119-263-57	Sequence 57, Appl
833	14	60.9	19	4	US-10-115-123-298	Sequence 298, App	906	14	60.9	20	3	US-09-119-263-58	Sequence 58, Appl
834	14	60.9	19	4	US-09-700-993-34	Sequence 34, Appl	907	14	60.9	20	3	US-09-119-263-59	Sequence 59, Appl
835	14	60.9	20	1	US-08-311-611A-54	Sequence 54, Appl	908	14	60.9	20	3	US-09-119-263-101	Sequence 101, App
836	14	60.9	20	1	US-08-311-611A-57	Sequence 57, Appl	909	14	60.9	20	3	US-09-119-263-150	Sequence 150, App
837	14	60.9	20	1	US-08-311-611A-58	Sequence 58, Appl	910	14	60.9	20	3	US-09-119-263-151	Sequence 151, App
838	14	60.9	20	1	US-08-311-611A-59	Sequence 59, Appl	911	14	60.9	20	3	US-09-119-263-152	Sequence 152, App
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866	14	60.9	20	1	US-08-321-625-50	Sequence 50, Appl	939	14	60.9	20	3	US-09-181-083-36	Sequence 36, Appl
867	14	60.9	20	1	US-08-306-473A-54	Sequence 54, Appl	940	14	60.9	20	3	US-09-181-083-50	Sequence 50, Appl
868	14	60.9	20	1	US-08-306-473A-57	Sequence 57, Appl	941	14	60.9	20	3	US-09-093-539-54	Sequence 54, Appl
869	14	60.9	20	1	US-08-306-473A-58	Sequence 58, Appl	942	14	60.9	20	3	US-08-927-597-76	Sequence 76, Appl
870	14	60.9	20	1	US-08-306-473A-59	Sequence 59, Appl	943	14	60.9	20	3	US-08-927-597-77	Sequence 77, Appl
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872	14	60.9	20	1	US-08-306-473A-150	Sequence 150, App	945	14	60.9	20	3	US-09-400-208B-1	Sequence 1, Appli
873	14	60.9	20	1	US-08-306-473A-151	Sequence 151, App	946	14	60.9	20	3	US-09-217-352-7	Sequence 7, Appli
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878	14	60.9	20	1	US-08-209-762-57	Sequence 57, Appl	951	14	60.9	20	3	US-09-217-352-148	Sequence 148, App
879	14	60.9	20	1	US-08-209-762-58	Sequence 58, Appl	952	14	60.9	20	3	US-08-860-656B-12	Sequence 12, Appl
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889	14	60.9	20	2	US-08-485-445A-54	Sequence 54, Appl	962	14	60.9	20	4	US-08-635-886C-33	Sequence 33, Appl
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898	14	60.9	20	2	US-08-485-445A-160	Sequence 160, App	971	14	60.9	20	4	US-09-664-945-23	Sequence 23, Appl
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901	14	60.9	20	2	US-08-714-537-17	Sequence 17, Appl	974	14	60.9	20	4	US-09-689-097-60	Sequence 60, Appl
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978 14 60.9 20 4 US-09-689-097-148 Sequence 148, App  
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980 14 60.9 20 4 US-09-689-097-156 Sequence 156, App  
981 14 60.9 20 4 US-09-689-097-157 Sequence 157, App  
982 14 60.9 20 4 US-08-974-685-32 Sequence 32, Appl  
983 14 60.9 20 4 US-08-974-685-33 Sequence 33, Appl  
984 14 60.9 20 4 US-08-974-685-39 Sequence 39, Appl  
985 14 60.9 20 4 US-09-674-973A-459 Sequence 459, App  
986 14 60.9 20 4 US-09-400-122A-1 Sequence 1, Appli  
987 14 60.9 20 4 US-09-695-437A-45 Sequence 45, Appl  
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993 14 60.9 20 5 PCT-US94-10356-17 Sequence 17, Appl  
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ALIGNMENTS

RESULT 1  
US-09-085-072-7  
; Sequence 7, Application US/09085072  
; Patent No. 6265150  
; GENERAL INFORMATION:  
; APPLICANT: L. Terstappen et al.  
; TITLE OF INVENTION: PHAGE ANTIBODIES  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hoffmann & Baron, LLP  
; STREET: 350 Jericho Turnpike  
; CITY: Jericho  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 11753  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/085,072  
; FILING DATE: 26-MAY-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Felt, Irving N.  
; REGISTRATION NUMBER: 28,601  
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; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-085-072-7

Query Match 73.9%; Score 17; DB 3; Length 13;  
Best Local Similarity 40.0%; Pred. No. 1.9e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

Sequence 147, App  
Sequence 148, App  
Sequence 149, App  
Sequence 156, App  
Sequence 157, App  
Sequence 32, Appl  
Sequence 33, Appl  
Sequence 39, Appl  
Sequence 459, App  
Sequence 1, Appli  
Sequence 45, Appl  
Sequence 61, Appl  
Sequence 54, Appl  
Sequence 57, Appl  
Sequence 58, Appl  
Sequence 59, Appl  
Sequence 101, App  
Sequence 150, App  
Sequence 151, App

QY 1 FXXXW 5  
| |  
Db 6 FASSW 10  
  
RESULT 2  
US-09-142-524D-87  
; Sequence 87, Application US/09142524D  
; Patent No. 6719976  
; GENERAL INFORMATION:  
; APPLICANT: Sone, Toshio  
; APPLICANT: Kume, Akinori  
; APPLICANT: Dairiki, Kazuo  
; APPLICANT: Iwama, Akiko  
; APPLICANT: Kino, Kohsuke  
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease  
; FILE REFERENCE: SPO-103  
; CURRENT APPLICATION NUMBER: US/09/142,524D  
; CURRENT FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: PCT/JP97/00740  
; PRIOR FILING DATE: 1997-03-10  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 87  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Cryptomeria japonica  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(15)  
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 4  
US-09-142-524D-87

Query Match 73.9%; Score 17; DB 4; Length 15;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 1 FXXXW 5  
| |  
Db 9 FSTAW 13

RESULT 3  
US-09-142-524D-88  
; Sequence 88, Application US/09142524D  
; Patent No. 6719976  
; GENERAL INFORMATION:  
; APPLICANT: Sone, Toshio  
; APPLICANT: Kume, Akinori  
; APPLICANT: Dairiki, Kazuo  
; APPLICANT: Iwama, Akiko  
; APPLICANT: Kino, Kohsuke  
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease  
; FILE REFERENCE: SPO-103  
; CURRENT APPLICATION NUMBER: US/09/142,524D  
; CURRENT FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: PCT/JP97/00740  
; PRIOR FILING DATE: 1997-03-10  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 88  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Cryptomeria japonica  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(15)  
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 5  
US-09-142-524D-88

Query Match 73.9%; Score 17; DB 4; Length 15;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 3; Gaps 0;



Qy 1 FXXW 5  
|  
Db 4 FSTW 8

RESULT 4

US-07-920-519-10  
; Sequence 10, Application US/07920519  
; Patent No. 5382518  
; GENERAL INFORMATION:  
; APPLICANT: CAPUT, DANIEL  
; APPLICANT: FERRARA, PASCUAL  
; APPLICANT: GUILLEMOT, JEAN-CLAUDE  
; APPLICANT: KAGHAD, MOURAD  
; APPLICANT: LEGOUX, RICHARD  
; APPLICANT: LOISON, GERARD  
; APPLICANT: LARBRE, ELIZABETH  
; APPLICANT: LUPKER, JOHANNES  
; APPLICANT: LEPLATOIS, PASCUAL  
; APPLICANT: SALOME, MARK  
; TITLE OF INVENTION: URATE OXIDASE ACTIVITY PROTEIN,  
; TITLE OF INVENTION: RECOMBINANT GENE CODING THEREFOR, EXPRESSION VECTOR,  
; TITLE OF INVENTION: MICRO-ORGANISMS AND TRANSFORMED CELLS  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/920,519  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/659,408  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 16781/276 BEDL  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; IMMEDIATE SOURCE:  
; CLONE: Hydrolysis product T 23  
US-07-920-519-10

Query Match 69.6%; Score 16; DB 1; Length 6;  
Best Local Similarity 40.0%; Pred. No. 4.1e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5  
|  
Db 1 FDTW 5

RESULT 5

US-08-086-410-7  
; Sequence 7, Application US/08086410  
; Patent No. 5407822  
; GENERAL INFORMATION:  
; APPLICANT: LEPLATOIS, Pascal  
; APPLICANT: LOISON, Gerard  
; APPLICANT: PESSEGUE, Bernard  
; APPLICANT: SHIRE, David  
; TITLE OF INVENTION: Artificial promoter for the expression  
; TITLE OF INVENTION: of proteins in yeast  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY & LARDNER  
; STREET: King Street Station, Suite 500, 1800 Diagonal  
; STREET: Road, PO Box 299  
; CITY: ALEXANDRIA  
; STATE: VIRGINIA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/086,410  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/768,083  
; FILING DATE: 02-OCT-1991  
; APPLICATION NUMBER: FR 89 17467  
; FILING DATE: 29-DEC-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SAXE, Bernhard D  
; REGISTRATION NUMBER: 28,665  
; REFERENCE/DOCKET NUMBER: 16781/318  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-9300  
; TELEFAX: (703) 683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; CLONE: hydrolysis product T23  
US-08-086-410-7

Query Match 69.6%; Score 16; DB 1; Length 6;  
Best Local Similarity 40.0%; Pred. No. 4.1e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5  
|  
Db 1 FDTW 5

RESULT 6

US-08-314-586-10  
; Sequence 10, Application US/08314586  
; Patent No. 5541098  
; GENERAL INFORMATION:  
; APPLICANT: CAPUT, DANIEL  
; APPLICANT: FERRARA, PASCUAL  
; APPLICANT: GUILLEMOT, JEAN-CLAUDE  
; APPLICANT: KAGHAD, MOURAD  
; APPLICANT: LEGOUX, RICHARD  
; APPLICANT: LOISON, GERARD  
; APPLICANT: LARBRE, ELIZABETH

```

; APPLICANT: LUPKER, JOHANNES
; APPLICANT: LEPLATOIS, PASCUAL
; APPLICANT: SALOME, MARK
; APPLICANT: LAURENT, PATRICK
; TITLE OF INVENTION: URATE OXIDASE ACTIVITY PROTEIN,
; TITLE OF INVENTION: RECOMBINANT GENE CODING THEREFOR, EXPRESSION VECTOR,
; TITLE OF INVENTION: MICROORGANISMS AND TRANSFORMED CELLS
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/314,586
; FILING DATE: 28-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/659,408
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16781/509/BEDL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; IMMEDIATE SOURCE:
; CLONE: Hydrolysis product T 23
;
US-08-314-586-10

Query Match          69.6%; Score 16; DB 1; Length 6;
Best Local Similarity 40.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
      |  |
Db      1 FDATAW 5

RESULT 7
US-09-774-639-284
; Sequence 284, Application US/09774639
; Patent No. 6806351
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P1
; CURRENT APPLICATION NUMBER: US/09/774,639
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 284
; LENGTH: 7
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-09-774-639-284

Query Match          69.6%; Score 16; DB 4; Length 7;
Best Local Similarity 40.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
      |  |
Db      2 FGTSW 6

RESULT 8
US-09-702-114A-28
; Sequence 28, Application US/09702114A
; Patent No. 6566078
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Aya Jakobovits
; APPLICANT: Mary Faris
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Steve Chappell Mitchell
; TITLE OF INVENTION: 36P6D5: SECRETED TUMOR ANTIGEN
; FILE REFERENCE: 129.22-US-U1
; CURRENT APPLICATION NUMBER: US/09/702,114A
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/162,417
; PRIOR FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-702-114A-28

Query Match          69.6%; Score 16; DB 4; Length 9;
Best Local Similarity 40.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
      |  |
Db      4 FRSSW 8

RESULT 9
US-08-208-886C-87
; Sequence 87, Application US/08208886C
; Patent No. 5597710
; GENERAL INFORMATION:
; APPLICANT: Dalie, Barbara
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Tindall, Stephen
; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/208,886C
; FILING DATE: March 10, 1994
; CLASSIFICATION: 424

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: JB0429
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908 298 2987
; TELEFAX: 908 298 5388
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-208-886C-87

Query Match 69.6%; Score 16; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 4 FSSYW 8

RESULT 10
US-08-704-744-89
; Sequence 89, Application US/08704744
; Patent No. 5705154
; GENERAL INFORMATION:
; APPLICANT: Dalie, Barbara
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Tindall, Stephen
; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5.3
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,744
; FILING DATE: 06-SEPT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/208886
; FILING DATE: 10-MAR-1994
; APPLICATION NUMBER: PCT/US/95/02400
; FILING DATE: 08-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: JB0429K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 298-2987
; TELEFAX: (908) 298-5388
; TELEX:
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-704-744-89

Query Match 69.6%; Score 16; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
DB 4 FSSYW 8

RESULT 11
US-08-469-557-68
; Sequence 68, Application US/08469557
; Patent No. 5770403
; GENERAL INFORMATION:
; APPLICANT: Dalie, Barbara
; APPLICANT: Le, Hung
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Nguyen, Hanh
; APPLICANT: Tindall, Stephen
; APPLICANT: Zavodny, Paul
; TITLE OF INVENTION: Cloning and Expression of
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; TITLE OF INVENTION: Against Human Interleukin-4
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,557
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/290,793
; FILING DATE: August 16, 1994
; APPLICATION NUMBER: PCT/US93/01301
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: US 07/841,659
; FILING DATE: 19-FEB-1992
; APPLICATION NUMBER: US 07/782,784
; FILING DATE: 24-OCT-1991
; APPLICATION NUMBER: US 07/499,327
; FILING DATE: 21-MAY-1990
; APPLICATION NUMBER: PCT/US88/03631
; FILING DATE: 21-OCT-1988
; APPLICATION NUMBER: US 07/655,966
; FILING DATE: 14-FEB-1991
; APPLICATION NUMBER: US 07/113,623
; FILING DATE: 26-OCT-1987
; APPLICATION NUMBER: US 06/881,553
; FILING DATE: 03-JUL-1986
; APPLICATION NUMBER: US 06/843,958
; FILING DATE: 25-MAR-1986
; APPLICATION NUMBER: US 06/799,668
; FILING DATE: 19-NOV-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: 2409K7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908 298-2987
; TELEFAX: 908-298-5388



```
; Sequence 17, Application US/08277660A
; Patent No. 5702908
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,660A
; FILING DATE: 20-JUL-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-60244/WHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-277-660A-17

Query Match 69.6%; Score 16; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5
Db 5 FSDAW 9

RESULT 15
US-08-424-957-29
; Sequence 29, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,957
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; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-424-957-29

Query Match 69.6%; Score 16; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 2.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5
Db 5 FSALW 9

RESULT 16
US-08-424-957-30
; Sequence 30, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,957
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
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US-08-424-957-30

Query Match 69.6%; Score 16; DB 1; Length 11;  
Best Local Similarity 40.0%; Pred. No. 2.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 5 FSDAW 9

RESULT 17

US-09-035-686-29  
; Sequence 29, Application US/09035686  
; Patent No. 6153391  
; GENERAL INFORMATION:  
; APPLICANT: Picksley, Steven M.  
; APPLICANT: Lane, David P.  
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/035,686  
; FILING DATE:

CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/424,957  
; FILING DATE: 19-APR-1995  
; APPLICATION NUMBER: US 08/277,660  
; FILING DATE: 20-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Walter H.  
; REGISTRATION NUMBER: 24,190  
; REFERENCE/DOCKET NUMBER: A-61228/WH  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
US-09-035-686-29

Query Match 69.6%; Score 16; DB 3; Length 11;  
Best Local Similarity 40.0%; Pred. No. 2.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 5 FSALW 9

RESULT 18

US-09-035-686-30  
; Sequence 30, Application US/09035686  
; Patent No. 6153391  
; GENERAL INFORMATION:  
; APPLICANT: Picksley, Steven M.

APPLICANT: Lane, David P.  
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53  
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/035,686  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/424,957  
; FILING DATE: 19-APR-1995  
; APPLICATION NUMBER: US 08/277,660  
; FILING DATE: 20-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Walter H.  
; REGISTRATION NUMBER: 24,190  
; REFERENCE/DOCKET NUMBER: A-61228/WH  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
US-09-035-686-30

Query Match 69.6%; Score 16; DB 3; Length 11;  
Best Local Similarity 40.0%; Pred. No. 2.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 5 FSDAW 9

RESULT 19

US-08-406-330-32  
; Sequence 32, Application US/08406330  
; Patent No. 5817748  
; GENERAL INFORMATION:  
; APPLICANT: Miller, Jonathan L.  
; APPLICANT: Lyle, Vicki A.  
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF  
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle  
; STREET: Clinton Square, P.O. Box 1051  
; CITY: Rochester  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 14603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/406,330  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Timian, Susan J.  
REGISTRATION NUMBER: 34,103  
REFERENCE/DOCKET NUMBER: 20884/100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1636  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-406-330-32

Query Match 69.6%; Score 16; DB 2; Length 12;  
Best Local Similarity 40.0%; Pred. No. 2.8e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5  
|  
Db 3 FSSVW 7

RESULT 20  
US-08-556-597-32  
Sequence 32, Application US/08556597  
Patent No. 5877155  
GENERAL INFORMATION:  
APPLICANT: Miller, Jonathan L.  
APPLICANT: Lyle, Vicki A.  
TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF  
TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: New York  
COUNTRY: USA  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/556,597  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/406,330  
FILING DATE: 17-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Timian, Susan J.  
REGISTRATION NUMBER: 34,103  
REFERENCE/DOCKET NUMBER: 20884/101  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1636  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-556-597-32

Query Match 69.6%; Score 16; DB 2; Length 12;  
Best Local Similarity 40.0%; Pred. No. 2.8e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5  
|  
Db 3 FSSVW 7

RESULT 21  
US-08-305-871A-23  
Sequence 23, Application US/08305871A  
Patent No. 5736142  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Gaeta, Federico  
APPLICANT: Grey, Howard M.  
APPLICANT: Sidney, John  
APPLICANT: Alexander, Jeffrey L.  
TITLE OF INVENTION: Alteration of Immune Response Using Pan  
TITLE OF INVENTION: DR-Binding Peptides  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/305,871A  
FILING DATE: 14-SEP-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/121,101  
FILING DATE: 14-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 14137-0062-10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1..13  
OTHER INFORMATION: /note= "Peptide wherein X is  
OTHER INFORMATION: tyrosine or phenylalanine."  
US-08-305-871A-23

Query Match 69.6%; Score 16; DB 1; Length 13;  
Best Local Similarity 40.0%; Pred. No. 2.9e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5  
|  
Db 3 FVAW 7

RESULT 22  
US-08-912-560-11





```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/218,025A
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/891,451
; FILING DATE: 29-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST33A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9206
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 139:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-218-025A-139

Query Match 69.6%; Score 16; DB 1; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels

QY 1 FXXXW 5
Db 1 FNSTW 5

RESULT 29
US-08-847-844A-22
; Sequence 22, Application US/08847844A
; Patent No. 6150160
; GENERAL INFORMATION:
; APPLICANT: KAZAZIAN JR., HAIG H.
; APPLICANT: BOEKE, JEF D.
; APPLICANT: MORAN, JOHN V.
; APPLICANT: DOMBROSKI, BETH A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF
; MAMMALIAN RETROTRANSPOSONS
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND FL.
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103-7086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,844A
; FILING DATE: 28-APR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/749,805
; FILING DATE: 16-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/006,831
; FILING DATE: 16-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DOYLE LEARY Ph.D., KATHRYN
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9596-23U2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/218,025A
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/891,451
; FILING DATE: 29-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST33A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9206
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 139:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-218-025A-139

Query Match 69.6%; Score 16; DB 1; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels

QY 1 FXXXW 5
Db 1 FNSTW 5

RESULT 29
US-08-847-844A-22
; Sequence 22, Application US/08847844A
; Patent No. 6150160
; GENERAL INFORMATION:
; APPLICANT: KAZAZIAN JR., HAIG H.
; APPLICANT: BOEKE, JEF D.
; APPLICANT: MORAN, JOHN V.
; APPLICANT: DOMBROSKI, BETH A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF
; MAMMALIAN RETROTRANSPOSONS
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND FL.
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103-7086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,844A
; FILING DATE: 28-APR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/749,805
; FILING DATE: 16-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/006,831
; FILING DATE: 16-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DOYLE LEARY Ph.D., KATHRYN
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9596-23U2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/218,025A
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/891,451
; FILING DATE: 29-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST33A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9206
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 139:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-218-025A-139

Query Match 69.6%; Score 16; DB 1; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels

QY 1 FXXXW 5
Db 1 FNSTW 5

RESULT 29
US-08-847-844A-22
; Sequence 22, Application US/08847844A
; Patent No. 6150160
; GENERAL INFORMATION:
; APPLICANT: KAZAZIAN JR., HAIG H.
; APPLICANT: BOEKE, JEF D.
; APPLICANT: MORAN, JOHN V.
; APPLICANT: DOMBROSKI, BETH A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF
; MAMMALIAN RETROTRANSPOSONS
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND FL.
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103-7086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,844A
; FILING DATE: 28-APR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/749,805
; FILING DATE: 16-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/006,831
; FILING DATE: 16-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DOYLE LEARY Ph.D., KATHRYN
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9596-23U2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/218,025A
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/891,451
; FILING DATE: 29-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST33A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9206
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 139:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-218-025A-139

Query Match 69.6%; Score 16; DB 1; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels

QY 1 FXXXW 5
Db 1 FNSTW 5

RESULT 29
US-08-847-844A-22
; Sequence 22, Application US/08847844A
; Patent No. 6150160
; GENERAL INFORMATION:
; APPLICANT: KAZAZIAN JR., HAIG H.
; APPLICANT: BOEKE, JEF D.
; APPLICANT: MORAN, JOHN V.
; APPLICANT: DOMBROSKI, BETH A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF
; MAMMALIAN RETROTRANSPOSONS
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND FL.
; CITY: PHILADELPHIA
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103-7086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/847,844A
; FILING DATE: 28-APR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/749,805
; FILING DATE: 16-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/006,831
; FILING DATE: 16-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DOYLE LEARY Ph.D., KATHRYN
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9596-23U2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/218,025A
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/891,451
; FILING DATE: 29-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST33A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9206
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 139:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-218-025A-139

Query Match 69.6%; Score 16; DB 1; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels

QY 1 FXXXW 5
Db 1 FNSTW 5

RESULT 29
US-08-847-844A-22
; Sequence 22, Application US/08847844A
; Patent No. 6150160
; GENERAL INFORMATION:
; APPLICANT: KAZAZIAN JR., HAIG H.
; APPLICANT: BOEKE, JEF D.
; APPLICANT: MORAN, JOHN V.
; APPLICANT: DOMBROSKI, BETH A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF
; MAMMALIAN RETROTRANSPOSONS
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND FL.
; CITY: PH
```

TELEFAX: 215-567-2991  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-847-844A-22

Query Match 69.6%; Score 16; DB 3; Length 15;  
Best Local Similarity 40.0%; Pred. No. 3.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5  
|  
Db 6 FIATW 10

RESULT 30

PCT-US93-08699-1  
Sequence 1, Application PC/TUS9308699  
GENERAL INFORMATION:  
APPLICANT: JOHNSON & JOHNSON and GEORGETOWN UNIVERSITY  
TITLE OF INVENTION: IMMUNOREACTIVE PEPTIDES FROM  
TITLE OF INVENTION: EPSTEIN-BARR VIRUS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East - Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/08699  
FILING DATE: 15-SEP-1993  
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: Wetherell, Jr., Ph.D., John R.,  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: FD-3033  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 455-5100  
TELEFAX: (619) 455-5110

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:

NAME/KEY: Peptide  
LOCATION: 1..15  
PCT-US93-08699-1

Query Match 69.6%; Score 16; DB 5; Length 15;  
Best Local Similarity 40.0%; Pred. No. 3.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5  
|  
Db 3 FTETW 7

RESULT 31

US-09-330-914A-11

Sequence 11, Application US/09330914A  
Patent No. 6432671  
GENERAL INFORMATION:  
APPLICANT: Flohe, Leopold  
No. 6432671ecke, Everson  
Kalisz, Henryk  
Montemartini, Marisa  
TITLE OF INVENTION: TRYPAREDOXIN, EXPRESSION PLASMID, PROCESS OF  
PRODUCTION, METHOD OF USE, TEST KIT, AND  
PHARMACEUTICAL COMPOSITION

NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Broun  
STREET: 233 South Wacker Drive/6300 Sears Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: Unites States of America  
ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/330,914A  
FILING DATE: 11-Jun-1999  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/EP97/06983  
FILING DATE: 12-DEC-1997  
ATTORNEY/AGENT INFORMATION:

NAME: Zeller, James P.  
REGISTRATION NUMBER: 28,491  
REFERENCE/DOCKET NUMBER: 29473/35678  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448

INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-330-914A-11

Query Match 69.6%; Score 16; DB 4; Length 16;  
Best Local Similarity 40.0%; Pred. No. 3.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5  
|  
Db 8 FAQSW 12

RESULT 32

US-08-413-233-3  
Sequence 3, Application US/08413233  
Patent No. 6506553

GENERAL INFORMATION:  
APPLICANT: Smith, Richard S.  
APPLICANT: Parks, D. Ellio  
TITLE OF INVENTION: METHOD FOR DIAGNOSIS OF EPSTEIN-BARR  
TITLE OF INVENTION: VIRUS ASSOCIATED DISEASE  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LOEB AND LOEB  
STREET: 1880 Century Park East, 5th Floor  
CITY: Los Angeles  
STATE: California

; COUNTRY: USA  
; ZIP: 90067  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/413,233  
; FILING DATE: 30-MAR-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Yang, Wei-ning  
; REGISTRATION NUMBER: 38,690  
; REFERENCE/DOCKET NUMBER: 7586D.4007  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (310) 553-5050  
; TELEFAX: (310) 553-4619  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1..16  
; US-08-413-233-3

Query Match 69.6%; Score 16; DB 4; Length 16;  
Best Local Similarity 40.0%; Pred. No. 3.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5  
|  
Db 3 FTETW 7

RESULT 33  
US-09-690-454-88  
; Sequence 88, Application US/09690454  
; Patent No. 6531447  
; GENERAL INFORMATION:  
; APPLICANT: Steven M. Ruben, et al.  
; TITLE OF INVENTION: 32 Human Secreted Proteins  
; FILE REFERENCE: PZ006P1  
; CURRENT APPLICATION NUMBER: US/09/690,454  
; CURRENT FILING DATE: 2000-10-18  
; PRIOR APPLICATION NUMBER: 09/189,144  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: 60/044,039  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,093  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,190  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/050,935  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,101  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,356  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/056,250  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,296  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,293  
; PRIOR FILING DATE: August 29, 1997  
; NUMBER OF SEQ ID NOS: 229  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 88  
; LENGTH: 16

; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-690-454-88  
  
Query Match 69.6%; Score 16; DB 4; Length 16;  
Best Local Similarity 40.0%; Pred. No. 3.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 FXXXW 5  
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Db 8 FRSAW 12  
  
RESULT 34  
US-09-170-496D-285  
; Sequence 285, Application US/09170496D  
; Patent No. 6555339  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-  
; FILE REFERENCE: AREN-0040  
; CURRENT APPLICATION NUMBER: US/09/170,496D  
; CURRENT FILING DATE: 1998-10-13  
; NUMBER OF SEQ ID NOS: 294  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 285  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: No. 6555339e1 Sequence  
; US-09-170-496D-285  
  
Query Match 69.6%; Score 16; DB 4; Length 16;  
Best Local Similarity 40.0%; Pred. No. 3.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 FXXXW 5  
|  
Db 5 FMSTW 9  
  
RESULT 35  
US-08-218-025A-115  
; Sequence 115, Application US/08218025A  
; Patent No. 5556744  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, David B.  
; APPLICANT: Ugen, Kenneth E.  
; APPLICANT: Williams, William V.  
; TITLE OF INVENTION: Methods and Compositions for Diagnosing  
; TITLE OF INVENTION: and Treating Certain HIV Infected Patients  
; NUMBER OF SEQUENCES: 197  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Howson and Howson  
; STREET: P.O. Box 457, 321 No. 5556744ristown Road  
; CITY: Spring House  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19477  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/218,025A  
; FILING DATE: 24-MAR-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/891,451  
FILING DATE: 29-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: WST33A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 540-9206  
TELEFAX: (215) 540-5818  
INFORMATION FOR SEQ ID NO: 115:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-218-025A-115

Query Match 69.6%; Score 16; DB 1; Length 17;  
Best Local Similarity 40.0%; Pred. No. 3.5e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5  
Db 13 FNSTW 17

RESULT 36  
US-08-746-283-7  
Sequence 7, Application US/08746283  
Patent No. 5834280  
GENERAL INFORMATION:  
APPLICANT: Oxenboll, Karen M.  
APPLICANT: Si, Joan Q.  
APPLICANT: Aagaard, Jesper  
TITLE OF INVENTION: Glucose Oxidases  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5834280 No. 5834280disk of No. 5834280th America  
STREET: 405 Lexington Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10174  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/746,283  
FILING DATE: 07-NOV-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Agis, Dr. Cheryl H.  
REGISTRATION NUMBER: 34,086  
REFERENCE/DOCKET NUMBER: 4158.214-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 867-0123  
TELEFAX: (212) 878-9655  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 5834280e  
US-08-746-283-7

Query Match 69.6%; Score 16; DB 2; Length 17;  
Best Local Similarity 40.0%; Pred. No. 3.5e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5

Db 3 FTSVW 7

RESULT 37  
US-08-746-257A-5  
Sequence 5, Application US/08746257A  
Patent No. 5879921  
GENERAL INFORMATION:  
APPLICANT: Cherry, Joel  
APPLICANT: Berka, Randy  
APPLICANT: Halkier, Torben  
TITLE OF INVENTION: Glucose Oxidases  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 5879921 No. 5879921disk of No. 5879921th America  
STREET: 405 Lexington Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10174  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/746,257A  
FILING DATE: 07-NOV-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Starnes, Robert L.  
REGISTRATION NUMBER: 41,324  
REFERENCE/DOCKET NUMBER: 4700.000-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 5879921e  
US-08-746-257A-5

Query Match 69.6%; Score 16; DB 2; Length 17;  
Best Local Similarity 40.0%; Pred. No. 3.5e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5  
Db 3 FTSVW 7

RESULT 38  
US-08-987-743-11  
Sequence 11, Application US/08987743  
Patent No. 6123938  
GENERAL INFORMATION:  
APPLICANT: Stern, Robert  
APPLICANT: Csoka, Anthony  
APPLICANT: Frost, Gregory I.  
APPLICANT: Wong, Tim M.  
TITLE OF INVENTION: Purification and Microsequencing of  
TITLE OF INVENTION: Hylauronidase Isozymes  
FILE REFERENCE: 9076/08CIP2  
CURRENT APPLICATION NUMBER: US/08/987,743  
CURRENT FILING DATE: 1997-12-09  
EARLIER APPLICATION NUMBER: 08/733,360  
EARLIER FILING DATE: 1996-10-17  
NUMBER OF SEQ ID NOS: 16

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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 17
; TYPE: PRT
; ORGANISM: H. sapiens
; US-08-987-743-11

Query Match      69.6%; Score 16; DB 3; Length 17;
Best Local Similarity 40.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 FXXW 5
Db      11 FTTW 15

RESULT 39
US-09-170-496D-286
; Sequence 286, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 286
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6555339e1 Sequence
; US-09-170-496D-286

Query Match      69.6%; Score 16; DB 4; Length 17;
Best Local Similarity 40.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 FXXW 5
Db      5 FMSTW 9

RESULT 40
US-08-934-915-125
; Sequence 125, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-934-915-125

Query Match      69.6%; Score 16; DB 2; Length 18;
Best Local Similarity 40.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 FXXW 5
Db      7 FSRTW 11

Search completed: October 18, 2005, 16:00:25
Job time : 35.7647 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:17:40 ; Search time 109.647 Seconds  
(without alignments)  
37.362 Million cell updates/sec

Title: US-09-214-371-10  
Perfect score: 23  
Sequence: 1 FXXXWXXX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : UniProt\_03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	17	73.9	9	1	AKH HELZE	P67787 heliothis z
2	17	73.9	13	2	Q9XLI2	Q9xli2 bemisia tab
3	17	73.9	26	2	Q9S880	Q9s880 spinacia ol
4	17	73.9	29	2	Q7RQ81	Q7rq81 plasmodium
5	17	73.9	32	2	O05602	O05602 pseudomonas
6	17	73.9	35	2	Q72FN9	Q72fn9 desulfovibr
7	17	73.9	36	2	Q9PV61	Q9pv61 mola mola (
8	17	73.9	38	1	PSA1 PROMA	O87786 prochloroco
9	17	73.9	38	2	Q7U4F1	Q7u4f1 synechococc
10	17	73.9	38	2	Q7V513	Q7v513 prochloroco
11	17	73.9	38	2	Q9PV63	Q9pv63 pseudopleur
12	17	73.9	40	2	Q9PT24	Q9pt24 oncorhynchu
13	17	73.9	40	2	Q9PT28	Q9ptz8 salarias sp
14	17	73.9	40	2	Q9PT29	Q9ptz9 epinephelus
15	17	73.9	40	2	Q9PU00	Q9pu00 dicentrarch
16	17	73.9	40	2	Q9PU01	Q9pu01 dendrochiru
17	17	73.9	40	2	Q9PU02	Q9pu02 zeus faber
18	17	73.9	40	2	Q9PU03	Q9pu03 sargocentro
19	17	73.9	40	2	Q9PU04	Q9pu04 fundulus he
20	17	73.9	40	2	Q9PU05	Q9pu05 hemiramphus
21	17	73.9	40	2	Q9PU06	Q9pu06 lampris sp.
22	17	73.9	40	2	Q9PV62	Q9pv62 ostracion s
23	17	73.9	40	2	Q9PV64	Q9pv64 channa sp.
24	17	73.9	40	2	Q9PV65	Q9pv65 colisa lali
25	17	73.9	40	2	Q9PV66	Q9pv66 stromateus
26	17	73.9	40	2	Q9PV68	Q9pv68 acanthurus
27	17	73.9	40	2	Q9PV69	Q9pv69 cryptocentr
28	17	73.9	40	2	Q9PV70	Q9pv70 dissostichu
29	17	73.9	40	2	Q9PV71	Q9pv71 mullus sp.
30	17	73.9	40	2	Q9PV72	Q9pv72 lates calca
31	17	73.9	40	2	Q9PV73	Q9pv73 mastacembel

32	17	73.9	40	2	Q9PV74	Q9pv74 hippocampus
33	17	73.9	40	2	Q9PV75	Q9pv75 poecilia la
34	17	73.9	40	2	Q9PV77	Q9pv77 mugil cepha
35	17	73.9	40	2	Q9PV78	Q9pv78 lophius sp.
36	17	73.9	40	2	Q9PV79	Q9pv79 galaxias ma
37	17	73.9	40	2	Q9PV80	Q9pv80 plecoglossu
38	17	73.9	40	2	Q9PV81	Q9pv81 esox lucius
39	17	73.9	40	2	Q9PV82	Q9pv82 barbus tetr
40	17	73.9	40	2	Q9PV84	Q9pv84 anguilla sp
41	17	73.9	40	2	Q9PV85	Q9pv85 osteoglossu
42	17	73.9	40	2	Q9PV88	Q9pv88 torpedo cal
43	17	73.9	40	2	Q9PV89	Q9pv89 triakis sp.
44	17	73.9	40	2	Q9PUU2	Q9puu2 polypterus
45	17	73.9	44	2	Q8XPJ4	Q8xpj4 ralstonia s
46	17	73.9	48	2	Q6H9V4	Q6h9v4 phage phi 4
47	17	73.9	49	2	Q8EF00	Q8ef00 shewanella
48	17	73.9	53	2	Q80077	Q80077 staphylococ
49	17	73.9	53	2	Q8SDM7	Q8sdm7 staphylococ
50	17	73.9	53	2	Q6R847	Q6r847 bacterioph
51	17	73.9	53	2	Q9B0G7	Q9b0g7 staphylococ
52	17	73.9	53	2	Q9G031	Q9g031 bacterioph
53	17	73.9	53	2	Q8NVM8	Q8nvm8 staphylococ
54	17	73.9	53	2	Q8NMG8	Q8nwg8 staphylococ
55	17	73.9	53	2	Q931J8	Q931j8 staphylococ
56	17	73.9	53	2	Q99SQ2	Q99sq2 staphylococ
57	17	73.9	53	2	Q6G7V0	Q6g7v0 staphylococ
58	17	73.9	53	2	Q6GAP3	Q6gap3 staphylococ
59	17	73.9	53	2	Q6GF65	Q6gf65 staphylococ
60	17	73.9	53	2	Q6GGM4	Q6ggm4 staphylococ
61	17	73.9	54	2	Q645F8	Q645f8 stereochilu
62	17	73.9	54	2	Q8VSJ2	Q8vsj2 shigella fl
63	17	73.9	54	2	Q6AQ08	Q6aq08 desulfotale
64	17	73.9	55	2	Q644C2	Q644c2 hydromantes
65	17	73.9	55	2	Q9MBS6	Q9mbs6 staphylococ
66	17	73.9	55	2	Q8FPA2	Q8fpa2 corynebacte
67	17	73.9	57	2	Q8WYF2	Q8wyf2 homo sapien
68	17	73.9	65	1	AKH MANSE	P67788 manduca sex
69	17	73.9	67	2	Q64109	Q64109 bacterioph
70	17	73.9	67	2	Q34509	Q34509 bacillus su
71	17	73.9	68	2	Q97736	Q97736 human immun
72	17	73.9	69	2	Q6YZN9	Q6yzn9 oryza sativ
73	17	73.9	69	2	Q84NAB	Q84nab arabidopsis
74	17	73.9	70	2	Q68I24	Q68i24 gasteroste
75	17	73.9	70	2	Q68I27	Q68i27 gasteroste
76	17	73.9	70	2	Q9MJL9	Q9mj19 scenedesmus
77	17	73.9	70	2	Q69587	Q69587 mycobacteri
78	17	73.9	72	2	Q88601	Q88601 tobacco mos
79	17	73.9	77	1	PUFQ RHOSH	P16069 rhodobacter
80	17	73.9	78	2	Q678B4	Q678b4 lymphocysti
81	17	73.9	79	2	Q82YT7	Q82yt7 enterococcu
82	17	73.9	81	2	Q984H4	Q984h4 rhizobium l
83	17	73.9	82	2	Q7EY23	Q7ey23 oryza sativ
84	17	73.9	84	1	Y149_ARCFU	Q30088 archaeoglob
85	17	73.9	84	2	Q60744	Q60744 homo sapien
86	17	73.9	85	2	Q42015	Q42015 arabidopsis
87	17	73.9	85	2	Q6ZLK9	Q6zlk9 oryza sativ
88	17	73.9	86	2	Q7PP04	Q7pp04 anopheles g
89	17	73.9	87	2	Q8U3P7	Q8u3p7 pyrococcus
90	17	73.9	87	2	Q6YVF4	Q6yvf4 oryza sativ
91	17	73.9	88	1	THI2 DICDI	P29446 dictyosteli
92	17	73.9	88	2	Q8PZQ6	Q8pzq6 methanosarc
93	17	73.9	89	2	Q6IG64	Q6ig64 drosophila
94	17	73.9	89	2	Q9B049	Q9b049 mycobacteri
95	17	73.9	89	2	Q7P017	Q7p017 chromobacte
96	17	73.9	92	2	Q9F1H3	Q9flh3 enterococcu
97	17	73.9	92	2	Q9LCU1	Q9lcul thermotoga
98	17	73.9	93	1	CD06_HUMAN	Q99440 homo sapien
99	17	73.9	93	2	Q8TL30	Q8tl30 methanosarc
100	17	73.9	95	2	Q7YX88	Q7yx88 caenorhabdi

ALIGNMENTS

```
RESULT 1
AKH_HELZE
ID AKH_HELZE STANDARD; PRT; 9 AA.
AC P67787; P08901;
DT 01-NOV-1988 (Rel. 09, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Adipokinetic hormone (Hez-AKH).
OS Heliothis zea (Corn earworm) (Bollworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Heliothinae; Helicoverpa.
OX NCBI_TaxID=7113;
RN [1]
RP SEQUENCE.
RX MEDLINE=86186794; PubMed=3964263;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Holman G.M.,
RA Wagner R.M., Ridgway R.L., Hayes D.K.;
RT "Isolation and primary structure of a peptide from the corpora
RT cardiaca of Heliothis zea with adipokinetic activity.";
RL Biochem. Biophys. Res. Commun. 135:622-628(1986).
CC -1- FUNCTION: This hormone, released from cells in the corpora
CC cardiaca after the beginning of flight, causes release of
CC diglycerides from the fat body and then stimulates the flight
CC muscles to use these diglycerides as an energy source.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.
DR PIR; A24244; A24244.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Amidation; Direct protein sequencing; Flight; Neuropeptide;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT MOD_RES 9 9 Glycine amide.
SQ SEQUENCE 9 AA; 1026 MW; 403665A5A1A9D1A7 CRC64;

Query Match 73.9%; Score 17; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
| |
Db 4 FTSSW 8

RESULT 2
Q9XLI2
ID Q9XLI2 PRELIMINARY; PRT; 13 AA.
AC Q9XLI2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome oxidase I (Fragment).
OS Bemisia tabaci (Sweetpotato whitefly).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aleyrodiformes;
OC Aleyrodidae; Aleyrodinae; Aleyrodinae; Bemisia.
OX NCBI_TaxID=7038;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=10583831;
RA Frohlich D.R., Torres-Jerez I., Bedford I.D., Markham P.G.,
RA Brown J.K.;
RT "A phylogeographical analysis of the Bemisia tabaci species complex
RT based on mitochondrial DNA markers.";
RL Mol. Ecol. 8:1683-1691(1999).
DR EMBL; AF110703; AAD28415.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1 1
SQ SEQUENCE 13 AA; 1639 MW; 8DD68729F5744365 CRC64;
```

```
Query Match 73.9%; Score 17; DB 2; Length 13;
Best Local Similarity 40.0%; Pred. No. 2.7e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
| |
Db 3 FTSSW 7

RESULT 3
Q9S880
ID Q9S880 PRELIMINARY; PRT; 26 AA.
AC Q9S880;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Thioredoxin H2 (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RX MEDLINE=91378382; PubMed=1897989;
RA Marcus F., Chamberlain S.H., Chu C., Masiarz F.R., Shin S., Yee B.C.,
RA Buchanan B.B.;
RT "Plant thioredoxin h: an animal-like thioredoxin occurring in multiple
RT cell compartments.";
RL Arch. Biochem. Biophys. 287:195-198(1991).
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; Thiored.
DR InterPro; IPR006663; Thioredoxin_dom2.
DR Pfam; PF00085; Thioredoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR PROSITE; PS00194; THIOREDOXIN; 1.
KW Redox-active center.
FT NON_TER 1 1
FT NON_TER 26 26
SQ SEQUENCE 26 AA; 2880 MW; A5317FC47DDB8863 CRC64;

Query Match 73.9%; Score 17; DB 2; Length 26;
Best Local Similarity 40.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5
| |
Db 6 FTASW 10

RESULT 4
Q7RQ81
ID Q7RQ81 PRELIMINARY; PRT; 29 AA.
AC Q7RQ81;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY01221;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
```

RA Florens L., Yates F.R. III, Raine J.D., Sindén R.E., Harris M.A.,  
Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,  
van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,  
Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,  
Carucci D.J.;  
RT "Genome sequence and comparative analysis of the model rodent malaria  
parasite Plasmodium yoelii yoelii";  
RL Nature 419:512-519(2002).  
CC -!- CAUTION: The sequence shown here is derived from an  
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
preliminary data.  
DR EMBL; AABL01000318; EAA20511.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 29 AA; 3408 MW; F36142D3148EE117 CRC64;  
  
Query Match 73.9%; Score 17; DB 2; Length 29;  
Best Local Similarity 40.0%; Pred. No. 5e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 FXXXW 5  
Db 11 FSASW 15  
  
RESULT 5  
O05602 PRELIMINARY; PRT; 32 AA.  
AC O05602;  
DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Transposon Tn5041 DNA (Fragment).  
OS Pseudomonas sp.  
OC Bacteria; Proteobacteria.  
OX NCBI\_TaxID=306;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=KHP41;  
RX MEDLINE=97419493; PubMed=9274008;  
RA Kholidii G.Y., Yurieva O.V., Gorlenko Z.M., Mindlin S.Z., Bass I.A.,  
RA Lomovskaya O.L., Kopteva A.V., Nikiforov V.G.;  
RT "Tn5041 : a chimeric mercury resistance transposon closely related to  
the toluene degradative transposon Tn4651.";  
RL Microbiology 143:2549-2556(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=KHP41;  
RX MEDLINE=22315381; PubMed=12427948;  
RA Kholidii G., Gorlenko Z., Mindlin S., Hobnan J., Nikiforov V.;  
RT "Tn5041-like transposons: molecular diversity, evolutionary  
relationships and distribution of distinct variants in environmental  
bacteria.";  
RL Microbiology 148:3569-3582(2002).  
DR EMBL; X98999; CAA67458.1; -.  
FT NON\_TER 1  
FT NON\_TER 32  
SQ SEQUENCE 32 AA; 3298 MW; AF42B5EEF917077A CRC64;  
  
Query Match 73.9%; Score 17; DB 2; Length 32;  
Best Local Similarity 40.0%; Pred. No. 5.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 FXXXW 5  
Db 11 FSASW 15

RESULT 6  
Q72FN9 PRELIMINARY; PRT; 35 AA.  
AC Q72FN9;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
GN OrderedLocNames=DVU0174;  
OS Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB  
8303).  
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;  
OC Desulfovibrionaceae; Desulfovibrio.  
OX NCBI\_TaxID=882;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=15077118; DOI=10.1038/nbt959;  
RA Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,  
RA Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,  
RA Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,  
RA Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,  
RA Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D.,  
RA Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,  
RA Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;  
RT "The genome sequence of the anaerobic, sulfate-reducing bacterium  
Desulfovibrio vulgaris Hildenborough.";  
RL Nat. Biotechnol. 22:554-559(2004).  
DR EMBL; AE017309; AAS94658.1; -.  
DR TIGR; DVU0174; -.  
KW Complete proteome.  
SQ SEQUENCE 35 AA; 3907 MW; CD423DA7D1422A7E CRC64;  
  
Query Match 73.9%; Score 17; DB 2; Length 35;  
Best Local Similarity 40.0%; Pred. No. 5.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 FXXXW 5  
Db 15 FATAW 19  
  
RESULT 7  
Q9PV61 PRELIMINARY; PRT; 36 AA.  
AC Q9PV61;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Dystrophin (Fragment).  
GN Name=Dyst;  
OS Mola mola (ocean sunfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Molidae; Mola.  
OX NCBI\_TaxID=94237;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93198697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate  
evolution.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF137130; AAD54215.1; -.  
DR HSSP; P11532; 1DXX.  
DR InterPro; IPR001715; Calponin-like.  
FT NON\_TER 1  
FT NON\_TER 36  
SQ SEQUENCE 36 AA; 4181 MW; DE01642A8CAAF18 CRC64;  
  
Query Match 73.9%; Score 17; DB 2; Length 36;  
Best Local Similarity 40.0%; Pred. No. 5.9e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5  
|  
Db 32 FSSW 36

## RESULT 8

PSAI\_PROMA STANDARD; PRT; 38 AA.

ID O87786;  
AC 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Photosystem I reaction center subunit VIII.  
GN Name=psaI; OrderedLocusNames=Pro1678;  
OS Prochlorococcus marinus.  
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;  
OC Prochlorococcus.  
OX NCBI\_TaxID=1219;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SARG / CCMP 1375 / SS120;  
RA van der Staay G.W.M., Moon-van der Staay S.Y., Garczarek L.,  
RA Partensky F.;  
RT "Characterization of the photosystem I subunits Psal and Psal from two  
RT strains of the marine oxyphototrophic";  
RL Photosyn. Res. 57:183-191(1998).  
RN [2]

RP SEQUENCE FROM N.A.  
RC STRAIN=SARG / CCMP 1375 / SS120;  
RX MEDLINE=22810154; PubMed=12917486; DOI=10.1073/pnas.1733211100;  
RA Dufresne A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M.,  
RA Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,  
RA Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B.,  
RA Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P.,  
RA Wolf Y.I., Hess W.R.;  
RT "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,  
RT a nearly minimal oxyphototrophic genome";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).  
CC -!- FUNCTION: May help in the organization of the psal subunit.  
CC -!- SIMILARITY: Belongs to the psaI family.

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-----  
DR EMBL; Z98594; CAB1178.1; ALT INIT.

DR EMBL; AE017166; AAQ00722.1; -.

DR HAMAP; MF 00431; atypical; 1.

DR InterPro; IPR001302; PSI\_8.

DR Pfam; PF00796; PSI\_8; 1.

KW Complete proteome; Photosynthesis; Photosystem I; Transmembrane.

FT TRANSMEM 12 32 Potential.

SQ SEQUENCE 38 AA; 4081 MW; 19DECDABA650A2F2 CRC64;

Query Match 73.9%; Score 17; DB 1; Length 38;  
Best Local Similarity 40.0%; Pred. No. 6.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5

|

Db 5 FAATW 9

## RESULT 9

Q7U4F1 PRELIMINARY; PRT; 38 AA.

ID Q7U4F1

AC Q7U4F1;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Photosystem I subunit VIII (Psal)  
GN Name=psaI; OrderedLocusNames=SYNW2117;  
OS Synechococcus sp. (strain WH8102).  
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.  
OX NCBI\_TaxID=84588;  
RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;

RA Palenik B., Brahmsha B., Larimer F.W., Land M.L., Hauser L.,

RA Chain P., Lamerdin J.E., Regala W., Allen E.E., McCarran J.,

RA Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.;

RT "The genome of a motile marine Synechococcus";

RL Nature 424:1037-1042(2003).

DR EMBL; BX569694; CAE08632.1; -.

KW Complete proteome.

SQ SEQUENCE 38 AA; 3975 MW; 75BEAB4500A52503 CRC64;

Query Match 73.9%; Score 17; DB 2; Length 38;  
Best Local Similarity 40.0%; Pred. No. 6.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5

|

Db 5 FAAA 9

## RESULT 10

Q7V513

ID Q7V513 PRELIMINARY; PRT; 38 AA.

AC Q7V513;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Photosystem I subunit VIII (Psal).

GN Name=psaI; OrderedLocusNames=PMT1767;

OS Prochlorococcus marinus (strain MIT 9313).

OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;

OC Prochlorococcus.

OX NCBI\_TaxID=74547;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;

RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,

RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,

RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,

RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,

RA Webb E.A., Zinser E.R., Chisholm S.W.;

RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic

RT niche differentiation";

RL Nature 424:1042-1047(2003).

DR EMBL; BX572100; CAE21942.1; -.

KW Complete proteome.

SQ SEQUENCE 38 AA; 4097 MW; 017DCC1CD4C3F4E2 CRC64;

Query Match 73.9%; Score 17; DB 2; Length 38;  
Best Local Similarity 40.0%; Pred. No. 6.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5

|

Db 5 FAATW 9

## RESULT 11

Q9PV63

ID Q9PV63 PRELIMINARY; PRT; 38 AA.

AC Q9PV63;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

```

DE Dystrophin (Fragment).
GN Name=Dyst;
OS Pseudopleuronectes americanus (Winter flounder) (Pleuronectes
OS americanus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidei; Pleuronectidae; Pseudopleuronectes.
OX NCBI_TaxID=8265;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137128; AAD54213.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
FT NON_TER 1
FT NON_TER 38
FT SEQUENCE 38 AA; 4424 MW; 41C67E01642A8CB0 CRC64;
SQ

Query Match 73.9%; Score 17; DB 2; Length 38;
Best Local Similarity 40.0%; Pred. No. 6.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 32 FSSSW 36

RESULT 12
Q9PT24 PRELIMINARY; PRT; 40 AA.
AC Q9PT24;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137093; AAD54187.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
FT SEQUENCE 40 AA; 4551 MW; B4865AA19BDB4B17 CRC64;
SQ

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 32 FSSSW 36

RESULT 13
Q9PT28 PRELIMINARY; PRT; 40 AA.
ID Q9PT28

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AC Q9PT28;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Salarias sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Blennioidei;
OC Blenniidae; Salarias.
OX NCBI_TaxID=94312;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137121; AAD54206.1; -.
DR EMBL; AF137120; AAD54206.1; JOINED.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
FT SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;
SQ

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 32 FSSSW 36

RESULT 14
Q9PT29 PRELIMINARY; PRT; 40 AA.
ID Q9PT29
AC Q9PT29;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Epinephelus coioides (Orange-spotted grouper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
OC Serranidae; Epinephelinae; Epinephelus.
OX NCBI_TaxID=94232;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137117; AAD54203.1; -.
DR EMBL; AF137116; AAD54203.1; JOINED.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
FT SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;
SQ

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 32 FSSSW 36

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Db 32 FSSW 36

RESULT 15

Q9PU00

ID Q9PU00 PRELIMINARY; PRT; 40 AA.

AC Q9PU00;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Dystrophin (Fragment).

GN Name=Dyst;

OS Dicertrarchus labrax (European sea bass).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;

OC Moronidae; Dicertrarchus.

OX NCBI\_TaxID=13489;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;

RA Venkatesh B., Ning Y., Brenner S.;

RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";

RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).

DR EMBL; AF137115; AAD54202.1; -.

DR EMBL; AF137114; AAD54202.1; JOINED.

DR HSSP; P11532; 1DXX.

DR InterPro; IPR001715; Calponin-like.

DR Pfam; PF00307; CH; 1.

FT NON\_TER 1 1

FT NON\_TER 40 40

SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;

Best Local Similarity 40.0%; Pred. No. 6.4e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5

Db 32 FSSW 36

RESULT 16

Q9PU01

ID Q9PU01 PRELIMINARY; PRT; 40 AA.

AC Q9PU01;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Dystrophin (Fragment).

GN Name=Dyst;

OS Dendrochirus zebra (Zebra turkeyfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;

OC Scorpaenidae; Scorpaenidae; Pteroinae; Dendrochirus.

OX NCBI\_TaxID=94308;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;

RA Venkatesh B., Ning Y., Brenner S.;

RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";

RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).

DR EMBL; AF137112; AAD54200.1; -.

DR EMBL; AF137111; AAD54200.1; JOINED.

DR HSSP; P11532; 1DXX.

DR InterPro; IPR001715; Calponin-like.

DR Pfam; PF00307; CH; 1.

FT NON\_TER 1 1

FT NON\_TER 40 40

SQ SEQUENCE 40 AA; 4638 MW; B49D49A67E0167E5 CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;

Best Local Similarity 40.0%; Pred. No. 6.4e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5

Db 32 FSSW 36

RESULT 17

Q9PU02

ID Q9PU02 PRELIMINARY; PRT; 40 AA.

AC Q9PU02;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Dystrophin (Fragment).

GN Name=Dyst;

OS Zeus faber (John Dory).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Zeiformes; Zeidae; Zeus.

OX NCBI\_TaxID=64108;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;

RA Venkatesh B., Ning Y., Brenner S.;

RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";

RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).

DR EMBL; AF137108; AAD55460.1; -.

DR EMBL; AF137107; AAD55460.1; JOINED.

DR HSSP; P11532; 1DXX.

DR InterPro; IPR001715; Calponin-like.

DR Pfam; PF00307; CH; 1.

FT NON\_TER 1 1

FT NON\_TER 40 40

SQ SEQUENCE 40 AA; 4645 MW; BA7D49A676A3642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;

Best Local Similarity 40.0%; Pred. No. 6.4e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5

Db 32 FSSW 36

RESULT 18

Q9PU03

ID Q9PU03 PRELIMINARY; PRT; 40 AA.

AC Q9PU03;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Dystrophin (Fragment).

GN Name=Dyst;

OS Sargocentron sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Beryciformes; Holocentridae;

OC Sargocentron.

OX NCBI\_TaxID=94226;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;

RA Venkatesh B., Ning Y., Brenner S.;

RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";

RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).

DR EMBL; AF137106; AAD54196.1; -.



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DR EMBL; AF137105; AAD54196.1; JOINED.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4579 MW; B49C92D67E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 32 FSSW 36

RESULT 19
Q9PU04
ID Q9PU04 PRELIMINARY; PRT; 40 AA.
AC Q9PU04;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Fundulus heteroclitus (Killifish) (Mummichog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Fundulidae; Fundulus.
OX NCBI_TaxID=8078;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137103; AAD54194.1; -.
DR EMBL; AF137102; AAD54194.1; JOINED.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 32 FSSW 36

RESULT 20
Q9PU05
ID Q9PU05 PRELIMINARY; PRT; 40 AA.
AC Q9PU05;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Hemiramphus sp.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Hemiramphidae; Hemiramphus.
OX NCBI_TaxID=94223;
RN [1]
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RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137101; AAD54193.1; -.
DR EMBL; AF137100; AAD54193.1; JOINED.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 32 FSSW 36

RESULT 21
Q9PU06
ID Q9PU06 PRELIMINARY; PRT; 40 AA.
AC Q9PU06;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Lampris sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Lampridiformes; Lampridae; Lampris.
OX NCBI_TaxID=94303;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137096; AAD54189.1; -.
DR EMBL; AF137095; AAD54189.1; JOINED.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 32 FSSW 36

RESULT 22
Q9PV62
ID Q9PV62 PRELIMINARY; PRT; 40 AA.
AC Q9PV62;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Ostracion sp. IMCB-2002.
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Ostraciidae; Ostracion; unclassified Ostracion.  
OX NCBI\_TaxID=188530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate  
RT evolution.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF137129; AAD54214.1; -.  
DR HSSP; P11532; 1DXX.  
DR InterPro; IPR001715; Calponin-like.  
DR Pfam; PF00307; CH; 1.  
FT NON\_TER 1 1  
FT NON\_TER 40 40  
SQ SEQUENCE 40 AA; 4582 MW; B49D4BCBEE01642A CRC64;  
  
Query Match 73.9%; Score 17; DB 2; Length 40;  
Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 FXXW 5  
Db 32 FSSW 36  
  
RESULT 23  
Q9PV64  
ID Q9PV64 PRELIMINARY; PRT; 40 AA.  
AC Q9PV64;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 21, Last annotation update)  
DE Dystrophin (Fragment).  
GN Names=Dyst;  
OS Channa sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Channoidae;  
OC Channidae; Channa.  
OX NCBI\_TaxID=94222;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate  
RT evolution.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF137127; AAD54212.1; -.  
DR HSSP; P11532; 1DXX.  
DR InterPro; IPR001715; Calponin-like.  
DR Pfam; PF00307; CH; 1.  
FT NON\_TER 1 1  
FT NON\_TER 40 40  
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;  
  
Query Match 73.9%; Score 17; DB 2; Length 40;  
Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 FXXW 5  
Db 32 FSSW 36  
  
RESULT 24  
Q9PV65  
ID Q9PV65 PRELIMINARY; PRT; 40 AA.  
AC Q9PV65;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 21, Last annotation update)  
DE Dystrophin (Fragment).  
GN Name=Dyst;  
OS Colisa lalia (dwarf gourami).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;  
OC Anabantoidei; Belontiidae; Colisa.  
OX NCBI\_TaxID=50373;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate  
RT evolution.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF137126; AAD54211.1; -.  
DR HSSP; P11532; 1DXX.  
DR InterPro; IPR001715; Calponin-like.  
DR Pfam; PF00307; CH; 1.  
FT NON\_TER 1 1  
FT NON\_TER 40 40  
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;  
  
Query Match 73.9%; Score 17; DB 2; Length 40;  
Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 FXXW 5  
Db 32 FSSW 36  
  
RESULT 25  
Q9PV66  
ID Q9PV66 PRELIMINARY; PRT; 40 AA.  
AC Q9PV66;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 21, Last annotation update)  
DE Dystrophin (Fragment).  
GN Name=Dyst;  
OS Stromateus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;  
OC Stromateoidei; Stromateidae; Stromateus.  
OX NCBI\_TaxID=94245;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate  
RT evolution.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF137125; AAD54210.1; -.  
DR HSSP; P11532; 1DXX.  
DR InterPro; IPR001715; Calponin-like.  
DR Pfam; PF00307; CH; 1.  
FT NON\_TER 1 1  
FT NON\_TER 40 40  
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;  
  
Query Match 73.9%; Score 17; DB 2; Length 40;  
Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 FXXW 5  
Db 32 FSSW 36

## RESULT 26

Q9PV68 ID Q9PV68 PRELIMINARY; PRT; 40 AA.  
 AC Q9PV68;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Dystrophin (Fragment).  
 GN Name=Dyst;  
 OS Acanthurus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;  
 OC Acanthuroidei; Acanthuridae; Acanthurus.  
 OX NCBI\_TaxID=94220;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
 RA Venkatesh B., Ning Y., Brenner S.;  
 RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
 DR EMBL; AF137123; AAD54208.1; -.  
 DR HSSP; P11532; 1DXX.  
 DR InterPro; IPR001715; Calponin-like.  
 DR Pfam; PF00307; CH; 1.  
 FT NON\_TER 1  
 FT NON\_TER 40  
 SQ SEQUENCE 40 AA; 4592 MW; B48FFE566BDB542A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;  
 Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
 Db 32 FSSSW 36

## RESULT 27

Q9PV69 ID Q9PV69 PRELIMINARY; PRT; 40 AA.  
 AC Q9PV69;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Dystrophin (Fragment).  
 GN Name=Dyst;  
 OS Cryptocentrus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Gobioidi;  
 OC Gobiidae; Cryptocentrus.  
 OX NCBI\_TaxID=94314;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
 RA Venkatesh B., Ning Y., Brenner S.;  
 RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
 DR EMBL; AF137122; AAD54207.1; -.  
 DR HSSP; P11532; 1DXX.  
 DR InterPro; IPR001715; Calponin-like.  
 DR Pfam; PF00307; CH; 1.  
 DR PROSITE; PS0021; CH; 1.  
 FT NON\_TER 1  
 FT NON\_TER 40  
 SQ SEQUENCE 40 AA; 4611 MW; B49D49A67E01756E CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;  
 Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
 Db 32 FSSSW 36

## RESULT 28

Q9PV70 ID Q9PV70 PRELIMINARY; PRT; 40 AA.  
 AC Q9PV70;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Dystrophin (Fragment).  
 GN Name=Dyst;  
 OS Dissostichus mawsoni (Antarctic cod).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;  
 OC Notothenioidi; Nototheniidae; Dissostichus.  
 OX NCBI\_TaxID=36200;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
 RA Venkatesh B., Ning Y., Brenner S.;  
 RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
 DR EMBL; AF137119; AAD54205.1; -.  
 DR HSSP; P11532; 1DXX.  
 DR InterPro; IPR001715; Calponin-like.  
 DR Pfam; PF00307; CH; 1.  
 FT NON\_TER 1  
 FT NON\_TER 40  
 SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;  
 Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
 Db 32 FSSSW 36

## RESULT 29

Q9PV71 ID Q9PV71 PRELIMINARY; PRT; 40 AA.  
 AC Q9PV71;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Dystrophin (Fragment).  
 GN Name=Dyst;  
 OS Mullus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidi;  
 OC Mullidae; Mullus.  
 OX NCBI\_TaxID=94224;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
 RA Venkatesh B., Ning Y., Brenner S.;  
 RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
 DR EMBL; AF137118; AAD54204.1; -.  
 DR HSSP; P11532; 1DXX.  
 DR InterPro; IPR001715; Calponin-like.  
 DR Pfam; PF00307; CH; 1.  
 FT NON\_TER 1  
 FT NON\_TER 40

```
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;
Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 32 FSSW 36

RESULT 30
Q9PV72 PRELIMINARY; PRT; 40 AA.
AC Q9PV72;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Lates calcarifer (Barramundi).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Centropomidae; Lates.
OX NCBI_TaxID=8187;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137113; AAD54201.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 32 FSSW 36

RESULT 31
Q9PV73 PRELIMINARY; PRT; 40 AA.
AC Q9PV73;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Mastacembelus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Synbranchiiformes;
OC Mastacembelidae; Mastacembelus.
OX NCBI_TaxID=94235;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137110; AAD54199.1; -.
DR
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DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 32 FSSW 36

RESULT 32
Q9PV74 PRELIMINARY; PRT; 40 AA.
AC Q9PV74;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Hippocampus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
OC Syngnathidae; Hippocampus.
OX NCBI_TaxID=72047;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137109; AAD54198.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
DR PROSITE; PS50021; CH; 1.
FT NON_TER 1 1
FT NON_TER 40 40
SQ SEQUENCE 40 AA; 4541 MW; B49D487D0E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 32 FSSW 36

RESULT 33
Q9PV75 PRELIMINARY; PRT; 40 AA.
AC Q9PV75;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Poecilia latipinna.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Poeciliidae; Poecilia.
OX NCBI_TaxID=48699;
RN [1]
RP SEQUENCE FROM N.A.
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RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137104; AAD54195.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
DR NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 32 FSSSW 36

RESULT 34
Q9PV77 PRELIMINARY; PRT; 40 AA.
AC Q9PV77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Mugil cephalus (Flathead mullet) (Mugil japonicus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Mugilomorpha; Mugilidae;
OC Mugil.
OX NCBI_TaxID=48193;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137098; AAD54191.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
DR NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 32 FSSSW 36

RESULT 35
Q9PV78 PRELIMINARY; PRT; 40 AA.
AC Q9PV78;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Lophius sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
```

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OC Acanthomorpha; Paracanthopterygii; Lophiiformes; Lophiidae; Lophius.
OX NCBI_TaxID=30791;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137097; AAD54190.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
DR NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4610 MW; B49D49A67E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 32 FSSSW 36

RESULT 36
Q9PV79 PRELIMINARY; PRT; 40 AA.
AC Q9PV79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
OS Galaxias maculatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Galaxiidae; Galaxias.
OX NCBI_TaxID=61620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137094; AAD54188.1; -.
DR HSSP; P11532; 1DXX.
DR InterPro; IPR001715; Calponin-like.
DR Pfam; PF00307; CH; 1.
DR NON_TER 1
FT NON_TER 40
SQ SEQUENCE 40 AA; 4613 MW; BA7C92D67E01642A CRC64;

Query Match 73.9%; Score 17; DB 2; Length 40;
Best Local Similarity 40.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 32 FSSSW 36

RESULT 37
Q9PV80 PRELIMINARY; PRT; 40 AA.
AC Q9PV80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Dystrophin (Fragment).
GN Name=Dyst;
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OS Placoglossus altivelis.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Osmeridae; Plecoglossus.  
OX NCBI\_TaxID=61084;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF137092; AAD54186.1; -.  
DR HSSP; P11532; IDXX.  
DR InterPro; IPR001715; Calponin-like.  
DR Pfam; PF00307; CH; 1.  
FT NON\_TER 1 1  
FT NON\_TER 40 40  
SQ SEQUENCE 40 AA; 4512 MW; B4931BF59BDB542A CRC64;  
  
Query Match 73.9%; Score 17; DB 2; Length 40;  
Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 FXXXW 5  
Db 32 FSSSW 36  
  
RESULT 38  
Q9PV81 ID Q9PV81 PRELIMINARY; PRT; 40 AA.  
AC Q9PV81;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Dystrophin (Fragment).  
GN Name=Dyst;  
OS Esoc lucius (Northern pike).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Esociformes;  
OC Esocidae; Esoc.  
OX NCBI\_TaxID=8010;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF137091; AAD54185.1; -.  
DR HSSP; P11532; IDXX.  
DR InterPro; IPR001715; Calponin-like.  
DR Pfam; PF00307; CH; 1.  
FT NON\_TER 1 1  
FT NON\_TER 40 40  
SQ SEQUENCE 40 AA; 4542 MW; 09165AA193794B14 CRC64;  
  
Query Match 73.9%; Score 17; DB 2; Length 40;  
Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 FXXXW 5  
Db 32 FSSSW 36  
  
RESULT 39  
Q9PV82 ID Q9PV82 PRELIMINARY; PRT; 40 AA.  
AC Q9PV82;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Dystrophin (Fragment).  
GN Name=Dyst;  
OS Barbus tetrazona.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Barbus.  
OX NCBI\_TaxID=94221;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF137090; AAD54184.1; -.  
DR HSSP; P11532; IDXX.  
DR InterPro; IPR001715; Calponin-like.  
DR Pfam; PF00307; CH; 1.  
FT NON\_TER 1 1  
FT NON\_TER 40 40  
SQ SEQUENCE 40 AA; 4573 MW; 459B37C19BC3E736 CRC64;  
  
Query Match 73.9%; Score 17; DB 2; Length 40;  
Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 FXXXW 5  
Db 32 FSSSW 36  
  
RESULT 40  
Q9PV84 ID Q9PV84 PRELIMINARY; PRT; 40 AA.  
AC Q9PV84;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Dystrophin (Fragment).  
GN Name=Dyst;  
OS Anguilla sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;  
OC Anguilla.  
OX NCBI\_TaxID=62126;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99398697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;  
RA Venkatesh B., Ning Y., Brenner S.;  
RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).  
DR EMBL; AF137088; AAD54182.1; -.  
DR HSSP; P11532; IDXX.  
DR InterPro; IPR001715; Calponin-like.  
DR Pfam; PF00307; CH; 1.  
DR PROSITE; PS50021; CH; 1.  
FT NON\_TER 1 1  
FT NON\_TER 40 40  
SQ SEQUENCE 40 AA; 4574 MW; 557846E66BDB5437 CRC64;  
  
Query Match 73.9%; Score 17; DB 2; Length 40;  
Best Local Similarity 40.0%; Pred. No. 6.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 FXXXW 5  
Db 32 FSSSW 36  
  
Search completed: October 18, 2005, 15:30:09  
Job time : 113.647 secs



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:31:13 ; Search time 109.176 Seconds  
(without alignments)  
28.340 Million cell updates/sec

Title: US-09-214-371-10  
Perfect score: 23  
Sequence: 1 FXXXWXXX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 716780

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : A Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	73.9	9	7	ADC07129 Honeybee
2	17	73.9	9	7	ADC07134 Painted 1
3	17	73.9	10	3	AAB10010
4	17	73.9	10	4	AAB86090 H. pylori
5	17	73.9	10	4	AAB86058 H. pylori
6	17	73.9	11	7	ADC07163 Painted 1
7	17	73.9	13	4	AAE05735
8	17	73.9	13	6	ABG75574 CDR3 pept
9	17	73.9	14	4	AAM98088 Human pep
10	17	73.9	15	2	AAR97874 Japan ced
11	17	73.9	15	2	AAR97875 Japan ced
12	17	73.9	15	2	AAW57758 Residues
13	17	73.9	19	5	AAE23038 Human thi
14	17	73.9	20	2	AAW42165 T-cell ep
15	17	73.9	20	4	AAG62999 Complemen
16	16	69.6	5	8	ADR68284 Androgen
17	16	69.6	6	2	AAW76953 Fusion im
18	16	69.6	6	6	ABR46309 Staphyloc
19	16	69.6	6	6	ABR46270 Staphyloc
20	16	69.6	6	6	ABR46702 Staphyloc
21	16	69.6	6	6	ABR47093 Staphyloc
22	16	69.6	6	6	ABR45149 Staphyloc
23	16	69.6	6	6	ABR45486 Staphyloc
24	16	69.6	6	6	ABR45878 Staphyloc
25	16	69.6	6	6	ABR46661 Staphyloc

26	16	69.6	6	6	ABR47053	Abr47053 Staphyloc
27	16	69.6	6	6	ABR45190	Abr45190 Staphyloc
28	16	69.6	6	6	ABR45877	Abr45877 Staphyloc
29	16	69.6	6	6	ABR46310	Abr46310 Staphyloc
30	16	69.6	6	6	ABR47094	Abr47094 Staphyloc
31	16	69.6	6	6	ABR46701	Abr46701 Staphyloc
32	16	69.6	6	6	ABR47054	Abr47054 Staphyloc
33	16	69.6	6	6	ABR45525	Abr45525 Staphyloc
34	16	69.6	6	6	ABR45918	Abr45918 Staphyloc
35	16	69.6	6	6	ABR45189	Abr45189 Staphyloc
36	16	69.6	6	6	ABR45485	Abr45485 Staphyloc
37	16	69.6	6	6	ABR45150	Abr45150 Staphyloc
38	16	69.6	6	6	ABR45526	Abr45526 Staphyloc
39	16	69.6	6	6	ABR46269	Abr46269 Staphyloc
40	16	69.6	6	6	ABR46662	Abr46662 Staphyloc
41	16	69.6	6	6	ABR45917	Abr45917 Staphyloc
42	16	69.6	6	7	ADL17086	Adl17086 Phage-dis
43	16	69.6	7	5	ABP53945	Abp53945 VEGFR-3 b
44	16	69.6	7	7	ADB47984	Adb47984 Novel hum
45	16	69.6	7	8	ADJ55539	Adj55539 Novel hum
46	16	69.6	8	2	AAV18082	Aay18082 Histamine
47	16	69.6	8	6	ABR53957	Abr53957 Beta-secr
48	16	69.6	8	6	ABR54100	Abr54100 Beta-secr
49	16	69.6	8	6	ABR54133	Abr54133 Beta-secr
50	16	69.6	8	6	ABR54102	Abr54102 Beta-secr
51	16	69.6	8	6	ABR54137	Abr54137 Beta-secr
52	16	69.6	8	6	ABR54108	Abr54108 Beta-secr
53	16	69.6	8	6	ABR54106	Abr54106 Beta-secr
54	16	69.6	8	6	ABR54135	Abr54135 Beta-secr
55	16	69.6	8	6	ABR53955	Abr53955 Beta-secr
56	16	69.6	8	6	ABR54129	Abr54129 Beta-secr
57	16	69.6	8	6	ABR54139	Abr54139 Beta-secr
58	16	69.6	8	6	ABR54104	Abr54104 Beta-secr
59	16	69.6	8	6	ABR54131	Abr54131 Beta-secr
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63	16	69.6	8	7	ADC07151	Adc07151 Libanasiid
64	16	69.6	8	7	ADC07141	Adc07141 Phymateus
65	16	69.6	8	7	ADC07150	Adc07150 Cricket A
66	16	69.6	8	7	ADC07130	Adc07130 Desert lo
67	16	69.6	8	7	ADC07137	Adc07137 Migratory
68	16	69.6	8	7	ADC07156	Adc07156 Onitis AK
69	16	69.6	8	8	ADR69591	Adr69591 Novel hyb
70	16	69.6	8	8	ADL27410	Adl27410 Amino aci
71	16	69.6	9	2	AAV48085	Aay48085 Immunogen
72	16	69.6	9	4	AAE01057	Aae01057 Human sec
73	16	69.6	9	5	ABP53956	Abp53956 VEGFR-3 b
74	16	69.6	9	5	ABP47522	Abp47522 N. mening
75	16	69.6	9	5	ABG97262	Abg97262 Human leu
76	16	69.6	9	5	AAE31347	Aae31347 Human tyr
77	16	69.6	9	8	ADH41183	Adh41183 Human rar
78	16	69.6	9	8	ADH41163	Adh41163 Human rar
79	16	69.6	9	8	ADK09130	Adk09130 Human pap
80	16	69.6	9	8	ADK09595	Adk09595 Human pap
81	16	69.6	9	8	ADN65877	Adn65877 HLA bindi
82	16	69.6	9	8	ADQ71598	Adq71598 Cancer re
83	16	69.6	9	8	ADQ72073	Adq72073 Cancer re
84	16	69.6	9	8	ADQ68606	Adq68606 Cancer re
85	16	69.6	9	8	ADQ72380	Adq72380 Cancer re
86	16	69.6	9	8	ADQ69652	Adq69652 Cancer re
87	16	69.6	9	8	ADQ72453	Adq72453 Cancer re
88	16	69.6	9	8	ADQ69664	Adq69664 Cancer re
89	16	69.6	9	8	ADQ71463	Adq71463 Cancer re
90	16	69.6	9	8	ADQ72148	Adq72148 Cancer re
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96	16	69.6	9	8	ADQ68180	Adq68180 Cancer re
97	16	69.6	9	8	ADQ70322	Adq70322 Cancer re
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99 16 69.6 9 ADP26276 Plasmodiu  
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103 16 69.6 10 AAB26393 Human CAS  
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150 16 69.6 11 ABP47662 N. mening  
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153 16 69.6 11 ADG15913 Synthetic  
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Aab13300 Caenorhab  
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Aam47919 Human cla  
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Aao20896 N-termina  
Aam47805 Miniature  
Abb77835 Peptide u  
Abr44352 N-termina  
Abp58627 Human end  
Adf12276 Drosophil  
Adq74628 Cancer re  
Adq74366 Cancer re  
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Adq74000 Cancer re  
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246	16	69.6	18	8	ADL78476	Adl78476 Albumin f	319	15	65.2	6	6	ABR46659	Abr46659 Staphyloc
247	16	69.6	19	3	AAB52193	Aab52193 Human ant	320	15	65.2	6	6	ABR46719	Abr46719 Staphyloc
248	16	69.6	19	4	AAM21012	Aam21012 Peptide #	321	15	65.2	6	6	ABR46759	Abr46759 Staphyloc
249	16	69.6	19	4	ABB43110	Abb43110 Peptide #	322	15	65.2	6	6	ABR45182	Abr45182 Staphyloc
250	16	69.6	19	4	AAM36940	Aam36940 Peptide #	323	15	65.2	6	6	ABR45517	Abr45517 Staphyloc
251	16	69.6	19	4	ABB26248	Abb26248 Protein #	324	15	65.2	6	6	ABR45518	Abr45518 Staphyloc
252	16	69.6	19	4	AAM76834	Aam76834 Human bon	325	15	65.2	6	6	ABR46301	Abr46301 Staphyloc
253	16	69.6	19	4	AAM64011	Aam64011 Human bra	326	15	65.2	6	6	ABR46379	Abr46379 Staphyloc
254	16	69.6	19	4	ABG58507	Abg58507 Human liv	327	15	65.2	6	6	ABR46439	Abr46439 Staphyloc
255	16	69.6	19	5	ABG45977	Abg45977 Human pep	328	15	65.2	6	6	ABR46475	Abr46475 Staphyloc
256	16	69.6	19	8	ADR68329	Adr68329 Androgen	329	15	65.2	6	6	ABR46495	Abr46495 Staphyloc
257	16	69.6	20	2	AAR63841	Aar63841 HIV-1 gp1	330	15	65.2	6	6	ABR46531	Abr46531 Staphyloc
258	16	69.6	20	2	AAW08045	Aaw08045 HIV pepti	331	15	65.2	6	6	ABR46694	Abr46694 Staphyloc
259	16	69.6	20	2	AAW08044	Aaw08044 HIV pepti	332	15	65.2	6	6	ABR45501	Abr45501 Staphyloc
260	16	69.6	20	2	AAR88352	Aar88352 Adenomato	333	15	65.2	6	6	ABR45510	Abr45510 Staphyloc
261	16	69.6	20	2	AAY02155	Aay02155 Peptide u	334	15	65.2	6	6	ABR45901	Abr45901 Staphyloc
262	16	69.6	20	3	AAY70799	Aay70799 Murine an	335	15	65.2	6	6	ABR45915	Abr45915 Staphyloc
263	16	69.6	20	3	AAB10376	Aab10376 HBV core	336	15	65.2	6	6	ABR46268	Abr46268 Staphyloc
264	16	69.6	20	4	ABB50791	Abb50791 Human sec	337	15	65.2	6	6	ABR45894	Abr45894 Staphyloc
265	16	69.6	20	5	AAE20323	Aae20323 Human B7-	338	15	65.2	6	6	ABR46308	Abr46308 Staphyloc
266	16	69.6	20	5	ABP30920	Abp30920 OE8 antib	339	15	65.2	6	6	ABR46435	Abr46435 Staphyloc
267	16	69.6	20	5	ABP30919	Abp30919 OE8 antib	340	15	65.2	6	6	ABR46535	Abr46535 Staphyloc
268	16	69.6	20	6	ABO45048	Abp45048 Novel hum	341	15	65.2	6	6	ABR46678	Abr46678 Staphyloc
269	16	69.6	20	7	ABO26528	Abp26528 Protein a	342	15	65.2	6	6	ABR45166	Abr45166 Staphyloc
270	16	69.6	20	7	ADA08565	Ada08565 Human OE8	343	15	65.2	6	6	ABR45181	Abr45181 Staphyloc
271	16	69.6	20	7	ADA08564	Ada08564 Human OE8	344	15	65.2	6	6	ABR46293	Abr46293 Staphyloc
272	16	69.6	20	7	ADC99562	Adc99562 Cancer-re	345	15	65.2	6	6	ABR46647	Abr46647 Staphyloc
273	16	69.6	20	7	ABW01365	Abw01365 Human HEA	346	15	65.2	6	6	ABR46693	Abr46693 Staphyloc
274	16	69.6	20	7	ADF08907	Adf08907 Secreted	347	15	65.2	6	6	ABR46699	Abr46699 Staphyloc
275	16	69.6	20	7	ADF08908	Adf08908 Secreted	348	15	65.2	6	6	ABR47077	Abr47077 Staphyloc
276	16	69.6	20	7	ADF09113	Adf09113 Secreted	349	15	65.2	6	6	ABR47092	Abr47092 Staphyloc
277	16	69.6	20	7	ADF09114	Adf09114 Secreted	350	15	65.2	6	6	ABR45147	Abr45147 Staphyloc
278	16	69.6	20	7	ADG46195	Adg46195 OE8 antib	351	15	65.2	6	6	ABR45187	Abr45187 Staphyloc
279	16	69.6	20	7	ADG46194	Adg46194 OE8 antib	352	15	65.2	6	6	ABR45484	Abr45484 Staphyloc
280	16	69.6	20	8	ADR05597	Adr05597 Novel ssd	353	15	65.2	6	6	ABR45509	Abr45509 Staphyloc
281	15	65.2	5	2	AAW17807	Aaw17807 Cyclic pe	354	15	65.2	6	6	ABR46267	Abr46267 Staphyloc
282	15	65.2	5	2	AAW17812	Aaw17812 Cyclic pe	355	15	65.2	6	6	ABR45909	Abr45909 Staphyloc
283	15	65.2	5	2	AAW17806	Aaw17806 Cyclic pe	356	15	65.2	6	6	ABR46383	Abr46383 Staphyloc
284	15	65.2	5	2	AAY33038	Aay33038 Carbohydr	357	15	65.2	6	6	ABR46715	Abr46715 Staphyloc
285	15	65.2	5	3	AAB07280	Aab07280 Motif bin	358	15	65.2	6	6	ABR46755	Abr46755 Staphyloc
286	15	65.2	5	5	ABP67371	Abp67371 Human CD6	359	15	65.2	6	6	ABR47070	Abr47070 Staphyloc
287	15	65.2	5	6	ABU87123	Abu87123 Carbohydr	360	15	65.2	6	6	ABR47085	Abr47085 Staphyloc
288	15	65.2	5	8	ADR68292	Adr68292 Androgen	361	15	65.2	6	6	ABR45502	Abr45502 Staphyloc
289	15	65.2	5	8	ADR68294	Adr68294 Androgen	362	15	65.2	6	6	ABR45876	Abr45876 Staphyloc
290	15	65.2	6	1	AAP50709	Aap50709 Hexapepti	363	15	65.2	6	6	ABR46294	Abr46294 Staphyloc
291	15	65.2	6	2	AAR54182	Aar54182 CHA255 li	364	15	65.2	6	6	ABR46419	Abr46419 Staphyloc
292	15	65.2	6	2	AAR89913	Aar89913 p53/MDM2	365	15	65.2	6	6	ABR46660	Abr46660 Staphyloc
293	15	65.2	6	2	AAR89915	Aar89915 p53 minim	366	15	65.2	6	6	ABR47052	Abr47052 Staphyloc
294	15	65.2	6	2	AAW13606	Aaw13606 p53 prote	367	15	65.2	6	6	ABR47078	Abr47078 Staphyloc
295	15	65.2	6	2	AAW04677	Aay04677 Peptide #	368	15	65.2	6	6	ABR45165	Abr45165 Staphyloc
296	15	65.2	6	3	AAH17074	Aab17074 Mdm/hdm a	369	15	65.2	6	6	ABR45483	Abr45483 Staphyloc
297	15	65.2	6	5	ABB73169	Abb73169 Mdm/hdm a	370	15	65.2	6	6	ABR45524	Abr45524 Staphyloc
298	15	65.2	6	5	ABP67361	Abp67361 Human CD6	371	15	65.2	6	6	ABR45910	Abr45910 Staphyloc
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306	15	65.2	6	6	ABR46491	Abr46491 Staphyloc	379	15	65.2	6	6	ABG73432	Abg73432 Human p53
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308	15	65.2	6	6	ABR46700	Abr46700 Staphyloc	381	15	65.2	6	7	ABR82526	AbR82526 Human apy
309	15	65.2	6	6	ABR45188	Abr45188 Staphyloc	382	15	65.2	6	7	ADJ73323	Adj73323 Mdm/hdm a
310	15	65.2	6	6	ABR45173	Abr45173 Staphyloc	383	15	65.2	6	8	ADJ52957	Adj52957 CH1 delet
311	15	65.2	6	6	ABR45523	Abr45523 Staphyloc	384	15	65.2	6	8	ADJ51918	Adj51918 CH1 delet
312	15	65.2	6	6	ABR45875	Abr45875 Staphyloc	385	15	65.2	7	1	AAP93327	Aap93327 Sequence
313	15	65.2	6	6	ABR45902	Abr45902 Staphyloc	386	15	65.2	7	2	AAR32880	Aar32880 Tryptic p
314	15	65.2	6	6	ABR46286	Abr46286 Staphyloc	387	15	65.2	7	2	AAR89921	Aar89921 Antibody
315	15	65.2	6	6	ABR46307	Abr46307 Staphyloc	388	15	65.2	7	2	AAR89925	Aar89925 p53 bindi
316	15	65.2	6	6	ABR47086	Abr47086 Staphyloc	389	15	65.2	7	2	AAY34151	Aay34151 Angiopoie
317	15	65.2	6	6	ABR45174	Abr45174 Staphyloc	390	15	65.2	7	2	AAW94141	Aaw94141 FG loop s

391	15	65.2	7	3	AAy82380	Aay82380 Heptaepet	464	15	65.2	8	6	ABR54070	Abr54070 Beta-secr
392	15	65.2	7	3	AAy57789	Aay57789 TRAM-inte	465	15	65.2	8	6	ABR54078	Abr54078 Beta-secr
393	15	65.2	7	3	AAB23205	Aab23205 Hsp47-bin	466	15	65.2	8	6	ABR54080	Abr54080 Beta-secr
394	15	65.2	7	3	AAB01512	Aab01512 Peptide w	467	15	65.2	8	6	ABR53951	Abr53951 Beta-secr
395	15	65.2	7	4	AAB73050	Aab73050 Luteinisi	468	15	65.2	8	6	ABR54049	Abr54049 Beta-secr
396	15	65.2	7	4	AAM47040	Aam47040 H11 bindi	469	15	65.2	8	6	ABR53996	Abr53996 Beta-secr
397	15	65.2	7	4	AAM46975	Aam46975 H11 bindi	470	15	65.2	8	6	ABR54000	Abr54000 Beta-secr
398	15	65.2	7	4	AAM46990	Aam46990 H11 bindi	471	15	65.2	8	6	ABR54047	Abr54047 Beta-secr
399	15	65.2	7	4	AAM46970	Aam46970 H11 bindi	472	15	65.2	8	6	ABR54025	Abr54025 Beta-secr
400	15	65.2	7	5	ABB94392	Abb94392 Ubiquitin	473	15	65.2	8	6	ABR53994	Abr53994 Beta-secr
401	15	65.2	7	5	ABP67352	Abp67352 Human CD6	474	15	65.2	8	6	ABR54023	Abr54023 Beta-secr
402	15	65.2	7	5	ABP67752	Abp67752 Human CD6	475	15	65.2	8	6	ABR54017	Abr54017 Beta-secr
403	15	65.2	7	5	ABG77724	Abg77724 Targettin	476	15	65.2	8	6	ADA44112	Ada44112 Human sec
404	15	65.2	7	7	ADL17146	Adl17146 Phage-dis	477	15	65.2	8	6	ABP71906	Abp71906 R. erythr
405	15	65.2	7	7	ADL17080	Adl17080 Phage-dis	478	15	65.2	8	7	ADC20439	Adc20439 Human sec
406	15	65.2	7	7	ADL17130	Adl17130 Phage-dis	479	15	65.2	8	7	ADC07142	Adc07142 Golden-wi
407	15	65.2	7	7	ADL17176	Adl17176 Phage-dis	480	15	65.2	8	7	ADC07143	Adc07143 Emperor d
408	15	65.2	7	7	ADL17077	Adl17077 Phage-dis	481	15	65.2	8	7	ADF10743	Adf10743 Human sec
409	15	65.2	7	7	ADL17227	Adl17227 Phage-dis	482	15	65.2	8	7	ADL17302	Adl17302 DENSIN-18
410	15	65.2	7	8	ADH08433	Adh08433 Ige produ	483	15	65.2	8	8	ADK01990	Adk01990 Hepatitis
411	15	65.2	7	8	ADI32411	Adi32411 PG loop p	484	15	65.2	8	8	ADK10578	Adk10578 Human pap
412	15	65.2	7	8	ADR68302	Adr68302 Androgen	485	15	65.2	8	8	ADQ28799	Adq28799 Human cel
413	15	65.2	8	2	AAR61038	Aar61038 Dynorphin	486	15	65.2	8	8	ADQ28800	Adq28800 Human cel
414	15	65.2	8	2	AAW94606	Aaw94606 Human ins	487	15	65.2	8	8	ADR69714	Adr69714 Novel hyb
415	15	65.2	8	2	AAy21268	Aay21268 Human sem	488	15	65.2	8	8	ADS00534	Ads00534 Human Apo
416	15	65.2	8	2	AAW37209	Aaw37209 Human onc	489	15	65.2	8	8	ADS00532	Ads00532 Human Apo
417	15	65.2	8	2	AAW37186	Aaw37186 Human onc	490	15	65.2	8	8	ADS00533	Ads00533 Human Apo
418	15	65.2	8	2	AAW37176	Aaw37176 Human onc	491	15	65.2	8	8	ADS00535	Ads00535 Human Apo
419	15	65.2	8	2	AAW37185	Aaw37185 Human onc	492	15	65.2	8	8	ADR99992	Adr99992 Human apo
420	15	65.2	8	2	AAW37206	Aaw37206 Human MDM	493	15	65.2	8	8	ADR99995	Adr99995 Human apo
421	15	65.2	8	2	AAW37177	Aaw37177 Human onc	494	15	65.2	8	8	ADR99994	Adr99994 Human apo
422	15	65.2	8	2	AAW37207	Aaw37207 Human MDM	495	15	65.2	8	8	ADR99993	Adr99993 Human apo
423	15	65.2	8	2	AAy25556	Aay25556 Human MHC	496	15	65.2	8	8	ADS54213	Ads54213 Human apo
424	15	65.2	8	3	AAy85386	Aay85386 IL-2 deri	497	15	65.2	8	8	ADS54215	Ads54215 Human apo
425	15	65.2	8	3	AAy85387	Aay85387 IL-2 deri	498	15	65.2	8	8	ADS54216	Ads54216 Human apo
426	15	65.2	8	3	AAy85388	Aay85388 IL-2 deri	499	15	65.2	8	8	ADS54214	Ads54214 Human apo
427	15	65.2	8	3	AAB09130	Aab09130 Hepatitis	500	15	65.2	9	2	AAR53342	Aar53342 Chimeric
428	15	65.2	8	4	AAB62220	Aab62220 Glycine m	501	15	65.2	9	2	AAW00686	Aaw00686 Peptide c
429	15	65.2	8	5	ABP67745	Abp67745 Human CD6	502	15	65.2	9	2	AAW45692	Aaw45692 HBV env 3
430	15	65.2	8	5	ABP67344	Abp67344 Human CD6	503	15	65.2	9	2	AAW39724	Aaw39724 Human car
431	15	65.2	8	6	ABP99660	Abp99660 Human sec	504	15	65.2	9	2	AAW43849	Aaw43849 Specific
432	15	65.2	8	6	ABP98083	Abp98083 Amino aci	505	15	65.2	9	2	AAW43845	Aaw43845 Specific
433	15	65.2	8	6	ABP98084	Abp98084 Amino aci	506	15	65.2	9	2	AAW81310	Aaw81310 Human iNO
434	15	65.2	8	6	ABP98081	Abp98081 Amino aci	507	15	65.2	9	2	AAW81250	Aaw81250 Human iNO
435	15	65.2	8	6	ABP98082	Abp98082 Amino aci	508	15	65.2	9	2	AAW72493	Aaw72493 Dengue vi
436	15	65.2	8	6	ABR01140	Abro1140 Human gen	509	15	65.2	9	2	AAW46351	Aaw46351 Amino aci
437	15	65.2	8	6	ADA98274	Ada98274 Human sec	510	15	65.2	9	2	AAW46349	Aaw46349 Amino aci
438	15	65.2	8	6	ABP68159	Abp68159 Bacillus	511	15	65.2	9	2	AAW46348	Aaw46348 Amino aci
439	15	65.2	8	6	ABP68163	Abp68163 Bacillus	512	15	65.2	9	2	AAW46350	Aaw46350 Amino aci
440	15	65.2	8	6	ABP68181	Abp68181 Bacillus	513	15	65.2	9	2	AAW37199	Aaw37199 Human onc
441	15	65.2	8	6	ABP68158	Abp68158 Bacillus	514	15	65.2	9	2	AAy46725	Aay46725 Immunogen
442	15	65.2	8	6	ABP68166	Abp68166 Bacillus	515	15	65.2	9	2	AAy25555	Aay25555 Human MHC
443	15	65.2	8	6	ABP68160	Abp68160 Bacillus	516	15	65.2	9	2	AAy27259	Aay27259 Human tum
444	15	65.2	8	6	ABR54027	Abr54027 Beta-secr	517	15	65.2	9	3	AAy84757	Aay84757 Antigenic
445	15	65.2	8	6	ABR54059	Abr54059 Beta-secr	518	15	65.2	9	3	AAy84765	Aay84765 Antigenic
446	15	65.2	8	6	ABR53990	Abr53990 Beta-secr	519	15	65.2	9	3	AAy84756	Aay84756 Antigenic
447	15	65.2	8	6	ABR54021	Abr54021 Beta-secr	520	15	65.2	9	3	AAy84758	Aay84758 Antigenic
448	15	65.2	8	6	ABR54074	Abr54074 Beta-secr	521	15	65.2	9	3	AAy84759	Aay84759 Antigenic
449	15	65.2	8	6	ABR53998	Abr53998 Beta-secr	522	15	65.2	9	3	AAy71328	Aay71328 Rat neur
450	15	65.2	8	6	ABR54015	Abr54015 Beta-secr	523	15	65.2	9	3	AAy71328	Aay71328 Phage dis
451	15	65.2	8	6	ABR53986	Abr53986 Beta-secr	524	15	65.2	9	3	AAAB23806	Aab23806 Human sec
452	15	65.2	8	6	ABR54072	Abr54072 Beta-secr	525	15	65.2	9	3	AAAB01629	Aab01629 Chimaeric
453	15	65.2	8	6	ABR54045	Abr54045 Beta-secr	526	15	65.2	9	4	AAAB46945	Aab46945 Human SAR
454	15	65.2	8	6	ABR54068	Abr54068 Beta-secr	527	15	65.2	9	4	ABM00050	Abm00050 Savinas a
455	15	65.2	8	6	ABR53988	Abr53988 Beta-secr	528	15	65.2	9	4	ABM00058	Abm00058 Savinas a
456	15	65.2	8	6	ABR54053	Abr54053 Beta-secr	529	15	65.2	9	4	ABM00059	Abm00059 Savinas a
457	15	65.2	8	6	ABR54055	Abr54055 Beta-secr	530	15	65.2	9	4	AAAB75691	Aab75691 HLA class
458	15	65.2	8	6	ABR54057	Abr54057 Beta-secr	531	15	65.2	9	4	AAAG63257	Aag63257 Complemen
459	15	65.2	8	6	ABR54076	Abr54076 Beta-secr	532	15	65.2	9	4	AAAM24637	Aam24637 Human MHC
460	15	65.2	8	6	ABR54082	Abr54082 Beta-secr	533	15	65.2	9	5	ABG79074	Abg79074 Human CEA
461	15	65.2	8	6	ABR54051	Abr54051 Beta-secr	534	15	65.2	9	5	ABG35129	Abg35129 Pancreati
462	15	65.2	8	6	ABR53992	Abr53992 Beta-secr	535	15	65.2	9	5	ABP47446	Abp47446 N. mening
463	15	65.2	8	6	ABR54019	Abr54019 Beta-secr	536	15	65.2	9	5	ABG97340	Abg97340 Human leu

537	15	65.2	9	5	ABG97341	Abg97341 Human leu	610	15	65.2	9	6	ABJ61113	Abj61113 184PIE2-r
538	15	65.2	9	5	AAO18872	Aao18872 Human CEA	611	15	65.2	9	6	ABJ61402	Abj61402 184PIE2-r
539	15	65.2	9	5	ABP67738	Abp67738 Human CD6	612	15	65.2	9	6	ABJ58361	Abj58361 184PIE2-r
540	15	65.2	9	5	ABP67337	Abp67337 Human CD6	613	15	65.2	9	6	ABJ60622	Abj60622 184PIE2-r
541	15	65.2	9	5	ABJ11741	Abj11741 Human 125	614	15	65.2	9	6	ABJ63441	Abj63441 184PIE2-r
542	15	65.2	9	5	ABJ12589	Abj12589 Human 125	615	15	65.2	9	6	ABJ63923	Abj63923 184PIE2-r
543	15	65.2	9	5	ABJ12352	Abj12352 Human 125	616	15	65.2	9	6	ABJ63965	Abj63965 184PIE2-r
544	15	65.2	9	5	ABJ11603	Abj11603 Human 125	617	15	65.2	9	6	ABJ57333	Abj57333 184PIE2-r
545	15	65.2	9	5	ABJ11833	Abj11833 Human 125	618	15	65.2	9	6	ABJ58971	Abj58971 184PIE2-r
546	15	65.2	9	5	ABJ12880	Abj12880 Human 125	619	15	65.2	9	6	ABJ60509	Abj60509 184PIE2-r
547	15	65.2	9	5	ABJ13175	Abj13175 Human 125	620	15	65.2	9	6	ABJ62494	Abj62494 184PIE2-r
548	15	65.2	9	5	ABJ12444	Abj12444 Human 125	621	15	65.2	9	6	ABJ64062	Abj64062 184PIE2-r
549	15	65.2	9	5	ABJ12211	Abj12211 Human 125	622	15	65.2	9	6	ABJ64839	Abj64839 184PIE2-r
550	15	65.2	9	5	ABJ09544	Abj09544 Hepatitis	623	15	65.2	9	6	ABJ65025	Abj65025 184PIE2-r
551	15	65.2	9	5	ABG60517	Abg60517 Selective	624	15	65.2	9	6	ABJ57376	Abj57376 184PIE2-r
552	15	65.2	9	5	AAE31317	Aae31317 Human p53	625	15	65.2	9	6	ABJ63110	Abj63110 184PIE2-r
553	15	65.2	9	5	AAE31316	Aae31316 Human p53	626	15	65.2	9	6	ABJ63111	Abj63111 184PIE2-r
554	15	65.2	9	5	AAE31395	Aae31395 Human p53	627	15	65.2	9	6	ABJ62218	Abj62218 184PIE2-r
555	15	65.2	9	5	AAU09701	Aau09701 Anti-mela	628	15	65.2	9	6	ABO27023	Abj627023 Yellow fe
556	15	65.2	9	5	AAU96014	Aau96014 Carcino e	629	15	65.2	9	6	ABO27024	Abj627024 West nile
557	15	65.2	9	6	ABJ20021	Abj20021 MHC bindi	630	15	65.2	9	6	ABO27025	Abj627025 Murray va
558	15	65.2	9	6	ABR56915	Abr56915 Pancreati	631	15	65.2	9	6	ABO27026	Abj627026 Kunjin v1
559	15	65.2	9	6	ABR24615	Abr24615 Human can	632	15	65.2	9	7	ADA07879	Ada07879 Viral pro
560	15	65.2	9	6	ABR24590	Abr24590 Human can	633	15	65.2	9	7	ADA07878	Ada07878 Viral pro
561	15	65.2	9	6	ABR25041	Abr25041 Human can	634	15	65.2	9	7	ADA07881	Ada07881 Viral pro
562	15	65.2	9	6	ABR25394	Abr25394 Human can	635	15	65.2	9	7	ADA07880	Ada07880 Viral pro
563	15	65.2	9	6	ABR24408	Abr24408 Human can	636	15	65.2	9	7	ADD26353	Add26353 Staphyloc
564	15	65.2	9	6	ABR24647	Abr24647 Human can	637	15	65.2	9	7	ADD94560	Add94560 Human SIM
565	15	65.2	9	6	ABR20240	Abr20240 Human can	638	15	65.2	9	7	ADD94768	Add94768 Human SIM
566	15	65.2	9	6	ABR25665	Abr25665 Human can	639	15	65.2	9	7	ADD94574	Add94574 Human SIM
567	15	65.2	9	6	ABR25205	Abr25205 Human can	640	15	65.2	9	7	ADG38574	Adg38574 Human car
568	15	65.2	9	6	ABR24809	Abr24809 Human can	641	15	65.2	9	7	ADG38572	Adg38572 Human car
569	15	65.2	9	6	ABR25596	Abr25596 Human can	642	15	65.2	9	7	AAO24240	Aao24240 MHC bindi
570	15	65.2	9	6	ABR23040	Abr23040 Human can	643	15	65.2	9	7	AAO24239	Aao24239 MHC bindi
571	15	65.2	9	6	ABR21629	Abr21629 Human can	644	15	65.2	9	7	ADI03011	Adi03011 Human mon
572	15	65.2	9	6	ABJ58972	Abj58972 184PIE2-r	645	15	65.2	9	7	ADL17217	Adl17217 Phage-dis
573	15	65.2	9	6	ABJ59510	Abj59510 184PIE2-r	646	15	65.2	9	7	ADL17251	Adl17251 Phage-dis
574	15	65.2	9	6	ABJ63247	Abj63247 184PIE2-r	647	15	65.2	9	7	ADL17455	Adl17455 Human SNT
575	15	65.2	9	6	ABJ65204	Abj65204 184PIE2-r	648	15	65.2	9	7	ADL17228	Adl17228 Phage-dis
576	15	65.2	9	6	ABJ61887	Abj61887 184PIE2-r	649	15	65.2	9	7	ADK65171	Adk65171 Human VEG
577	15	65.2	9	6	ABJ63999	Abj63999 184PIE2-r	650	15	65.2	9	7	ADK65120	Adk65120 Human VEG
578	15	65.2	9	6	ABJ64840	Abj64840 184PIE2-r	651	15	65.2	9	8	ADG89640	Adg89640 Class I H
579	15	65.2	9	6	ABJ60510	Abj60510 184PIE2-r	652	15	65.2	9	8	ADK39506	Adk39506 Hepatitis
580	15	65.2	9	6	ABJ62064	Abj62064 184PIE2-r	653	15	65.2	9	8	ADK10586	Adk10586 Human pap
581	15	65.2	9	6	ABJ62495	Abj62495 184PIE2-r	654	15	65.2	9	8	ADK03265	Adk03265 Hepatitis
582	15	65.2	9	6	ABJ65468	Abj65468 184PIE2-r	655	15	65.2	9	8	ADK05899	Adk05899 Hepatitis
583	15	65.2	9	6	ABJ58585	Abj58585 184PIE2-r	656	15	65.2	9	8	ADK10587	Adk10587 Human pap
584	15	65.2	9	6	ABJ59876	Abj59876 184PIE2-r	657	15	65.2	9	8	ADK05107	Adk05107 Hepatitis
585	15	65.2	9	6	ABJ59965	Abj59965 184PIE2-r	658	15	65.2	9	8	ADK10585	Adk10585 Human pap
586	15	65.2	9	6	ABJ61159	Abj61159 184PIE2-r	659	15	65.2	9	8	ADK05911	Adk05911 Hepatitis
587	15	65.2	9	6	ABJ64098	Abj64098 184PIE2-r	660	15	65.2	9	8	ADK10584	Adk10584 Human pap
588	15	65.2	9	6	ABJ64452	Abj64452 184PIE2-r	661	15	65.2	9	8	ADM12337	Adm12337 MHC class
589	15	65.2	9	6	ABJ60738	Abj60738 184PIE2-r	662	15	65.2	9	8	ADL19695	Adl19695 125P5C8 p
590	15	65.2	9	6	ABJ65172	Abj65172 184PIE2-r	663	15	65.2	9	8	ADL19077	Adl19077 125P5C8 p
591	15	65.2	9	6	ABJ59130	Abj59130 184PIE2-r	664	15	65.2	9	8	ADL18847	Adl18847 125P5C8 p
592	15	65.2	9	6	ABJ59833	Abj59833 184PIE2-r	665	15	65.2	9	8	ADL19603	Adl19603 125P5C8 p
593	15	65.2	9	6	ABJ59945	Abj59945 184PIE2-r	666	15	65.2	9	8	ADL19840	Adl19840 125P5C8 p
594	15	65.2	9	6	ABJ60623	Abj60623 184PIE2-r	667	15	65.2	9	8	ADL18985	Adl18985 125P5C8 p
595	15	65.2	9	6	ABJ63529	Abj63529 184PIE2-r	668	15	65.2	9	8	ADL20131	Adl20131 125P5C8 p
596	15	65.2	9	6	ABJ65631	Abj65631 184PIE2-r	669	15	65.2	9	8	ADL20425	Adl20425 125P5C8 p
597	15	65.2	9	6	ABJ60467	Abj60467 184PIE2-r	670	15	65.2	9	8	ADL19462	Adl19462 125P5C8 p
598	15	65.2	9	6	ABJ61114	Abj61114 184PIE2-r	671	15	65.2	9	8	ADO38557	Ado38557 Carcinoem
599	15	65.2	9	6	ABJ63481	Abj63481 184PIE2-r	672	15	65.2	9	8	ADP25801	Adp25801 Plasmodi
600	15	65.2	9	6	ABJ61514	Abj61514 184PIE2-r	673	15	65.2	9	8	ADQ28798	Adq28798 Human cel
601	15	65.2	9	6	ABJ61798	Abj61798 184PIE2-r	674	15	65.2	9	8	ADP79788	Adp79788 Human HLA
602	15	65.2	9	6	ABJ62063	Abj62063 184PIE2-r	675	15	65.2	9	8	ADP80098	Adp80098 Human HLA
603	15	65.2	9	6	ABJ62639	Abj62639 184PIE2-r	676	15	65.2	10	2	AAR89917	Aar89917 Human p53
604	15	65.2	9	6	ABJ58529	Abj58529 184PIE2-r	677	15	65.2	10	2	AAR89918	Aar89918 Mouse p53
605	15	65.2	9	6	ABJ63337	Abj63337 184PIE2-r	678	15	65.2	10	2	AAW32713	Aaw32713 Human pla
606	15	65.2	9	6	ABJ64453	Abj64453 184PIE2-r	679	15	65.2	10	2	AAW13605	Aaw13605 p53 prote
607	15	65.2	9	6	ABJ61556	Abj61556 184PIE2-r	680	15	65.2	10	2	AAW37961	Aaw37961 Peptide s
608	15	65.2	9	6	ABJ62994	Abj62994 184PIE2-r	681	15	65.2	10	2	AAW62010	Aaw62010 Heavy cha
609	15	65.2	9	6	ABJ61053	Abj61053 184PIE2-r	682	15	65.2	10	2	AAW37198	Aaw37198 Human onc



683	15	65.2	10	2	AAY25554	Aay25554 Human MHC	756	15	65.2	10	6	ABJ67907	Abj67907 184P1E2-r
684	15	65.2	10	2	AAY40548	Aay40648 S2 deriva	757	15	65.2	10	6	ABJ68931	Abj68931 184P1E2-r
685	15	65.2	10	3	AAY82337	Aay82337 Humanised	758	15	65.2	10	6	ABJ65862	Abj65862 184P1E2-r
686	15	65.2	10	3	AAB29987	Aab29987 Scaffold	759	15	65.2	10	6	ABJ66586	Abj66586 184P1E2-r
687	15	65.2	10	4	AAM24682	Aam24682 Human MHC	760	15	65.2	10	6	ABJ67496	Abj67496 184P1E2-r
688	15	65.2	10	4	AAB76236	Aab76236 Tumour as	761	15	65.2	10	6	ABJ66002	Abj66002 184P1E2-r
689	15	65.2	10	4	AAB76069	Aab76069 Tumour as	762	15	65.2	10	6	ABJ67609	Abj67609 184P1E2-r
690	15	65.2	10	4	AAG87403	Aag87403 Saccharom	763	15	65.2	10	6	ABJ69115	Abj69115 184P1E2-r
691	15	65.2	10	4	AAG87402	Aag87402 Saccharom	764	15	65.2	10	6	ABJ65863	Abj65863 184P1E2-r
692	15	65.2	10	4	ABB52377	Abb52377 Human API	765	15	65.2	10	6	ABJ58400	Abj58400 184P1E2-r
693	15	65.2	10	4	AAB35294	Aab35294 Murine PS	766	15	65.2	10	6	ABJ68318	Abj68318 184P1E2-r
694	15	65.2	10	5	ABB06172	Abb06172 Gonadotro	767	15	65.2	10	6	ABJ68081	Abj68081 184P1E2-r
695	15	65.2	10	5	ABG70414	Abg70414 CDR1/H1 r	768	15	65.2	10	6	ABJ68082	Abj68082 184P1E2-r
696	15	65.2	10	5	AAU98467	Aau98467 Novel hum	769	15	65.2	10	6	ABJ68164	Abj68164 184P1E2-r
697	15	65.2	10	5	ABP67331	Abp67331 Human CD6	770	15	65.2	10	7	ADC07158	Adc07158 Platypleu
698	15	65.2	10	5	ABP67732	Abp67732 Human CD6	771	15	65.2	10	7	ADD94159	Add94159 Mouse HUI
699	15	65.2	10	5	ABJ13821	Abj13821 Human 125	772	15	65.2	10	7	ADD94141	Add94141 Mouse HUI
700	15	65.2	10	5	ABJ11673	Abj11673 Human 125	773	15	65.2	10	7	ADD94158	Add94158 Mouse HUI
701	15	65.2	10	5	ABJ13682	Abj13682 Human 125	774	15	65.2	10	7	ADD94162	Add94162 Mouse HUI
702	15	65.2	10	5	ABJ14107	Abj14107 Human 125	775	15	65.2	10	7	ADD94161	Add94161 Mouse HUI
703	15	65.2	10	5	ABJ13459	Abj13459 Human 125	776	15	65.2	10	7	ADD94160	Add94160 Mouse HUI
704	15	65.2	10	5	ABJ13896	Abj13896 Human 125	777	15	65.2	10	7	ADD94632	Add94632 Human SIM
705	15	65.2	10	5	ABJ11759	Abj11759 Human 125	778	15	65.2	10	7	ADF10400	Adf10400 Serum alb
706	15	65.2	10	5	ABJ14159	Abj14159 Human 125	779	15	65.2	10	7	ADL17313	Adl17313 DENGIN-18
707	15	65.2	10	5	AAU82450	Aau82450 Llama CDR	780	15	65.2	10	7	ADL17226	Adl17226 Phage-dis
708	15	65.2	10	5	AAU82812	Aau82812 Human Cal	781	15	65.2	10	7	ADL17327	Adl17327 Human scr
709	15	65.2	10	5	AAU82829	Aau82829 Human Cal	782	15	65.2	10	7	ADL17218	Adl17218 Phage-dis
710	15	65.2	10	6	ABP70583	Abp70583 Hepatitis	783	15	65.2	10	7	ADL17215	Adl17215 Phage-dis
711	15	65.2	10	6	ABO10708	Abol10708 Murine J4	784	15	65.2	10	7	ADL17219	Adl17219 Phage-dis
712	15	65.2	10	6	ABR25335	Abr25335 Human can	785	15	65.2	10	7	ADM07751	Adm07751 Canine im
713	15	65.2	10	6	ABR25737	Abr25737 Human can	786	15	65.2	10	7	ADM07748	Adm07748 Canine im
714	15	65.2	10	6	ABR25754	Abr25754 Human can	787	15	65.2	10	7	ADM07744	Adm07744 Canine im
715	15	65.2	10	6	ABR23106	Abr23106 Human can	788	15	65.2	10	8	ADG38998	Adg38998 Humanised
716	15	65.2	10	6	ABR21698	Abr21698 Human can	789	15	65.2	10	8	ADG78885	Adg78885 Human p53
717	15	65.2	10	6	ABR22470	Abr22470 Human can	790	15	65.2	10	8	ADI82158	Adi82158 Plasma re
718	15	65.2	10	6	ABR24908	Abr24908 Human can	791	15	65.2	10	8	ADJ50603	Adj50603 Human ser
719	15	65.2	10	6	ABR23870	Abr23870 Human can	792	15	65.2	10	8	ADK10594	Adk10594 Human pap
720	15	65.2	10	6	ABR25307	Abr25307 Human can	793	15	65.2	10	8	ADK03263	Adk03263 Hepatitis
721	15	65.2	10	6	ABR24723	Abr24723 Human can	794	15	65.2	10	8	ADK03268	Adk03268 Hepatitis
722	15	65.2	10	6	ABR20303	Abr20303 Human can	795	15	65.2	10	8	ADK10595	Adk10595 Human pap
723	15	65.2	10	6	ABR25496	Abr25496 Human can	796	15	65.2	10	8	ADK10596	Adk10596 Human pap
724	15	65.2	10	6	ABR24681	Abr24681 Human can	797	15	65.2	10	8	ADK05932	Adk05932 Hepatitis
725	15	65.2	10	6	ABR24520	Abr24520 Human can	798	15	65.2	10	8	ADK10593	Adk10593 Human pap
726	15	65.2	10	6	ABR21070	Abr21070 Human can	799	15	65.2	10	8	ADK10592	Adk10592 Human pap
727	15	65.2	10	6	ABR59148	Abr59148 Alzheimer	800	15	65.2	10	8	ADK03267	Adk03267 Hepatitis
728	15	65.2	10	6	ABR44652	Abr44652 Murine J4	801	15	65.2	10	8	ADL21058	Adl21058 125P5C8 p
729	15	65.2	10	6	ABR47280	Abr47280 Staphyloc	802	15	65.2	10	8	ADL21133	Adl21133 125P5C8 p
730	15	65.2	10	6	ABJ57466	Abj57466 184P1E2-r	803	15	65.2	10	8	ADL19003	Adl19003 125P5C8 p
731	15	65.2	10	6	ABJ58687	Abj58687 184P1E2-r	804	15	65.2	10	8	ADL21344	Adl21344 125P5C8 p
732	15	65.2	10	6	ABJ66221	Abj66221 184P1E2-r	805	15	65.2	10	8	ADL21396	Adl21396 125P5C8 p
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734	15	65.2	10	6	ABJ68257	Abj68257 184P1E2-r	807	15	65.2	10	8	ADL18917	Adl18917 125P5C8 p
735	15	65.2	10	6	ABJ69492	Abj69492 184P1E2-r	808	15	65.2	10	8	ADL20919	Adl20919 125P5C8 p
736	15	65.2	10	6	ABJ66633	Abj66633 184P1E2-r	809	15	65.2	10	8	ADN32081	Adn32081 Human Alz
737	15	65.2	10	6	ABJ66805	Abj66805 184P1E2-r	810	15	65.2	10	8	ADN48959	Adn48959 Peptide #
738	15	65.2	10	6	ABJ69386	Abj69386 184P1E2-r	811	15	65.2	10	8	ADN64792	Adn64792 HLA bindi
739	15	65.2	10	6	ABJ68555	Abj68555 184P1E2-r	812	15	65.2	10	8	ADO49156	Ado49156 Human car
740	15	65.2	10	6	ABJ69580	Abj69580 184P1E2-r	813	15	65.2	10	8	ADO77933	Ado77933 Gonadotro
741	15	65.2	10	6	ABJ58245	Abj58245 184P1E2-r	814	15	65.2	10	8	ADP47005	Adp47005 Murine he
742	15	65.2	10	6	ABJ67497	Abj67497 184P1E2-r	815	15	65.2	10	8	ADP47213	Adp47213 Human pho
743	15	65.2	10	6	ABJ66765	Abj66765 184P1E2-r	816	15	65.2	10	8	ADQ92367	Adq92367 Human hul
744	15	65.2	10	6	ABJ68357	Abj68357 184P1E2-r	817	15	65.2	10	8	ADQ92369	Adq92369 Human hul
745	15	65.2	10	6	ABJ58624	Abj58624 184P1E2-r	818	15	65.2	10	8	ADQ92371	Adq92371 Human hul
746	15	65.2	10	6	ABJ57961	Abj57961 184P1E2-r	819	15	65.2	10	8	ADQ92373	Adq92373 Human hul
747	15	65.2	10	6	ABJ66841	Abj66841 184P1E2-r	820	15	65.2	10	8	ADQ80558	Adq80558 TNF-alpha
748	15	65.2	10	6	ABJ57757	Abj57757 184P1E2-r	821	15	65.2	10	8	ADQ80562	Adq80562 TNF-alpha
749	15	65.2	10	6	ABJ67608	Abj67608 184P1E2-r	822	15	65.2	10	8	ADQ80556	Adq80556 TNF-alpha
750	15	65.2	10	6	ABJ67679	Abj67679 184P1E2-r	823	15	65.2	10	8	ADQ80560	Adq80560 TNF-alpha
751	15	65.2	10	6	ABJ68752	Abj68752 184P1E2-r	824	15	65.2	10	8	ADQ90780	Adq90780 Mouse com
752	15	65.2	10	6	ABJ68831	Abj68831 184P1E2-r	825	15	65.2	10	8	ADR03382	Adr03382 Humanised
753	15	65.2	10	6	ABJ68832	Abj68832 184P1E2-r	826	15	65.2	10	8	ADR03384	Adr03384 Humanised
754	15	65.2	10	6	ABJ68968	Abj68968 184P1E2-r	827	15	65.2	10	8	ADR03385	Adr03385 Humanised
755	15	65.2	10	6	ABJ69385	Abj69385 184P1E2-r	828	15	65.2	10	8	ADQ90923	Adq90923 Pancreati

829	15	65.2	10	8	ADS18661	Adsl8661 Peptide s	902	15	65.2	12	5	ABB81664	Abb81664 Yellow me
830	15	65.2	10	8	ADP79877	Adp79877 Human HLA	903	15	65.2	12	6	AAE30893	Aae30893 MDM2-bind
831	15	65.2	10	8	ADP80344	Adp80344 Human HLA	904	15	65.2	12	6	AAE30886	Aae30886 MDM2-bind
832	15	65.2	10	8	ADT02867	Adt02867 Human p53	905	15	65.2	12	6	ABP71371	Abp71371 Anti-OPGL
833	15	65.2	10	8	ADR70840	Adr70840 Synthetic	906	15	65.2	12	6	ABR00856	Abr00856 Bioactive
834	15	65.2	11	1	AAF71510	Aap71510 Growth ho	907	15	65.2	12	7	ADC35960	Adc35960 Peptidic
835	15	65.2	11	1	AAP82068	Aap82068 Polypepti	908	15	65.2	12	7	ADC36035	Adc36035 Chemokine
836	15	65.2	11	2	AAW05784	Aaw05784 Presenili	909	15	65.2	12	7	ADE78490	Ade78490 Peptide 3
837	15	65.2	11	2	AAW11231	Aaw11231 Peptide A	910	15	65.2	12	7	ADI03010	Adi03010 Human mon
838	15	65.2	11	2	AAW12288	Aaw12288 Mycobacte	911	15	65.2	12	7	ADL17289	Adl17289 DENGIN-18
839	15	65.2	11	2	AAW62114	Aaw62114 Human MDM	912	15	65.2	12	7	ADJ73326	Adj73326 Mdm/hdm a
840	15	65.2	11	2	AAW25553	Aay25553 Human MHC	913	15	65.2	12	7	ADJ73330	Adj73330 Mdm/hdm a
841	15	65.2	11	4	AAU27152	Aau27152 Human Leu	914	15	65.2	12	7	ADJ73339	Adj73339 Mdm/hdm a
842	15	65.2	11	4	AAU26842	Aau26842 Human Leu	915	15	65.2	12	7	ADJ73324	Adj73324 Mdm/hdm a
843	15	65.2	11	5	ABP47586	Abp47586 N. mening	916	15	65.2	12	7	ADJ73336	Adj73336 Mdm/hdm a
844	15	65.2	11	5	ABP67727	Abp67727 Human CD6	917	15	65.2	12	7	ADJ73327	Adj73327 Mdm/hdm a
845	15	65.2	11	5	ABP67326	Abp67326 Human CD6	918	15	65.2	12	7	ADJ73337	Adj73337 Mdm/hdm a
846	15	65.2	11	5	AAU93631	Aau93631 Granulocy	919	15	65.2	12	7	ADJ73338	Adj73338 Mdm/hdm a
847	15	65.2	11	5	AAW52269	Aam52269 Miniature	920	15	65.2	12	7	ADJ73325	Adj73325 Mdm/hdm a
848	15	65.2	11	5	ABG67493	Abg67493 Human ADP	921	15	65.2	12	8	ADI34264	Adi34264 Wild type
849	15	65.2	11	6	ABR59507	Abr59507 S. aureus	922	15	65.2	12	8	ADJ52964	Adj52964 CH1 delet
850	15	65.2	11	6	ADA23607	Ada23607 Alzheimer	923	15	65.2	12	8	ADJ52960	Adj52960 CH1 delet
851	15	65.2	11	8	ADG15910	Adg15910 Synthetic	924	15	65.2	12	8	ADJ52959	Adj52959 CH1 delet
852	15	65.2	11	8	ADG15914	Adg15914 Synthetic	925	15	65.2	12	8	ADJ52971	Adj52971 CH1 delet
853	15	65.2	11	8	ADJ25786	Adj25786 MDM2 bind	926	15	65.2	12	8	ADJ52972	Adj52972 CH1 delet
854	15	65.2	11	8	ADJ25912	Adj25912 MDM2 bind	927	15	65.2	12	8	ADJ52970	Adj52970 CH1 delet
855	15	65.2	11	8	ADN64806	Adn64806 HLA bindi	928	15	65.2	12	8	ADJ52958	Adj52958 CH1 delet
856	15	65.2	11	8	ADR20392	Adr20392 Tryptic d	929	15	65.2	12	8	ADJ52961	Adj52961 CH1 delet
857	15	65.2	11	8	ADP80368	Adp80368 Human HLA	930	15	65.2	12	8	ADJ52973	Adj52973 CH1 delet
858	15	65.2	12	1	AAP93573	Aap93573 Extracell	931	15	65.2	12	8	ADJ51921	Adj51921 CH1 delet
859	15	65.2	12	2	AAR77621	Aar77621 Ascorbate	932	15	65.2	12	8	ADJ51922	Adj51922 CH1 delet
860	15	65.2	12	2	AAR83344	Aar83344 Kb-bindin	933	15	65.2	12	8	ADJ51920	Adj51920 CH1 delet
861	15	65.2	12	2	AAW29957	Aaw29957 Cysteine	934	15	65.2	12	8	ADJ51932	Adj51932 CH1 delet
862	15	65.2	12	2	AAW18715	Aaw18715 C-src exo	935	15	65.2	12	8	ADJ51931	Adj51931 CH1 delet
863	15	65.2	12	2	AAW81309	Aaw81309 Human iNO	936	15	65.2	12	8	ADJ51919	Adj51919 CH1 delet
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865	15	65.2	12	2	AAW37190	Aaw37190 Human onc	938	15	65.2	12	8	ADJ51925	Adj51925 CH1 delet
866	15	65.2	12	2	AAW37184	Aaw37184 Human onc	939	15	65.2	12	8	ADJ51933	Adj51933 CH1 delet
867	15	65.2	12	2	AAW37195	Aaw37195 Human onc	940	15	65.2	12	8	ADJ57768	Adj57768 Surface g
868	15	65.2	12	2	AAW37171	Aaw37171 Human onc	941	15	65.2	12	8	ADJ57296	Adj57296 Provasopr
869	15	65.2	12	2	AAW37182	Aaw37182 Human onc	942	15	65.2	12	8	ADN65746	Adn65746 HLA bindi
870	15	65.2	12	2	AAW37181	Aaw37181 Human p53	943	15	65.2	12	8	ADR42787	Adr42787 Modulator
871	15	65.2	12	2	AAW37188	Aaw37188 Human onc	944	15	65.2	13	2	AAR49316	Aar49316 Beta2m po
872	15	65.2	12	2	AAW37189	Aaw37189 Human onc	945	15	65.2	13	2	AAW59205	Aaw59205 Seq ID 10
873	15	65.2	12	2	AAW37222	Aaw37222 MDM2 bind	946	15	65.2	13	2	AAW40094	Aaw40094 Seq ID 10
874	15	65.2	12	2	AAW25552	Aay25552 Human MHC	947	15	65.2	13	2	AAW67036	Aaw67036 Polioviru
875	15	65.2	12	3	AAW66808	Aay66808 T cell an	948	15	65.2	13	2	AAW25551	Aay25551 Human MHC
876	15	65.2	12	3	AAB17076	Aab17076 Mdm/hdm a	949	15	65.2	13	3	AAW57799	Aay57799 TRAM-inte
877	15	65.2	12	3	AAB17087	Aab17087 Mdm/hdm a	950	15	65.2	13	4	AAB20427	Aab20427 Anti-FIX/
878	15	65.2	12	3	AAB17089	Aab17089 Mdm/hdm a	951	15	65.2	13	4	AAB20390	Aab20390 Anti-FIX/
879	15	65.2	12	3	AAB17081	Aab17081 Mdm/hdm a	952	15	65.2	13	4	AAB86009	Aab86009 DCM-assoc
880	15	65.2	12	3	AAB17078	Aab17078 Mdm/hdm a	953	15	65.2	13	4	AAB86007	Aab86007 DCM-assoc
881	15	65.2	12	3	AAB17090	Aab17090 Mdm/hdm a	954	15	65.2	13	4	AAB86006	Aab86006 DCM-assoc
882	15	65.2	12	3	AAB17088	Aab17088 Mdm/hdm a	955	15	65.2	13	5	ABP68836	Abp68836 Marine sn
883	15	65.2	12	3	AAB17075	Aab17075 Mdm/hdm a	956	15	65.2	13	5	ABP67720	Abp67720 Human CD6
884	15	65.2	12	3	AAB17077	Aab17077 Mdm/hdm a	957	15	65.2	13	5	ABP67319	Abp67319 Human CD6
885	15	65.2	12	3	AAW93809	Aay93809 Reactive	958	15	65.2	13	5	ABP59059	Abp59059 Peptide #
886	15	65.2	12	3	AAW93867	Aay93867 Reactive	959	15	65.2	13	5	ADG67226	Adg67226 Human 5G1
887	15	65.2	12	4	AAB86005	Aab86005 DCM-assoc	960	15	65.2	13	5	ADG66202	Adg66202 Human pro
888	15	65.2	12	5	ABW06167	Abb06167 Gonadotro	961	15	65.2	13	5	ADG66200	Adg66200 Human pro
889	15	65.2	12	5	ABG78401	Abg78401 Memapsin	962	15	65.2	13	5	ADG67227	Adg67227 Human 5G1
890	15	65.2	12	5	ABB73170	Abb73170 Mdm/hdm a	963	15	65.2	13	5	ADG66203	Adg66203 Human pro
891	15	65.2	12	5	ABB73172	Abb73172 Mdm/hdm a	964	15	65.2	13	5	ADG67228	Adg67228 Human 5G1
892	15	65.2	12	5	ABB73185	Abb73185 Mdm/hdm a	965	15	65.2	13	5	ADG66201	Adg66201 Human pro
893	15	65.2	12	5	ABB73184	Abb73184 Mdm/hdm a	966	15	65.2	13	5	ADG67229	Adg67229 Human 5G1
894	15	65.2	12	5	ABB73176	Abb73176 Mdm/hdm a	967	15	65.2	13	6	ABP76124	Abp76124 Human GEN
895	15	65.2	12	5	ABB73183	Abb73183 Mdm/hdm a	968	15	65.2	13	6	ABP76126	Abp76126 Human GEN
896	15	65.2	12	5	ABB73173	Abb73173 Mdm/hdm a	969	15	65.2	13	6	ABP76127	Abp76127 Human GEN
897	15	65.2	12	5	ABB73171	Abb73171 Mdm/hdm a	970	15	65.2	13	6	ABP76125	Abp76125 Human GEN
898	15	65.2	12	5	ABB73182	Abb73182 Mdm/hdm a	971	15	65.2	13	7	AAO30274	Aao30274 Trichoder
899	15	65.2	12	5	ABP67723	Abp67723 Human CD6	972	15	65.2	13	7	ADE36957	Ade36957 Interfaci
900	15	65.2	12	5	ABP67322	Abp67322 Human CD6	973	15	65.2	13	7	ADF75892	Adf75892 Antimicro
901	15	65.2	12	5	ABG60547	Abg60547 Selective	974	15	65.2	13	7	ADF75888	Adf75888 Antimicro



975 15 65.2 13 7 ADF75890 Adf75890 Antimicro  
976 15 65.2 13 7 ADI57984 Adi57984 Anti-TNF-  
977 15 65.2 13 7 ADI57985 Adi57985 Anti-TNF-  
978 15 65.2 13 7 ADI57983 Adi57983 Anti-TNF-  
979 15 65.2 13 7 ADI57986 Adi57986 Anti-TNF-  
980 15 65.2 13 8 ADH94540 Lecithin  
981 15 65.2 13 8 ADO57860 Human for  
982 15 65.2 13 8 ADO24819 Polioviru  
983 15 65.2 13 8 ADR05553 Novel ssD  
984 15 65.2 14 2 AAW09477 Thrombopo  
985 15 65.2 14 2 AAW36764 Thrombopo  
986 15 65.2 14 2 AAW36628 Thrombopo  
987 15 65.2 14 2 AAW53471 P2 predom  
988 15 65.2 14 2 AAW37197 Human onc  
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990 15 65.2 14 2 AAY42867 Vpr-bind  
991 15 65.2 14 3 AAB17012 TPO-mimet  
992 15 65.2 14 3 AAB13866 L2/HNK1 c  
993 15 65.2 14 4 AAB20428 Anti-FIX/  
994 15 65.2 14 4 AAM98166 Human pep  
995 15 65.2 14 4 AAM98390 Human pep  
996 15 65.2 14 4 AAM00740 Human pro  
997 15 65.2 14 4 AAM00739 Human pro  
998 15 65.2 14 4 AAU25847 Human thr  
999 15 65.2 14 4 AAG98212 Human SNP  
1000 15 65.2 14 4 AAB86012 DCM-assoc

ALIGNMENTS

RESULT 1  
ADC07129  
ID ADC07129 standard; peptide; 9 AA.  
XX  
AC ADC07129;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Honeybee AKH peptide.  
XX  
KW lipid mobilisation; insect; adipokinetic hormone; AKH; anorectic;  
KW antidiabetic; hypotensive; cardiant; antiarthritic; cytostatic;  
KW nephrotropic; hepatotropic; analgesic; cerebroprotective; uropathic;  
KW obesity; type II diabetes; cholelithiasis; hypertension;  
KW coronary heart disease; atherosclerosis; glycosenosis; arthritis; cancer;  
KW renal failure; liver; chronic pain; sleep apnea; stroke;  
KW urinary incontinence; honeybee.  
XX  
OS Synthetic.  
OS Apis mellifera.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /label= OTHER  
FT /note= "OTHER = Pyroglutamic acid"  
FT Misc-difference 9 /note= "Preferably C-terminal amide"  
FT /note= "Preferably C-terminal amide"  
XX  
PN WO2003066080-A1.  
XX  
PD 14-AUG-2003.  
XX  
PF 07-FEB-2003; 2003WO-US003800.  
XX  
PR 07-FEB-2002; 2002US-00072419.  
XX  
PA (BLMB-) BLM GROUP.  
XX  
PI Schacter BZ, Schacter LP;  
XX  
DR WPI; 2003-712542/67.  
XX

PT Pharmaceutical composition useful for promoting weight loss, comprises an  
PT insect adipokinetic hormone, having a pyroglutamate residue at its amino  
PT terminus.  
XX  
PS Claim 29; Page 20; 82pp; English.  
XX  
CC The invention relates to a novel method of promoting lipid mobilisation  
CC in a human which comprises administering an insect adipokinetic hormone  
CC (AKH). The hormone of the invention demonstrates anorectic, antidiabetic,  
CC hypotensive, cardiant, antiarthritic, cytostatic, nephrotropic,  
CC hepatotropic, analgesic, cerebroprotective and uropathic activities. The  
CC method of the invention may be useful for treating obesity, type II  
CC diabetes, cholelithiasis, hypertension, coronary heart disease,  
CC atherosclerosis, types I to VI glycosenosis, arthritis, cancer, renal  
CC failure, liver disease, chronic pain, sleep apnea, stroke and urinary  
CC incontinence. The current sequence is that of the honeybee AKH peptide of  
CC the invention.  
XX  
SQ Sequence 9 AA;  
Query Match 73.9%; Score 17; DB 7; Length 9;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 FXXXW 5  
Db | |  
4 FTSSW 8  
RESULT 2  
ADC07134  
ID ADC07134 standard; peptide; 9 AA.  
XX  
AC ADC07134;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Painted lady AKH peptide.  
XX  
KW lipid mobilisation; insect; adipokinetic hormone; AKH; anorectic;  
KW antidiabetic; hypotensive; cardiant; antiarthritic; cytostatic;  
KW nephrotropic; hepatotropic; analgesic; cerebroprotective; uropathic;  
KW obesity; type II diabetes; cholelithiasis; hypertension;  
KW coronary heart disease; atherosclerosis; glycosenosis; arthritis; cancer;  
KW renal failure; liver; chronic pain; sleep apnea; stroke;  
KW urinary incontinence; painted lady.  
XX  
OS Synthetic.  
OS Vanessa cardui.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /label= OTHER  
FT /note= "OTHER = Pyroglutamic acid"  
FT Misc-difference 9 /note= "Preferably C-terminal amide"  
FT /note= "Preferably C-terminal amide"  
XX  
PN WO2003066080-A1.  
XX  
PD 14-AUG-2003.  
XX  
PF 07-FEB-2003; 2003WO-US003800.  
XX  
PR 07-FEB-2002; 2002US-00072419.  
XX  
PA (BLMB-) BLM GROUP.  
XX  
PI Schacter BZ, Schacter LP;  
XX  
DR WPI; 2003-712542/67.  
XX  
PT Pharmaceutical composition useful for promoting weight loss, comprises an  
PT insect adipokinetic hormone, having a pyroglutamate residue at its amino

terminus.  
Claim 29; Page 20; 82pp; English.  
The invention relates to a novel method of promoting lipid mobilisation in a human which comprises administering an insect adipokinetic hormone (AKH). The hormone of the invention demonstrates anorectic, antidiabetic, hypotensive, cardiant, antiarthritic, cytostatic, nephrotropic, hepatotropic, analgesic, cerebroprotective and uropathic activities. The method of the invention may be useful for treating obesity, type II diabetes, cholelithiasis, hypertension, coronary heart disease, atherosclerosis, types I to VI glycogenosis, arthritis, cancer, renal failure, liver disease, chronic pain, sleep apnea, stroke and urinary incontinence. The current sequence is that of the painted lady AKH peptide of the invention.

XX  
SQ Sequence 9 AA;  
Query Match 73.9%; Score 17; DB 7; Length 9;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 FXXXW 5  
| |  
Db 4 FTSSW 8

RESULT 3  
AAB10010  
ID AAB10010 standard; protein; 10 AA.  
XX  
AC AAB10010;  
XX  
DT 01-NOV-2000 (first entry)  
DE H. pylori beta-urease-binding antibody heavy chain CDR1 protein #2.  
XX  
KW Acid-resistant microorganism; detection; faecal; intestine; infection;  
KW monoclonal antibody; heavy chain; complementarity determining region;  
KW CDR; beta-urease.  
XX  
OS Unidentified.  
XX  
PN WO200026671-A1.  
XX  
PD 11-MAY-2000.  
XX  
PF 29-OCT-1999; 99WO-EP008212.  
XX  
PR 29-OCT-1998; 98EP-00120517.  
PR 06-NOV-1998; 98EP-00120687.  
XX  
PA (CONN-) CONNEX GMBH.  
XX  
PI Reiter C, Cullmann G, Friedrichs U, Heppner P, Lakner M;  
PI Ringeis A;  
XX  
DR WPI; 2000-365747/31.  
DR N-PSDB; AAA40166.  
XX  
PT Detecting infection by acid-fast microbes for diagnosis of Helicobacter  
PT pylori, comprises reacting a fecal sample with two binding reagents for  
PT antigens that survive intestinal passage.  
XX  
PS Claim 26; Page 22; 84pp; German.  
XX  
CC This invention describes a novel method for the detection of a mammalian  
CC infection by an acid-resistant microorganism (A) by treating a faecal  
CC sample with at least two different monoclonal antibodies (MAb) (or their  
CC fragments or derivatives) or aptamers (collectively (I)) and detecting  
CC formation of a complex (C) between (I) and the corresponding antigen of  
CC (A). The first and second (I) bind to epitopes of different antigens  
CC (Ag). These epitopes are present, after passage through the intestines,

CC in at least some mammals, and have either: (i) their native structure; or  
CC (ii) a structure against which an antibody is produced by an animal  
CC infected or immunized with (A), or its extract, lysate, derived protein  
CC or fragment, or with a synthetic peptide. Practically all mammals display  
CC at least one of the specified epitopes. The method is used to detect  
CC infection by acid-fast bacteria, particularly of the genera Helicobacter,  
CC Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus, M.  
CC tuberculosis, C. jejuni and C. pylori. (I) may also be used  
CC therapeutically. The method is direct and non-invasive, and provides an  
CC inexpensive and easily standardizable diagnosis, despite possible  
CC degradation of antigens during passage through the intestines. This  
CC sequence represents a fragment of a H. pylori beta-urease-binding  
CC antibody heavy chain complementarity determining region CDR1 which is  
CC used to illustrate the method of the invention  
XX  
SQ Sequence 10 AA;  
Query Match 73.9%; Score 17; DB 3; Length 10;  
Best Local Similarity 40.0%; Pred. No. 3.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 FXXXW 5  
| |  
Db 4 FSTSW 8

RESULT 4  
AAB86090  
ID AAB86090 standard; peptide; 10 AA.  
XX  
AC AAB86090;  
XX  
DT 17-JUL-2001 (first entry)  
DE H. pylori beta-urease derived antibody light chain CDR1 #1.  
XX  
KW Catalase; beta-urease; antibody; antigen; detection; infection; epitope;  
KW acid-resistant microorganism; complementarity determining region; CDR;  
KW feces; heavy chain; light chain.  
XX  
OS Unidentified.  
XX  
PN WO200127612-A2.  
XX  
PD 19-APR-2001.  
XX  
PF 12-OCT-2000; 2000WO-EP010057.  
XX  
PR 12-OCT-1999; 99EP-00120351.  
PR 16-MAR-2000; 2000EP-00105592.  
PR 31-MAR-2000; 2000EP-00107028.  
PR 10-MAY-2000; 2000EP-00110110.  
XX  
PA (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.  
XX  
PI Reiter C, Cullmann G, Lakner M, Truee A, Dehnert S, Schwartz G;  
PI  
XX  
DR WPI; 2001-282086/29.  
DR N-PSDB; AAF88117.  
XX  
PT Detecting infections by acid-resistant microorganisms, particularly for  
PT diagnosing Helicobacter pylori, comprises immunochromatographic detection  
PT of antigen in feces.  
XX  
PS Claim 27; Page 27; 90pp; German.  
XX  
CC This invention describes a novel method for detecting infection by an  
CC acid-resistant microorganism (A), in a mammal, using  
CC immunochromatography. The method is used to diagnose infection by an acid  
CC -resistant microorganism (A), in a mammal, such as Helicobacter,  
CC Campylobacter or Mycobacterium, particularly H. pylori (most preferred),  
CC H. hepatica, C. jejuni and M. tuberculosis. The method is rapid, simple,  
CC inexpensive and non-invasive, and may indicate the stage of infection. A

CC test strip used in the method may include a filter to eliminate particles  
CC present in the sample and only a single receptor provides a reasonably  
CC secure diagnosis, with specificity and selectivity improved by detecting  
CC several epitopes (of catalase) or different antigens (catalase and beta-  
CC urease). The method can be automated. This sequence represents a  
CC complementarity determining region (CDR) from an antibody raised against  
CC the H. pylori catalase or beta-urease antigen which is used to illustrate  
XX the method of the invention  
SQ Sequence 10 AA;

Query Match 73.9%; Score 17; DB 4; Length 10;  
Best Local Similarity 40.0%; Pred. No. 3.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 4 FSTSW 8

RESULT 5  
AAB86058  
ID AAB86058 standard; peptide; 10 AA.

XX AAB86058;

AC 17-JUL-2001 (first entry)

DT H. pylori beta-urease derived antibody light chain CDR1 #1.

XX Heavy chain; light chain; catalase; beta-urease; detection; CDR; antigen;  
KW infection; acid-resistant microorganism; fecal; antibody; diagnosis;  
KW antibacterial; complementarity determining region.

XX Unidentified.

OS WO200127613-A2.

XX 19-APR-2001.

PD 12-OCT-2000; 2000WO-EP010058.

PF 12-OCT-1999; 99EP-00120351.

XX 16-MAR-2000; 2000EP-00105592.

PR 31-MAR-2000; 2000EP-00107028.

PR 10-MAY-2000; 2000EP-00110110.

XX (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.

PI Reiter C, Cullmann G, Heppner P, Ringeis A, Mueller H, Haindl E;

XX WPI; 2001-282087/29.

DR N-PSDB; AAF88060.

XX Claim 23; Page 17; 89pp; German.

CC This invention describes a novel method for detecting, in a mammal,  
CC infection by an acid-resistant microorganism (A) which comprises reacting  
CC a fecal sample with: (i) a receptor (R) such that a complex is formed  
CC with an antigen (Ag) of (A); or (ii) two different R so that a three-part  
CC complex is formed with Ag, and the formation of a complex detected. R are  
CC specific for an Ag which, after passage through the intestines, at least  
CC in some mammals, retains a native (or corresponding) structure against  
CC which the mammal produces antibodies (when immunized or infected with  
CC (A), or its extracts, lysates or derived proteins (or fragments) or  
CC synthetic peptides). The products of the invention have antibacterial  
CC activity. The method is used to diagnose infection by Helicobacter,  
CC Campylobacter or Mycobacterium, particularly H. pylori (most preferred),  
CC H. hepatica, C. jejuni and M. tuberculosis, and also to monitor the

CC progress of treatment. Receptors, particularly antibodies, directed  
CC against Ag can be used therapeutically for treatment of infections. The  
CC method requires only one R to provide a reasonably secure diagnosis  
CC (although use of two R improves sensitivity), so is relatively  
CC inexpensive and more easily standardized. Also it is direct, non-  
CC invasive, suitable for automation and may indicate the stage of an  
CC infection. This sequence represents a complementarity determining region  
CC (CDR) from an antibody generated against a Helicobacter pylori antigen  
CC (catalase or beta-urease) which is used to illustrate the method of the  
XX invention  
SQ Sequence 10 AA;

Query Match 73.9%; Score 17; DB 4; Length 10;  
Best Local Similarity 40.0%; Pred. No. 3.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 4 FSTSW 8

RESULT 6  
ADC07163  
ID ADC07163 standard; peptide; 11 AA.

XX ADC07163;

AC 18-DEC-2003 (first entry)

DT Painted lady AKH peptide 2.

XX lipid mobilisation; insect; adipokinetic hormone; AKH; anorectic;  
KW antidiabetic; hypotensive; cardiant; antiarthritic; cytostatic;  
KW nephrotropic; hepatotropic; analgesic; cerebroprotective; uropathic;  
KW obesity; type II diabetes; cholelithiasis; hypertension;  
KW coronary heart disease; atherosclerosis; glycogenosis; arthritis; cancer;  
KW renal failure; liver; chronic pain; sleep apnea; stroke;  
KW urinary incontinence; painted lady.

OS Synthetic.

OS Vanessa cardui.

XX Key Location/Qualifiers

FT Modified-site 1

FT /label= OTHER

FT /note= "OTHER = Pyroglutamic acid"

FT Misc-difference 11

FT /note= "Preferably C-terminal amide"

XX WO2003066080-A1.

XX 14-AUG-2003.

XX 07-FEB-2003; 2003WO-US003800.

XX 07-FEB-2002; 2002US-00072419.

XX (BLMB-) BLM GROUP.

XX Schacter BZ, Schacter LP;

XX WPI; 2003-712542/67.

XX Pharmaceutical composition useful for promoting weight loss, comprises an  
XX insect adipokinetic hormone, having a pyroglutamate residue at its amino  
XX terminus.  
XX Claim 29; Page 20; 82pp; English.  
XX The invention relates to a novel method of promoting lipid mobilisation  
XX in a human which comprises administering an insect adipokinetic hormone  
XX (AKH). The hormone of the invention demonstrates anorectic, antidiabetic,



Db | 6 FASSW 10

RESULT 9

AAM98088

ID AAM98088 standard; peptide; 14 AA.

XX AC AAM98088;

XX DT 24-JAN-2002 (first entry)

XX DE Human peptide #1363 encoded by a SNP oligonucleotide.

XX KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; cancer; amyloid protein; angiopoietin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinein; cytokine; interferon; interleukin; G-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection; nervous system disease.

XX OS Homo sapiens.

XX PN WO200147944-A2.

XX PD 05-JUL-2001.

XX PF 28-DEC-2000; 2000WO-US035498.

XX PK 28-DEC-1999; 99US-0173419P.

XX PR 27-DEC-2000; 2000US-00173419.

XX (CURA-) CURAGEN CORP.

XX PI Shimkets RA, Leach M;

XX WPI; 2001-465210/50.

XX PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.

XX PS Disclosure; Page 3967; 4143pp; English.

XX CC The present invention relates to oligonucleotides (see AAL26793-AAL34659) encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases.

XX CC The present sequence is a peptide encoded by one such oligonucleotide.

XX CC The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic organisms

XX SQ Sequence 14 AA;

Query Match 73.9%; Score 17; DB 4; Length 14;

Best Local Similarity 40.0%; Pred. No. 4.4e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db | 6 FASTW 10

RESULT 10

AAR97874

ID AAR97874 standard; peptide; 15 AA.

XX AC AAR97874;

XX DT 16-AUG-1996 (first entry)

XX DE Japan cedar pollen mature allergen Cry j II amino acids 16-30.

XX KW Allergen; epitope; overlapping peptide; Cry j II; cedar pollen; Sugi pollinosis; diagnosis; treatment.

XX OS Cryptomeria japonica.

XX PN JP08047392-A.

XX PD 20-FEB-1996.

XX PF 07-NOV-1994; 94JP-00297840.

XX PR 05-NOV-1993; 93JP-00276773.

XX PR 26-MAY-1994; 94JP-00134868.

XX (MEIP ) MEIJI MILK PROD CO LTD.

XX WPI; 1996-166249/17.

XX PT Japan cedar pollen allergen Cry j II epitope - comprises at least part of specified 460 aminoacid protein.

XX PS Claim 8; Fig 3; 17pp; Japanese.

XX CC AAR97871-R97960 are overlapping peptides used for the epitope mapping of the Japan cedar pollen allergen Cry j II. Cry j II and allergenic peptides of it are useful in the diagnosis, prevention and treatment of Sugi pollinosis, the allergic reaction to Japan cedar pollen. Significant regions of the allergen were identified using the overlapping peptides of the full epitope derived from a Cry j II antigen-specific T cell line.

XX CC Amino acids 66-80 (AAR97884) and 186-200 (R978908) of the full mature 460 amino acid allergen are the most allergenic of the 90 peptides tested

XX SQ Sequence 15 AA;

Query Match 73.9%; Score 17; DB 2; Length 15;

Best Local Similarity 40.0%; Pred. No. 4.7e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db | 9 FSTAW 13

RESULT 11

AAR97875

ID AAR97875 standard; peptide; 15 AA.

XX AC AAR97875;

XX DT 16-AUG-1996 (first entry)

XX DE Japan cedar pollen mature allergen Cry j II amino acids 21-35.

XX KW Allergen; epitope; overlapping peptide; Cry j II; cedar pollen; Sugi pollinosis; diagnosis; treatment.

XX OS Cryptomeria japonica.

XX PN JP08047392-A.

XX PD 20-FEB-1996.





```
SQ      Sequence 19 AA;
Query Match      73.9%; Score 17; DB 5; Length 19;
Best Local Similarity 40.0%; Pred. No. 5.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
      | |
Db      4 FSATW 8

RESULT 14
AAW42165
ID      AAW42165 standard; peptide; 20 AA.
XX
AC      AAW42165;
XX
DT      27-AUG-2003 (revised)
DT      25-MAR-2003 (revised)
DT      16-JUN-1998 (first entry)
XX
DE      T-cell epitope peptide 45 from Japanese cypress pollen antigen Chao2.
XX
KW      Japanese cypress pollen; antigen; T-cell epitope; Chao1; Chao2;
KW      diagnosis; allergy; spring tree pollen disease; pollinosis.
XX
OS      Chamaecyparis obtusa.
XX
PN      WO9747648-A1.
XX
PD      18-DEC-1997.
XX
PF      12-JUN-1997; 97WO-JP002031.
XX
PR      14-JUN-1996; 96JP-00153527.
XX
PA      (MEIP ) MEIJI MILK PROD CO LTD.
XX
PI      Kino K, Dairiri K;
XX
WPI; 1998-052242/05.
XX
T-cell epitope peptide portion of Japanese cypress pollen antigens Chao1
and Chao2 - used for diagnosis and treatment of spring tree pollen
disease.
XX
Claim 2; Page 36; 71pp; Japanese.
XX
The present sequence represents a T-cell epitope peptide from Japanese
cypress pollen antigen Chao2. The present invention describes peptides
which correspond to the T-cell epitope sites on Japanese cypress pollen
antigens Chao1 and Chao2. The peptides can be used as a reagent for the
diagnosis of allergy to Japanese cypress pollen, and as an antigen in the
treatment and prevention of spring tree pollen disease in which the
pollinosis involves reactivity to Japanese cypress pollen. (Updated on 25
-MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS
field.)
XX
SQ      Sequence 20 AA;
Query Match      73.9%; Score 17; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 5.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
      | |
Db      8 FATTW 12

RESULT 15
AAG62999
ID      AAG62999 standard; peptide; 20 AA.
XX
AC      AAG62999;
XX
DT      01-OCT-2001 (first entry)
XX
DE      Complementarity determining region 3 (CDR3) of VH chain of clone G101.
XX
KW      Antibody; light chain; VL; amyloid protein; blood brain barrier;
KW      endothelial cell; brain cell antigen; inflammation; adhesion molecule;
KW      transferrin receptor; neurological disease; Alzheimer's disease;
KW      prion disease; AIDS-related dementia; epilepsy; brain injury.
XX
OS      Homo sapiens.
XX
PN      WO200144300-A2.
XX
PD      21-JUN-2001.
XX
PF      27-NOV-2000; 2000WO-GB0004501.
XX
PR      13-DEC-1999; 99US-0170599P.
XX
PA      (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI      Webster C, Osbourn J, Ward G, Miller K;
XX
WPI; 2001-398131/42.
XX
Mixture or panel of antibodies for selecting specific binding members
that cross the blood brain barrier, for use in delivering different
molecules and treating neurological diseases.
XX
Claim 1; Page 76; 109pp; English.
XX
AAG62970-AAG63005 represent complementarity determining region 3 (CDR3)
of VL and VH chains of antibodies of the invention. The specification
describes a mixture or panel of 5 different specific binding members,
each comprising an antibody VH and/or VL variable domain and capable,
when displayed on the surface of filamentous bacteriophage particles or
in the case of a specific binding member comprising the D5 VH and/or VL
variable domain when bound to human serum amyloid protein, to pass
through a mammalian blood brain barrier (BBB). The panel is useful for
the selection of specific binding members with a desired property such as
ability to cross BBB, ability to bind endothelial cells or other brain
cell antigen, ability to bind areas of inflammation in the brain or BBB
breakdown or ability to bind intracellular adhesion molecules and to bind
transferrin receptor. The antibodies are useful in diagnosis, prophylaxis
and treatment of human or animal body, including neurological diseases,
such as Alzheimer's disease, prion disease, AIDS-related dementia,
epilepsy and traumatic brain injury and any diseases involving
inflammation occurring within the brain or central nervous system
XX
SQ      Sequence 20 AA;
Query Match      73.9%; Score 17; DB 4; Length 20;
Best Local Similarity 40.0%; Pred. No. 5.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
      | |
Db      4 FSSSW 8

RESULT 16
ADR68284
ID      ADR68284 standard; peptide; 5 AA.
XX
AC      ADR68284;
XX
DT      02-DEC-2004 (first entry)
XX
DE      Androgen receptor interacting peptide SEQ ID NO:2.
XX
KW      androgen receptor binding peptide; androgen receptor interacting peptide;
```



KW androgen receptor; cytostatic; gene therapy; prostate cancer.  
XX Mammalia.  
OS Synthetic.  
XX WO2004076473-A2.  
PN 10-SEP-2004.  
XX 10-FEB-2004; 2004WO-US003774.  
PF 12-FEB-2003; 2003US-0446955P.  
XX (KARO-) KARO BIO AB.  
PA Buehrer BM, Barnett TR;  
XX WPI; 2004-653365/63.  
XX New polypeptides that bind to the androgen receptor, useful for  
PT diagnosing or treating diseases associated with abnormal levels of  
PT activation of androgen receptor, e.g. prostate cancer, or in biological  
PT research.  
XX Disclosure; SEQ ID NO 2; 46pp; English.  
PS The present invention describes a polypeptide that binds to the androgen  
XX receptor, or a polypeptide that comprises at least 50% amino acid  
CC sequence identity to the polypeptide. Also described: (1) methods of  
CC analysing the surface conformation of a protein using one or more of the  
CC polypeptide sequences mentioned above; (2) methods of identifying  
CC modulators of protein function using one or more of the polypeptide  
CC sequences mentioned above; (3) a pharmaceutical composition comprising a  
CC pharmaceutical carrier and one or more of the polypeptide sequences  
CC described above; (4) a peptide that binds to the androgen receptor, the  
CC binding being competitively inhibited by the polypeptide described above;  
CC (5) a chimeric protein comprising the above polypeptide and at least a  
CC portion of a filamentous phage protein, the portion of the filamentous  
CC phage protein being sufficient for integration of the chimeric protein  
CC into the coat of phage particles for display of the polypeptide; (6) a  
CC filamentous phage displaying the above polypeptide; (7) a method of  
CC diagnosing a disease in a patient characterised by abnormal levels of  
CC fluid or tissue of the patient, comprising providing a sample of body  
CC activated androgen receptor in the body fluid or tissue of the patient;  
CC and (8) a method of treating a patient suffering from a disease  
CC characterised by abnormal levels of activation of androgen receptor,  
CC comprising administering to the patient a therapeutic amount of the  
CC pharmaceutical composition described above. The androgen receptor  
CC interacting polypeptide has cytostatic activity, and can be used in gene  
CC therapy. The composition and methods are useful for diagnosing or  
CC treating patients suffering from diseases characterised by abnormal  
CC levels of activation of androgen receptor, such as prostate cancer. They  
CC may also be used in biological research, as therapeutics or for in vitro  
CC or in vivo classification of compounds. The present sequence represents  
CC an androgen receptor interacting peptide, which is used in the  
CC exemplification of the present invention.  
XX  
SQ Sequence 5 AA;  
Query Match 69.6%; Score 16; DB 8; Length 5;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 FXXXW 5  
|  
Db 1 FAALW 5  
RESULT 17  
AAW76953  
ID AAW76953 standard; peptide; 6 AA.

XX AAW76953;  
AC 25-JAN-1999 (first entry)  
DT Fusion immunoglobulin heavy chain HIV gp120 B cell epitope #93.  
XX B cell; T cell; epitope; immunoglobulin; heavy chain; gp120; IgH;  
KW human immune deficiency virus; HIV; tolerance; treatment; therapy;  
KW prophylaxis; vaccine; chemotherapy; immune response; modifier; tumour;  
KW microbial infection; autoimmune disease; antibody; apoptosis;  
KW antiviral T cell immunity.  
XX Mus sp.  
OS Homo sapiens.  
XX WO9836087-A1.  
PN 20-AUG-1998.  
XX 13-FEB-1998; 98WO-US002766.  
PF 13-FEB-1997; 97US-0040581P.  
XX (AMNA-) AMERICAN NAT RED CROSS.  
PA Scott D, Zambidis E;  
XX WPI; 1998-506315/43.  
XX New fusion immunoglobulin heavy chain including gp120 epitopes and  
PT related complete antibodies - DNA, vectors and transformed cells, used to  
PT induce tolerance to the epitopes for treatment of human immune deficiency  
PT virus infection.  
XX Disclosure; Page 40; 154pp; English.  
PS This sequence is an epitope used in the construction of a novel fusion  
XX immunoglobulin heavy chain (IgH) protein with a mammalian, especially  
CC human, IgH chain fused in frame at its N-terminus to one or more human  
CC immune deficiency virus (HIV) gp120 epitopes. Fusion Ig proteins and/or  
CC transfected cells are used to tolerate subjects to gp120 epitopes and to  
CC maintain this tolerance, particularly for treatment of HIV infection,  
CC optionally together with other therapeutic/prophylactic agents such as  
CC vaccines, chemotherapeutic agents and immune response modifiers. Such  
CC proteins can be used against other diseases where an immune response is  
CC deleterious, e.g. microbial infection, tumours or autoimmune disease.  
CC Induction of tolerance suppresses production of antibodies against gp120,  
CC so prevents or inhibits 'bystander' apoptosis of uninfected T cells that  
CC are bound to gp120 protein, maximising induction of protective antiviral  
CC T cell immunity  
XX Sequence 6 AA;  
SQ Query Match 69.6%; Score 16; DB 2; Length 6;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 FXXXW 5  
|  
Db 2 FNSTW 6  
RESULT 18  
ABR46309  
ID ABR46309 standard; peptide; 6 AA.  
XX  
AC ABR46309;  
XX 10-JUN-2003 (first entry)  
DT Staphylococcus aureus CHIPS-related peptide #1499.  
DE  
XX

KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;  
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;  
KW inflammation; cardiovascular disease; central nervous system disease;  
KW gastrointestinal disease; skin disease; genitourinary disease;  
KW joint disease; respiratory disease; HIV infection; antiinflammatory;  
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;  
KW gynecological; immunosuppressive; anti-HIV.  
XX  
OS Staphylococcus aureus.  
OS Synthetic.  
PN WO2003006048-A1.  
XX  
PD 23-JAN-2003.  
XX  
PF 11-JUL-2001; 2001WO-EP008004.  
XX  
PR 11-JUL-2001; 2001WO-EP008004.  
XX  
XX (JARI-) JARI PHARM BV.  
XX  
PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;  
PI Van Strijp JAG;  
XX  
DR WPI; 2003-256333/25.  
XX  
XX Combination of peptides derived from chemotaxis inhibiting protein from  
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in  
PT prophylaxis and treatment of inflammation, cardiovascular, skin and  
PT kidney diseases.  
XX  
PS Disclosure; Page 16; 89pp; English.  
XX  
CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164  
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from  
CC Staphylococcus aureus. The peptide fragments are useful in the  
CC prophylaxis or treatment of diseases or disorders involving the C5a-  
CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,  
CC monocytes and endothelial cells or involving acute or chronic  
CC inflammation reactions. The diseases or disorders include cardiovascular  
CC diseases, disease of the central nervous system, gastrointestinal  
CC diseases, skin diseases, genitourinary diseases, joint diseases,  
CC respiratory diseases and HIV infection  
XX  
SQ Sequence 6 AA;  
  
Query Match 69.6%; Score 16; DB 6; Length 6;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 FXXXW 5  
|  
Db 1 FSFSW 5  
  
RESULT 19  
ABR46270  
ID ABR46270 standard; peptide; 6 AA.  
XX  
AC ABR46270;  
XX  
DT 10-JUN-2003 (first entry)  
XX  
DE Staphylococcus aureus CHIPS-related peptide #1460.  
XX  
KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;  
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;  
KW inflammation; cardiovascular disease; central nervous system disease;  
KW gastrointestinal disease; skin disease; genitourinary disease;  
KW joint disease; respiratory disease; HIV infection; antiinflammatory;  
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;  
KW gynecological; immunosuppressive; anti-HIV.  
XX

OS Staphylococcus aureus.  
OS Synthetic.  
XX  
PN WO2003006048-A1.  
XX  
PD 23-JAN-2003.  
XX  
PF 11-JUL-2001; 2001WO-EP008004.  
XX  
PR 11-JUL-2001; 2001WO-EP008004.  
XX  
XX (JARI-) JARI PHARM BV.  
XX  
PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;  
PI Van Strijp JAG;  
XX  
DR WPI; 2003-256333/25.  
XX  
XX Combination of peptides derived from chemotaxis inhibiting protein from  
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in  
PT prophylaxis and treatment of inflammation, cardiovascular, skin and  
PT kidney diseases.  
XX  
PS Disclosure; Page 16; 89pp; English.  
XX  
CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164  
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from  
CC Staphylococcus aureus. The peptide fragments are useful in the  
CC prophylaxis or treatment of diseases or disorders involving the C5a-  
CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,  
CC monocytes and endothelial cells or involving acute or chronic  
CC inflammation reactions. The diseases or disorders include cardiovascular  
CC diseases, disease of the central nervous system, gastrointestinal  
CC diseases, skin diseases, genitourinary diseases, joint diseases,  
CC respiratory diseases and HIV infection  
XX  
SQ Sequence 6 AA;  
  
Query Match 69.6%; Score 16; DB 6; Length 6;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 FXXXW 5  
|  
Db 1 FTFW 5  
  
RESULT 20  
ABR46702  
ID ABR46702 standard; peptide; 6 AA.  
XX  
AC ABR46702;  
XX  
DT 10-JUN-2003 (first entry)  
XX  
DE Staphylococcus aureus CHIPS-related peptide #1892.  
XX  
KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;  
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;  
KW inflammation; cardiovascular disease; central nervous system disease;  
KW gastrointestinal disease; skin disease; genitourinary disease;  
KW joint disease; respiratory disease; HIV infection; antiinflammatory;  
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;  
KW gynecological; immunosuppressive; anti-HIV.  
XX  
OS Staphylococcus aureus.  
OS Synthetic.  
XX  
PN WO2003006048-A1.  
XX  
PD 23-JAN-2003.  
XX  
PF 11-JUL-2001; 2001WO-EP008004.

```
XX 11-JUL-2001; 2001WO-EP008004.
XX (JARI-) JARI PHARM BV.
XX Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
XX Van Strijp JAG;
XX WPI; 2003-256333/25.
XX Combination of peptides derived from chemotaxis inhibiting protein from
XX Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
XX prophylaxis and treatment of inflammation, cardiovascular, skin and
XX kidney diseases.
XX Disclosure; Page 17; 89pp; English.
XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
XX -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
XX Staphylococcus aureus. The peptide fragments are useful in the
XX prophylaxis or treatment of diseases or disorders involving the C5a-
XX receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
XX monocytes and endothelial cells or involving acute or chronic
XX inflammation reactions. The diseases or disorders include cardiovascular
XX diseases, disease of the central nervous system, gastrointestinal
XX diseases, skin diseases, genitourinary diseases, joint diseases,
XX respiratory diseases and HIV infection
XX Sequence 6 AA;
XX Query Match 69.6%; Score 16; DB 6; Length 6;
XX Best Local Similarity 40.0%; Pred. No. 1.8e+06;
XX Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX QY 1 FXXXW 5
XX | |
XX 1 FTFSW 5
XX DB
XX RESULT 21
XX ABR47093
XX ID ABR47093 standard; peptide; 6 AA.
XX AC ABR47093;
XX DT 10-JUN-2003 (first entry)
XX DE Staphylococcus aureus CHIPS-related peptide #2283.
XX KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
XX formulated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
XX inflammation; cardiovascular disease; central nervous system disease;
XX gastrointestinal disease; skin disease; genitourinary disease;
XX joint disease; respiratory disease; HIV infection; antiinflammatory;
XX cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
XX gynecological; immunosuppressive; anti-HIV.
XX OS Staphylococcus aureus.
XX OS Synthetic.
XX PN WO2003006048-A1.
XX PD 23-JAN-2003.
XX PF 11-JUL-2001; 2001WO-EP008004.
XX PR 11-JUL-2001; 2001WO-EP008004.
XX XX (JARI-) JARI PHARM BV.
XX PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
XX PI Van Strijp JAG;
XX WPI; 2003-256333/25.
XX Combination of peptides derived from chemotaxis inhibiting protein from
XX Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
XX prophylaxis and treatment of inflammation, cardiovascular, skin and
XX kidney diseases.
XX Disclosure; Page 17; 89pp; English.
XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
XX -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
XX Staphylococcus aureus. The peptide fragments are useful in the
XX prophylaxis or treatment of diseases or disorders involving the C5a-
XX receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,
XX monocytes and endothelial cells or involving acute or chronic
XX inflammation reactions. The diseases or disorders include cardiovascular
XX diseases, disease of the central nervous system, gastrointestinal
XX diseases, skin diseases, genitourinary diseases, joint diseases,
XX respiratory diseases and HIV infection
XX Sequence 6 AA;
XX Query Match 69.6%; Score 16; DB 6; Length 6;
XX Best Local Similarity 40.0%; Pred. No. 1.8e+06;
XX Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX QY 1 FXXXW 5
XX | |
XX 1 FTFSW 5
XX DB
XX RESULT 22
XX ABR45149
XX ID ABR45149 standard; peptide; 6 AA.
XX AC ABR45149;
XX DT 10-JUN-2003 (first entry)
XX DE Staphylococcus aureus CHIPS-related peptide #339.
XX KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
XX formulated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
XX inflammation; cardiovascular disease; central nervous system disease;
XX gastrointestinal disease; skin disease; genitourinary disease;
XX joint disease; respiratory disease; HIV infection; antiinflammatory;
XX cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
XX gynecological; immunosuppressive; anti-HIV.
XX OS Staphylococcus aureus.
XX OS Synthetic.
XX PN WO2003006048-A1.
XX PD 23-JAN-2003.
XX PF 11-JUL-2001; 2001WO-EP008004.
XX PR 11-JUL-2001; 2001WO-EP008004.
XX XX (JARI-) JARI PHARM BV.
XX PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
XX PI Van Strijp JAG;
XX WPI; 2003-256333/25.
XX Combination of peptides derived from chemotaxis inhibiting protein from
XX Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
XX prophylaxis and treatment of inflammation, cardiovascular, skin and
XX kidney diseases.
XX Disclosure; Page 11; 89pp; English.
```

XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164  
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from  
CC Staphylococcus aureus. The peptide fragments are useful in the  
CC prophylaxis or treatment of diseases or disorders involving the C5a-  
CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,  
CC monocytes and endothelial cells or involving acute or chronic  
CC inflammation reactions. The diseases or disorders include cardiovascular  
CC diseases, disease of the central nervous system, gastrointestinal  
CC diseases, skin diseases, genitourinary diseases, joint diseases,  
CC respiratory diseases and HIV infection  
XX  
SQ Sequence 6 AA;  
  
Query Match 69.6%; Score 16; DB 6; Length 6;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 FXXXW 5  
Db 1 FSFAW 5  
  
RESULT 23  
ABR45486  
ID ABR45486 standard; peptide; 6 AA.  
XX  
AC ABR45486;  
XX  
DT 10-JUN-2003 (first entry)  
XX  
DE Staphylococcus aureus CHIPS-related peptide #676.  
XX  
KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;  
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;  
KW inflammation; cardiovascular disease; central nervous system disease;  
KW gastrointestinal disease; skin disease; genitourinary disease;  
KW joint disease; respiratory disease; HIV infection; antiinflammatory;  
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;  
KW gynecological; immunosuppressive; anti-HIV.  
XX  
OS Staphylococcus aureus.  
OS Synthetic.  
XX  
PN WO2003006048-A1.  
XX  
PD 23-JAN-2003.  
XX  
PF 11-JUL-2001; 2001WO-EP008004.  
XX  
PR 11-JUL-2001; 2001WO-EP008004.  
XX  
PA (JARI-) JARI PHARM BV.  
XX  
PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;  
PI Van Strijp JAG;  
XX  
DR WPI; 2003-256333/25.  
XX  
XX Combination of peptides derived from chemotaxis inhibiting protein from  
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in  
PT prophylaxis and treatment of inflammation, cardiovascular, skin and  
PT kidney diseases.  
XX  
PS Disclosure; Page 13; 89pp; English.  
XX  
CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164  
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from  
CC Staphylococcus aureus. The peptide fragments are useful in the  
CC prophylaxis or treatment of diseases or disorders involving the C5a-  
CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,  
CC monocytes and endothelial cells or involving acute or chronic  
CC inflammation reactions. The diseases or disorders include cardiovascular  
XX

CC diseases, disease of the central nervous system, gastrointestinal  
CC diseases, skin diseases, genitourinary diseases, joint diseases,  
CC respiratory diseases and HIV infection  
XX  
SQ Sequence 6 AA;  
  
Query Match 69.6%; Score 16; DB 6; Length 6;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 FXXXW 5  
Db 1 FTFAW 5  
  
RESULT 24  
ABR45878  
ID ABR45878 standard; peptide; 6 AA.  
XX  
AC ABR45878;  
XX  
DT 10-JUN-2003 (first entry)  
XX  
DE Staphylococcus aureus CHIPS-related peptide #1068.  
XX  
KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;  
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;  
KW inflammation; cardiovascular disease; central nervous system disease;  
KW gastrointestinal disease; skin disease; genitourinary disease;  
KW joint disease; respiratory disease; HIV infection; antiinflammatory;  
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;  
KW gynecological; immunosuppressive; anti-HIV.  
XX  
OS Staphylococcus aureus.  
OS Synthetic.  
XX  
PN WO2003006048-A1.  
XX  
PD 23-JAN-2003.  
XX  
PF 11-JUL-2001; 2001WO-EP008004.  
XX  
PR 11-JUL-2001; 2001WO-EP008004.  
XX  
PA (JARI-) JARI PHARM BV.  
XX  
PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;  
PI Van Strijp JAG;  
XX  
DR WPI; 2003-256333/25.  
XX  
XX Combination of peptides derived from chemotaxis inhibiting protein from  
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in  
PT prophylaxis and treatment of inflammation, cardiovascular, skin and  
PT kidney diseases.  
XX  
PS Disclosure; Page 14; 89pp; English.  
XX  
CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164  
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from  
CC Staphylococcus aureus. The peptide fragments are useful in the  
CC prophylaxis or treatment of diseases or disorders involving the C5a-  
CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,  
CC monocytes and endothelial cells or involving acute or chronic  
CC inflammation reactions. The diseases or disorders include cardiovascular  
CC diseases, disease of the central nervous system, gastrointestinal  
CC diseases, skin diseases, genitourinary diseases, joint diseases,  
CC respiratory diseases and HIV infection  
XX  
SQ Sequence 6 AA;  
  
Query Match 69.6%; Score 16; DB 6; Length 6;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Matches	2;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
Qy	1	FXXW 5							
Db	1	FTFAW 5							
RESULT 25									
ABR46661									
ID	ABR46661 standard; peptide; 6 AA.								
XX									
AC	ABR46661;								
XX									
DT	10-JUN-2003 (first entry)								
XX									
DE	Staphylococcus aureus CHIPS-related peptide #1851.								
XX									
KW	CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR; formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell; inflammation; cardiovascular disease; central nervous system disease; gastrointestinal disease; skin disease; genitourinary disease; joint disease; respiratory disease; HIV infection; antiinflammatory; cardiant; cerebroprotective; neuroprotective; nootropic; dermatological; gynecological; immunosuppressive; anti-HIV.								
XX									
OS	Staphylococcus aureus.								
OS	Synthetic.								
XX									
PN	WO2003006048-A1.								
XX									
PD	23-JAN-2003.								
XX									
PF	11-JUL-2001; 2001WO-EP008004.								
XX									
PR	11-JUL-2001; 2001WO-EP008004.								
XX									
PA	(JARI-) JARI PHARM BV.								
XX									
PI	Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;								
PI	Van Strijp JAG;								
XX									
DR	WPI; 2003-256333/25.								
XX									
PT	Combination of peptides derived from chemotaxis inhibiting protein from Staphylococcus aureus (CHIPS) having CHIPS activity, useful in prophylaxis and treatment of inflammation, cardiovascular, skin and kidney diseases.								
XX									
PS	Disclosure; Page 17; 89pp; English.								
XX									
CC	The present invention relates to peptides (ABR44811-ABR47162 and ABR47164 -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from Staphylococcus aureus. The peptide fragments are useful in the prophylaxis or treatment of diseases or disorders involving the C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial cells or involving acute or chronic inflammation reactions. The diseases or disorders include cardiovascular diseases, disease of the central nervous system, gastrointestinal diseases, skin diseases, genitourinary diseases, joint diseases, respiratory diseases and HIV infection								
XX									
SQ	Sequence 6 AA;								
Query Match 69.6%; Score 16; DB 6; Length 6;									
Best Local Similarity 40.0%; Pred. No. 1.8e+06;									
Matches	2;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
Qy	1	FXXW 5							
Db	1	FSFAW 5							
RESULT 26									

ABR47053						
ID	ABR47053 standard; peptide; 6 AA.					
XX						
AC	ABR47053;					
XX						
DT	10-JUN-2003 (first entry)					
XX						
DE	Staphylococcus aureus CHIPS-related peptide #2243.					
XX						
KW	CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR; formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell; inflammation; cardiovascular disease; central nervous system disease; gastrointestinal disease; skin disease; genitourinary disease; joint disease; respiratory disease; HIV infection; antiinflammatory; cardiant; cerebroprotective; neuroprotective; nootropic; dermatological; gynecological; immunosuppressive; anti-HIV.					
XX						
OS	Staphylococcus aureus.					
OS	Synthetic.					
XX						
PN	WO2003006048-A1.					
XX						
PD	23-JAN-2003.					
XX						
PF	11-JUL-2001; 2001WO-EP008004.					
XX						
PR	11-JUL-2001; 2001WO-EP008004.					
XX						
PA	(JARI-) JARI PHARM BV.					
XX						
PI	Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;					
PI	Van Strijp JAG;					
XX						
DR	WPI; 2003-256333/25.					
XX						
PT	Combination of peptides derived from chemotaxis inhibiting protein from Staphylococcus aureus (CHIPS) having CHIPS activity, useful in prophylaxis and treatment of inflammation, cardiovascular, skin and kidney diseases.					
PT						
PT						
PT						
XX						
PS	Disclosure; Page 19; 89pp; English.					
XX						
CC	The present invention relates to peptides (ABR44811-ABR47162 and ABR47164 -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from Staphylococcus aureus. The peptide fragments are useful in the prophylaxis or treatment of diseases or disorders involving the C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial cells or involving acute or chronic inflammation reactions. The diseases or disorders include cardiovascular diseases, disease of the central nervous system, gastrointestinal diseases, skin diseases, genitourinary diseases, joint diseases, respiratory diseases and HIV infection					
XX						
SQ	Sequence 6 AA;					
Query Match 69.6%; Score 16; DB 6; Length 6;						
Best Local Similarity 40.0%; Pred. No. 1.8e+06;						
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;						
Qy	1 FXXXW 5					
Db	1 FSFAW 5					
RESULT 27						
ABR45190						
ID	ABR45190 standard; peptide; 6 AA.					
XX						
AC	ABR45190;					
XX						
DT	10-JUN-2003 (first entry)					
XX						
DE	Staphylococcus aureus CHIPS-related peptide #380.					

XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;  
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;  
KW inflammation; cardiovascular disease; central nervous system disease;  
KW gastrointestinal disease; skin disease; genitourinary disease;  
KW joint disease; respiratory disease; HIV infection; antiinflammatory;  
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;  
KW gynecological; immunosuppressive; anti-HIV.  
XX  
OS Staphylococcus aureus.  
OS Synthetic.  
XX  
PN WO2003006048-A1.  
XX  
PD 23-JAN-2003.  
XX  
PF 11-JUL-2001; 2001WO-EP008004.  
XX  
PR 11-JUL-2001; 2001WO-EP008004.  
XX  
PA (JARI-) JARI PHARM BV.  
XX  
PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;  
PI Van Strijp JAG;  
XX  
DR WPI; 2003-256333/25.  
XX  
XX Combination of peptides derived from chemotaxis inhibiting protein from  
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in  
PT prophylaxis and treatment of inflammation, cardiovascular, skin and  
PT kidney diseases.  
XX  
PS Disclosure; Page 12; 89pp; English.  
XX  
XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164  
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from  
CC Staphylococcus aureus. The peptide fragments are useful in the  
CC prophylaxis or treatment of diseases or disorders involving the C5a-  
CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,  
CC monocytes and endothelial cells or involving acute or chronic  
CC inflammation reactions. The diseases or disorders include cardiovascular  
CC diseases, disease of the central nervous system, gastrointestinal  
CC diseases, skin diseases, genitourinary diseases, joint diseases,  
CC respiratory diseases and HIV infection  
XX  
SQ Sequence 6 AA;  
Query Match 69.6%; Score 16; DB 6; Length 6;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 FXXHW 5  
Db 1 FTFSW 5  
RESULT 28  
ABR45877  
ID ABR45877 standard; peptide; 6 AA.  
XX  
AC ABR45877;  
XX  
DT 10-JUN-2003 (first entry)  
XX  
DE Staphylococcus aureus CHIPS-related peptide #1067.  
XX  
KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;  
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;  
KW inflammation; cardiovascular disease; central nervous system disease;  
KW gastrointestinal disease; skin disease; genitourinary disease;  
KW joint disease; respiratory disease; HIV infection; antiinflammatory;  
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;  
KW gynecological; immunosuppressive; anti-HIV.

XX Staphylococcus aureus.  
OS Synthetic.  
XX  
PN WO2003006048-A1.  
XX  
PD 23-JAN-2003.  
XX  
PF 11-JUL-2001; 2001WO-EP008004.  
XX  
PR 11-JUL-2001; 2001WO-EP008004.  
XX  
PA (JARI-) JARI PHARM BV.  
XX  
PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;  
PI Van Strijp JAG;  
XX  
DR WPI; 2003-256333/25.  
XX  
XX Combination of peptides derived from chemotaxis inhibiting protein from  
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in  
PT prophylaxis and treatment of inflammation, cardiovascular, skin and  
PT kidney diseases.  
XX  
PS Disclosure; Page 14; 89pp; English.  
XX  
XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164  
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from  
CC Staphylococcus aureus. The peptide fragments are useful in the  
CC prophylaxis or treatment of diseases or disorders involving the C5a-  
CC receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,  
CC monocytes and endothelial cells or involving acute or chronic  
CC inflammation reactions. The diseases or disorders include cardiovascular  
CC diseases, disease of the central nervous system, gastrointestinal  
CC diseases, skin diseases, genitourinary diseases, joint diseases,  
CC respiratory diseases and HIV infection  
XX  
SQ Sequence 6 AA;  
Query Match 69.6%; Score 16; DB 6; Length 6;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 FXXHW 5  
Db 1 FSPAW 5  
RESULT 29  
ABR46310  
ID ABR46310 standard; peptide; 6 AA.  
XX  
AC ABR46310;  
XX  
DT 10-JUN-2003 (first entry)  
XX  
DE Staphylococcus aureus CHIPS-related peptide #1500.  
XX  
KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;  
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;  
KW inflammation; cardiovascular disease; central nervous system disease;  
KW gastrointestinal disease; skin disease; genitourinary disease;  
KW joint disease; respiratory disease; HIV infection; antiinflammatory;  
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;  
KW gynecological; immunosuppressive; anti-HIV.  
XX  
OS Staphylococcus aureus.  
OS Synthetic.  
XX  
PN WO2003006048-A1.  
XX  
PD 23-JAN-2003.  
XX









Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5  
|  
Db 1 FSFSW 5

RESULT 34  
ABR45918  
ID ABR45918 standard; peptide; 6 AA.  
XX  
AC ABR45918;  
XX  
DT 10-JUN-2003 (first entry)  
XX  
DE Staphylococcus aureus CHIPS-related peptide #1108.  
XX

KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;  
KW formulated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;  
KW inflammation; cardiovascular disease; central nervous system disease;  
KW gastrointestinal disease; skin disease; genitourinary disease;  
KW joint disease; respiratory disease; HIV infection; antiinflammatory;  
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;  
KW gynecological; immunosuppressive; anti-HIV.  
XX

OS Staphylococcus aureus.  
OS Synthetic.

XX WO2003006048-A1.

XX 23-JAN-2003.

XX 11-JUL-2001; 2001WO-EP008004.

XX 11-JUL-2001; 2001WO-EP008004.

XX (JARI-) JARI PHARM BV.

PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;  
PI Van Strijp JAG;

XX WPI; 2003-256333/25.

XX Combination of peptides derived from chemotaxis inhibiting protein from  
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in  
PT prophylaxis and treatment of inflammation, cardiovascular, skin and  
PT kidney diseases.

PS Disclosure; Page 14; 89pp; English.

XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164  
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from  
CC Staphylococcus aureus. The peptide fragments are useful in the  
CC prophylaxis or treatment of diseases or disorders involving the C5a-  
CC receptor (C5aR) and/or formulated peptide receptor (FPR) or neutrophils,  
CC monocytes and endothelial cells or involving acute or chronic  
CC inflammation reactions. The diseases or disorders include cardiovascular  
CC diseases, disease of the central nervous system, gastrointestinal  
CC diseases, skin diseases, genitourinary diseases, joint diseases,  
CC respiratory diseases and HIV infection

XX Sequence 6 AA;

Query Match 69.6%; Score 16; DB 6; Length 6;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5  
|  
Db 1 FTFSW 5

RESULT 35  
ABR45189  
ID ABR45189 standard; peptide; 6 AA.  
XX

AC ABR45189;

XX 10-JUN-2003 (first entry)

XX Staphylococcus aureus CHIPS-related peptide #379.

DE  
XX  
KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;  
KW formulated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;  
KW inflammation; cardiovascular disease; central nervous system disease;  
KW gastrointestinal disease; skin disease; genitourinary disease;  
KW joint disease; respiratory disease; HIV infection; antiinflammatory;  
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;  
KW gynecological; immunosuppressive; anti-HIV.  
XX

OS Staphylococcus aureus.

OS Synthetic.

XX WO2003006048-A1.

XX 23-JAN-2003.

XX 11-JUL-2001; 2001WO-EP008004.

XX 11-JUL-2001; 2001WO-EP008004.

XX (JARI-) JARI PHARM BV.

PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;  
PI Van Strijp JAG;

XX WPI; 2003-256333/25.

XX Combination of peptides derived from chemotaxis inhibiting protein from  
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in  
PT prophylaxis and treatment of inflammation, cardiovascular, skin and  
PT kidney diseases.

PS Disclosure; Page 12; 89pp; English.

XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164  
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from  
CC Staphylococcus aureus. The peptide fragments are useful in the  
CC prophylaxis or treatment of diseases or disorders involving the C5a-  
CC receptor (C5aR) and/or formulated peptide receptor (FPR) or neutrophils,  
CC monocytes and endothelial cells or involving acute or chronic  
CC inflammation reactions. The diseases or disorders include cardiovascular  
CC diseases, disease of the central nervous system, gastrointestinal  
CC diseases, skin diseases, genitourinary diseases, joint diseases,  
CC respiratory diseases and HIV infection

XX Sequence 6 AA;

Query Match 69.6%; Score 16; DB 6; Length 6;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5  
|  
Db 1 FSFSW 5

RESULT 36  
ABR45485  
ID ABR45485 standard; peptide; 6 AA.  
XX

AC ABR45485;

XX 10-JUN-2003 (first entry)

XX

DE Staphylococcus aureus CHIPS-related peptide #675.  
XX  
KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;  
formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;  
inflammation; cardiovascular disease; central nervous system disease;  
gastrointestinal disease; skin disease; genitourinary disease;  
joint disease; respiratory disease; HIV infection; antiinflammatory;  
cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;  
gynecological; immunosuppressive; anti-HIV.  
XX  
OS Staphylococcus aureus.  
Synthetic.  
XX  
PN WO2003006048-A1.  
XX  
PD 23-JAN-2003.  
XX  
PF 11-JUL-2001; 2001WO-EP008004.  
XX  
PR 11-JUL-2001; 2001WO-EP008004.  
XX  
PA (JARI-) JARI PHARM BV.  
XX  
PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;  
PI Van Strijp JAG;  
XX  
DR WPI; 2003-256333/25.  
XX  
PT Combination of peptides derived from chemotaxis inhibiting protein from  
Staphylococcus aureus (CHIPS) having CHIPS activity, useful in  
prophylaxis and treatment of inflammation, cardiovascular, skin and  
kidney diseases.  
XX  
PS Disclosure; Page 13; 89pp; English.  
XX  
CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164  
-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from  
Staphylococcus aureus. The peptide fragments are useful in the  
prophylaxis or treatment of diseases or disorders involving the C5a-  
receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,  
monocytes and endothelial cells or involving acute or chronic  
inflammation reactions. The diseases or disorders include cardiovascular  
diseases, skin diseases, genitourinary diseases, joint diseases,  
respiratory diseases and HIV infection  
XX  
SQ Sequence 6 AA;  
Query Match 69.6%; Score 16; DB 6; Length 6;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 FXXXW 5  
|  
Db 1 FSFAW 5  
RESULT 37  
ABR45150  
ID ABR45150 standard; peptide; 6 AA.  
XX  
AC ABR45150;  
XX  
DT 10-JUN-2003 (first entry)  
XX  
DE Staphylococcus aureus CHIPS-related peptide #340.  
XX  
KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;  
formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;  
inflammation; cardiovascular disease; central nervous system disease;  
gastrointestinal disease; skin disease; genitourinary disease;  
joint disease; respiratory disease; HIV infection; antiinflammatory;  
cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;  
gynecological; immunosuppressive; anti-HIV.

KW gynecological; immunosuppressive; anti-HIV.  
XX  
OS Staphylococcus aureus.  
Synthetic.  
XX  
PN WO2003006048-A1.  
XX  
PD 23-JAN-2003.  
XX  
PF 11-JUL-2001; 2001WO-EP008004.  
XX  
PR 11-JUL-2001; 2001WO-EP008004.  
XX  
PA (JARI-) JARI PHARM BV.  
XX  
PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;  
PI Van Strijp JAG;  
XX  
DR WPI; 2003-256333/25.  
XX  
PT Combination of peptides derived from chemotaxis inhibiting protein from  
Staphylococcus aureus (CHIPS) having CHIPS activity, useful in  
prophylaxis and treatment of inflammation, cardiovascular, skin and  
kidney diseases.  
XX  
PS Disclosure; Page 11; 89pp; English.  
XX  
CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164  
-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from  
Staphylococcus aureus. The peptide fragments are useful in the  
prophylaxis or treatment of diseases or disorders involving the C5a-  
receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils,  
monocytes and endothelial cells or involving acute or chronic  
inflammation reactions. The diseases or disorders include cardiovascular  
diseases, skin diseases, genitourinary diseases, joint diseases,  
respiratory diseases and HIV infection  
XX  
SQ Sequence 6 AA;  
Query Match 69.6%; Score 16; DB 6; Length 6;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 FXXXW 5  
|  
Db 1 FTFAW 5  
RESULT 38  
ABR45526  
ID ABR45526 standard; peptide; 6 AA.  
XX  
AC ABR45526;  
XX  
DT 10-JUN-2003 (first entry)  
XX  
DE Staphylococcus aureus CHIPS-related peptide #716.  
XX  
KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;  
formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;  
inflammation; cardiovascular disease; central nervous system disease;  
gastrointestinal disease; skin disease; genitourinary disease;  
joint disease; respiratory disease; HIV infection; antiinflammatory;  
cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;  
gynecological; immunosuppressive; anti-HIV.  
XX  
OS Staphylococcus aureus.  
Synthetic.  
XX  
PN WO2003006048-A1.  
XX  
PD 23-JAN-2003.

```
XX 11-JUL-2001; 2001WO-EP008004.
XX
XX
PR 11-JUL-2001; 2001WO-EP008004.
XX
XX (JARI-) JARI PHARM BV.
XX
PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
PI Van Strijp JAG;
XX
XX WPI; 2003-256333/25.
XX
XX Combination of peptides derived from chemotaxis inhibiting protein from
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
PT prophylaxis and treatment of inflammation, cardiovascular, skin and
PT kidney diseases.
XX
XX Disclosure; Page 13; 89pp; English.
XX
XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
CC Staphylococcus aureus. The peptide fragments are useful in the
CC prophylaxis or treatment of diseases or disorders involving the C5a-
CC receptor (C5aR) and/or formulated peptide receptor (FPR) or neutrophils,
CC monocytes and endothelial cells or involving acute or chronic
CC inflammation reactions. The diseases or disorders include cardiovascular
CC diseases, disease of the central nervous system, gastrointestinal
CC diseases, skin diseases, genitourinary diseases, joint diseases,
CC respiratory diseases and HIV infection
XX
XX Sequence 6 AA;
XX
XX Query Match 69.6%; Score 16; DB 6; Length 6;
XX Best Local Similarity 40.0%; Pred. No. 1.8e+06;
XX Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1 FXXXW 5
Db 1 FTFSW 5
XX
XX
RESULT 39
ABR46269
ID ABR46269 standard; peptide; 6 AA.
XX
XX ABR46269;
AC
XX
XX 10-JUN-2003 (first entry)
DT
XX
XX Staphylococcus aureus CHIPS-related peptide #1459.
DE
XX
XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
KW formulated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
KW inflammation; cardiovascular disease; central nervous system disease;
KW gastrointestinal disease; skin disease; genitourinary disease;
KW joint disease; respiratory disease; HIV infection; antiinflammatory;
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
KW gynecological; immunosuppressive; anti-HIV.
XX
XX Staphylococcus aureus.
OS
XX Synthetic.
OS
XX WO2003006048-A1.
PN
XX
XX 23-JAN-2003.
PD
XX
XX 11-JUL-2001; 2001WO-EP008004.
PF
XX
XX 11-JUL-2001; 2001WO-EP008004.
PR
XX (JARI-) JARI PHARM BV.
PA
XX
XX Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
PI Van Strijp JAG;
XX
XX WPI; 2003-256333/25.
XX
XX Combination of peptides derived from chemotaxis inhibiting protein from
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
PT prophylaxis and treatment of inflammation, cardiovascular, skin and
PT kidney diseases.
XX
XX
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```
PI Van Strijp JAG;
XX
XX WPI; 2003-256333/25.
XX
XX Combination of peptides derived from chemotaxis inhibiting protein from
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
PT prophylaxis and treatment of inflammation, cardiovascular, skin and
PT kidney diseases.
XX
XX Disclosure; Page 16; 89pp; English.
XX
XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
CC Staphylococcus aureus. The peptide fragments are useful in the
CC prophylaxis or treatment of diseases or disorders involving the C5a-
CC receptor (C5aR) and/or formulated peptide receptor (FPR) or neutrophils,
CC monocytes and endothelial cells or involving acute or chronic
CC inflammation reactions. The diseases or disorders include cardiovascular
CC diseases, disease of the central nervous system, gastrointestinal
CC diseases, skin diseases, genitourinary diseases, joint diseases,
CC respiratory diseases and HIV infection
XX
XX Sequence 6 AA;
XX
XX Query Match 69.6%; Score 16; DB 6; Length 6;
XX Best Local Similarity 40.0%; Pred. No. 1.8e+06;
XX Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1 FXXXW 5
Db 1 FSFAW 5
XX
XX
RESULT 40
ABR46662
ID ABR46662 standard; peptide; 6 AA.
XX
XX ABR46662;
AC
XX
XX 10-JUN-2003 (first entry)
DT
XX
XX Staphylococcus aureus CHIPS-related peptide #1852.
DE
XX
XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
KW formulated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
KW inflammation; cardiovascular disease; central nervous system disease;
KW gastrointestinal disease; skin disease; genitourinary disease;
KW joint disease; respiratory disease; HIV infection; antiinflammatory;
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
KW gynecological; immunosuppressive; anti-HIV.
XX
XX Staphylococcus aureus.
OS
XX Synthetic.
OS
XX WO2003006048-A1.
PN
XX
XX 23-JAN-2003.
PD
XX
XX 11-JUL-2001; 2001WO-EP008004.
PF
XX
XX 11-JUL-2001; 2001WO-EP008004.
PR
XX (JARI-) JARI PHARM BV.
PA
XX
XX Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
PI Van Strijp JAG;
XX
XX WPI; 2003-256333/25.
XX
XX Combination of peptides derived from chemotaxis inhibiting protein from
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
PT prophylaxis and treatment of inflammation, cardiovascular, skin and
PT kidney diseases.
XX
XX
```

XX Disclosure; Page 17; 89pp; English.  
PS  
XX  
CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164  
CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from  
CC Staphylococcus aureus. The peptide fragments are useful in the  
CC prophylaxis or treatment of diseases or disorders involving the C5a-  
CC receptor (C5ar) and/or formylated peptide receptor (FPR) or neutrophils,  
CC monocytes and endothelial cells or involving acute or chronic  
CC inflammation reactions. The diseases or disorders include cardiovascular  
CC diseases, disease of the central nervous system, gastrointestinal  
CC diseases, skin diseases, genitourinary diseases, joint diseases,  
CC respiratory diseases and HIV infection  
XX  
SQ Sequence 6 AA;

Query Match 69.6%; Score 16; DB 6; Length 6;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
| |  
Db 1 FTFW 5

Search completed: October 18, 2005, 15:54:56  
Job time : 135.176 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 18, 2005, 15:18:31 ; Search time 23.0588 Seconds  
(without alignments)  
33.381 Million cell updates/sec

Title: US-09-214-371-10  
Perfect score: 23  
Sequence: 1 FXXXWXXX 8

Scoring table: BLOSUM62  
Gapop 10.0 ; Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	73.9	9	2	A24244 adipokinetic hormo
2	17	73.9	53	2	T00172 hypothetical prote
3	17	73.9	53	2	D89989 hypothetical prote
4	17	73.9	63	2	T29202 hypothetical prote
5	17	73.9	65	1	A32613 adipokinetic hormo
6	17	73.9	67	2	T12860 hypothetical prote
7	17	73.9	70	2	A86942 hypothetical prote
8	17	73.9	72	2	S15137 thioredoxin h2 - s
9	17	73.9	77	2	S18581 pufQ protein - Rho
10	17	73.9	77	2	T50756 pufQ protein [impo
11	17	73.9	84	2	E69268 hypothetical prote
12	17	73.9	88	2	B46264 thioredoxin 2 - sl
13	17	73.9	98	2	F47624 Ig heavy chain V-I
14	17	73.9	99	2	S37444 gene E2 protein -
15	17	73.9	99	2	S37441 gene E2 protein -
16	17	73.9	99	2	S37448 gene E2 protein -
17	17	73.9	99	2	S37442 gene E2 protein -
18	17	73.9	102	2	G71043 GTP-binding protei
19	17	73.9	102	2	B56956 thioredoxin - rabb
20	17	73.9	104	1	A28086 thioredoxin - chic
21	17	73.9	105	1	A30006 thioredoxin [valid
22	17	73.9	105	1	JH0568 thioredoxin - rhes
23	17	73.9	105	1	JS0667 thioredoxin - mous
24	17	73.9	105	1	S04107 thioredoxin - rat
25	17	73.9	105	1	S04352 thioredoxin [impor
26	17	73.9	107	2	T33843 Ig heavy chain V r
27	17	73.9	108	2	AH2101
28	17	73.9	112	2	PH0980
29	17	73.9			

30	17	73.9	112	2	AF2549	hypothetical prote
31	17	73.9	113	1	S57775	thioredoxin h, cyt
32	17	73.9	114	1	JQ2242	thioredoxin h - Ar
33	17	73.9	115	1	G3HUN	Ig heavy chain V-I
34	17	73.9	115	2	PL0238	Ig heavy chain V r
35	17	73.9	115	2	G72642	probable surface p
36	17	73.9	116	2	T10739	thioredoxin - comm
37	17	73.9	117	2	PL0237	Ig heavy chain V r
38	17	73.9	117	2	PL0234	Ig heavy chain V r
39	17	73.9	117	2	PL0235	Ig heavy chain V r
40	17	73.9	118	1	S34812	thioredoxin h2 - c
41	17	73.9	118	2	S58118	thioredoxin (clone
42	17	73.9	118	2	S58120	thioredoxin (clone
43	17	73.9	118	2	T10170	thioredoxin - cast
44	17	73.9	118	2	PL0231	Ig heavy chain V r
45	17	73.9	118	2	F82424	diacylglycerol kin
46	17	73.9	119	2	T08142	thioredoxin h homo
47	17	73.9	119	2	D86330	F6F9.21 protein -
48	17	73.9	119	2	T50867	thioredoxin-like p
49	17	73.9	119	2	A24672	Ig heavy chain pre
50	17	73.9	119	2	B72526	hypothetical prote
51	17	73.9	122	2	T04090	probable thioredox
52	17	73.9	123	2	S34009	Ig heavy chain V r
53	17	73.9	125	2	T50866	probable thioredox
54	17	73.9	125	2	S58119	thioredoxin (clone
55	17	73.9	126	1	S16590	thioredoxin h1 - c
56	17	73.9	131	2	T50862	thioredoxin-like p
57	17	73.9	131	2	T50863	thioredoxin-like p
58	17	73.9	131	2	T50864	thioredoxin-like p
59	17	73.9	131	2	T50865	thioredoxin-like p
60	17	73.9	133	2	S58123	thioredoxin (clone
61	17	73.9	136	2	AI0124	probable prepilin
62	17	73.9	138	2	S03526	Ig heavy chain pre
63	17	73.9	141	2	T17760	hypothetical prote
64	17	73.9	141	2	S50690	hypothetical prote
65	17	73.9	141	2	C95330	probable nucleotid
66	17	73.9	142	2	I47190	Ig heavy chain var
67	17	73.9	144	2	A36324	growth arrest-spec
68	17	73.9	146	2	AI1809	hypothetical prote
69	17	73.9	147	2	F87432	hypothetical prote
70	17	73.9	149	2	T23939	hypothetical prote
71	17	73.9	150	2	D69100	probable protein d
72	17	73.9	152	2	F72702	hypothetical prote
73	17	73.9	156	2	T48047	hypothetical prote
74	17	73.9	158	2	S74730	hypothetical prote
75	17	73.9	160	2	A53293	flm3-region hypoth
76	17	73.9	160	2	S76328	hypothetical prote
77	17	73.9	161	2	AC0966	probable PTS syste
78	17	73.9	174	2	S73301	hypothetical prote
79	17	73.9	174	2	T02276	hypothetical prote
80	17	73.9	174	2	T29491	hypothetical prote
81	17	73.9	180	2	G70028	conserved hypotet
82	17	73.9	180	2	T51724	phosphotransferase
83	17	73.9	182	2	T17625	hypothetical prote
84	17	73.9	182	2	S53822	fucoxanthin chloro
85	17	73.9	183	2	T38917	hypothetical prote
86	17	73.9	189	2	T51064	hypothetical prote
87	17	73.9	191	2	S76398	hypothetical prote
88	17	73.9	194	2	T00482	probable thioredox
89	17	73.9	201	2	AC3593	probable integral
90	17	73.9	204	2	B82410	conserved hypotet
91	17	73.9	205	2	S75300	hypothetical prote
92	17	73.9	206	2	E83515	conserved hypotet
93	17	73.9	207	2	AC0006	probable membrane
94	17	73.9	207	2	T46415	hypothetical prote
95	17	73.9	208	1	D71802	hypothetical prote
96	17	73.9	208	1	G64715	conserved hypotet
97	17	73.9	211	2	S53824	fucoxanthin chloro
98	17	73.9	212	2	B47698	hemagglutinin hag2
99	17	73.9	216	2	S53821	fucoxanthin chloro
100	17	73.9	217	2	C70629	probable mutT3 pro

ALIGNMENTS

RESULT 1  
A24244  
adipokinet hormone - bollworm  
N;Alternate names: Hex-AKH  
C;Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)  
C;Date: 31-Mar-1988 #sequence\_revision 23-Mar-1995 #text\_change 09-Jul-2004  
C;Accession: A24244  
R;Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway  
Biochem. Biophys. Res. Commun. 135, 622-628, 1986  
A;Title: Isolation and primary structure of a peptide from the corpora cardiaca of Helio  
A;Reference number: A24244; MUID:86186794; PMID:3964263  
A;Accession: A24244  
A;Molecule type: protein  
A;Residues: 1-9 <JAF>  
A;Cross-references: UNIPROT:P08901  
C;Superfamily: adipokinet hormone  
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 73.9%; Score 17; DB 2; Length 9;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5  
| |  
Db 4 FTSSW 8

RESULT 2  
T00172  
hypothetical protein 38 - Staphylococcus aureus phage phi PVL  
C;Species: Staphylococcus aureus phage phi PVL  
C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C;Accession: T00172  
R;Kaneko, J.; Kimura, T.; Kawakami, Y.; Tomita, T.; Kamio, Y.  
Biosci. Biotechnol. Biochem. 61, 1960-1962, 1997  
A;Title: Pantone-Valentine leukocidin genes in a phage-like particle isolated from mitomy  
A;Reference number: Z14119; MUID:98067870; PMID:9404084  
A;Accession: T00172  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-53 <KAN>  
A;Cross-references: UNIPROT:O80077; EMBL:AB009866; NID:d1204727; PIDN:BAA31912.1; PID:d1

Query Match 73.9%; Score 17; DB 2; Length 53;  
Best Local Similarity 40.0%; Pred. No. 1.3e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5  
| |  
Db 28 FTTAW 32

RESULT 3  
D89989  
hypothetical protein SAS063 [imported] - Staphylococcus aureus (strain N315)  
C;Species: Staphylococcus aureus  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C;Accession: D89989  
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc  
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;  
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
Lancet 357, 1225-1240, 2001  
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.  
A;Reference number: A89758; MUID:21311952; PMID:11418146  
A;Accession: D89989  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-53 <KUR>

A;Cross-references: UNIPROT:Q99SQ2; GB:BA000018; PID:g13701784; PIDN:BAB43077.1; GSPDB:GN  
A;Experimental source: strain N315  
C;Genetics:  
A;Gene: SAS063

Query Match 73.9%; Score 17; DB 2; Length 53;  
Best Local Similarity 40.0%; Pred. No. 1.3e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5  
| |  
Db 28 FTTAW 32

RESULT 4  
T29202  
hypothetical protein F28F9.3 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T29202  
R;Nelson, J.; Wohldmann, P.  
submitted to the EMBL Data Library, September 1996  
A;Description: The sequence of C. elegans cosmid F28F9.  
A;Reference number: Z20587  
A;Accession: T29202  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-63 <NEL>  
A;Cross-references: UNIPROT:Q94194; EMBL:U70850; PIDN:AAB09124.1; GSPDB:GN00022; CBSP:F28  
A;Experimental source: strain Bristol N2; clone F28F9  
C;Genetics:  
A;Gene: CBSP:F28F9.3  
A;Map position: 4  
A;Introns: 38/1

Query Match 73.9%; Score 17; DB 2; Length 63;  
Best Local Similarity 40.0%; Pred. No. 1.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5  
| |  
Db 30 FATAW 34

RESULT 5  
A32613  
adipokinet hormone precursor - tobacco hornworm  
C;Species: Manduca sexta (tobacco hornworm)  
C;Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 09-Jul-2004  
C;Accession: A32613  
R;Bradfield, J.Y.; Keeley, L.L.  
J. Biol. Chem. 264, 12791-12793, 1989.  
A;Title: Adipokinet hormone gene sequence from Manduca sexta.  
A;Reference number: A32613; MUID:89327232; PMID:2753887  
A;Accession: A32613  
A;Molecule type: DNA  
A;Residues: 1-65 <BRA>  
A;Cross-references: UNIPROT:P08901; GB:J04972; NID:g159478; PIDN:AAA29299.1; PID:g159479  
C;Genetics:  
A;Introns: #status absent  
C;Superfamily: adipokinet hormone  
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-28/Product: adipokinet hormone #status predicted <MAT>  
F;20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted  
F;28/Modified site: amidated carboxyl end (Gly) (amide in mature form from following gly

Query Match 73.9%; Score 17; DB 1; Length 65;  
Best Local Similarity 40.0%; Pred. No. 1.5e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5  
| |



Db 23 FTSSW 27

RESULT 6

T12860

hypothetical protein yopZ - Bacillus subtilis phage SPBc2

C;Species: Bacillus subtilis phage SPBc2

C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004

C;Accession: T12860; H69918

R;Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Mael, C.; Karamata, D.

submitted to the EMBL Data Library, August 1997

A;Description: The complete nucleotide sequence of the Bacillus subtilis SPbetac2 prophage

A;Reference number: Z17583

A;Accession: T12860

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-67 <LAZ>

A;Cross-references: UNIPROT:O64109; EMBL:AF020713; NID:g3025478; PIDN:AAC1

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertet

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: H69918

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-67 <KUN>

A;Cross-references: GB:Z99114; GB:Z99115; GB:AL009126; NID:g2634478; PIDN:CAB13989.1; PI

A;Experimental source: strain 168

C;Genetics:

A;Gene: yopZ

Query Match 73.9%; Score 17; DB 2; Length 67;

Best Local Similarity 40.0%; Pred. No. 1.5e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db 49 FASSW 53

RESULT 7

A86942

hypothetical protein [imported] - Mycobacterium leprae

C;Species: Mycobacterium leprae

C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004

C;Accession: A86942

R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho

R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,

eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq

A;Title: Massive gene decay in the leprosy bacillus.

A;Reference number: A86909; MUID:21128732; PMID:11234002

A;Accession: A86942

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-70 <STO>

A;Cross-references: UNIPROT:O69587; GB:AL450380; NID:g13092599; PIDN:CAC29773.1; GSPDB:G

C;Genetics:

A;Gene: ML0265

Query Match 73.9%; Score 17; DB 2; Length 77;

Best Local Similarity 40.0%; Pred. No. 1.7e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db 60 FASAW 64

RESULT 8

S15137

thioredoxin h2 - spinach (fragments)

C;Species: Spinacia oleracea (spinach)

C;Date: 25-Feb-1994 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004

C;Accession: S15137

R;Marcus, F.; Chamberlain, S.H.; Chu, C.; Masiarz, F.R.; Shin, S.; Yee, B.C.; Buchanan,

Arch. Biochem. Biophys. 287, 195-198, 1991

A;Title: Plant thioredoxin h: an animal-like thioredoxin occurring in multiple cell comp

A;Reference number: S15137; MUID:91378382; PMID:1897989

A;Accession: S15137

A;Molecule type: protein

A;Residues: 1-72 <MAR>

A;Cross-references: UNIPROT:Q9S881

C;Superfamily: thioredoxin; thioredoxin homology

C;Keywords: redox-active disulfide

Query Match 73.9%; Score 17; DB 2; Length 72;

Best Local Similarity 40.0%; Pred. No. 1.6e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db 6 FTASW 10

RESULT 9

S18581

pufQ protein - Rhodobacter sphaeroides

C;Species: Rhodobacter sphaeroides

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004

C;Accession: S18581; S32854

R;Hunter, C.N.; McGlynn, P.; Ashby, M.K.; Burgess, J.G.; Olsen, J.D.

Mol. Microbiol. 5, 2649-2661, 1991

A;Title: DNA sequencing and complementation/deletion analysis of the bchA-puf operon reg

A;Reference number: S18580; MUID:92140030; PMID:1779756

A;Accession: S18581

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-77 <HUN>

A;Cross-references: UNIPROT:P16069; EMBL:X68795; NID:g49170; PID:g49175

C;Genetics:

A;Gene: pufQ

C;Superfamily: pufQ protein

Query Match 73.9%; Score 17; DB 2; Length 77;

Best Local Similarity 40.0%; Pred. No. 1.7e+03;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db 60 FASAW 64

RESULT 10

T50756

pufQ protein [imported] - Rhodobacter sphaeroides

C;Species: Rhodobacter sphaeroides

C;Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 09-Jul-2004

C;Accession: T50756

R;Choudhary, M.; Kaplan, S.

Nucleic Acids Res. 28, 862-867, 2000

A;Title: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides 2

A;Reference number: Z25222; MUID:20115911; PMID:10648776

A;Accession: T50756  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-77 <CHO>  
A;Cross-references: UNIPROT:P16069; EMBL:AF195122; PIDN:AAF24300.1  
A;Experimental source: strain 2.4.1  
C;Genetics:  
A;Gene: pufQ  
C;Superfamily: pufQ protein

Query Match 73.9%; Score 17; DB 2; Length 77;  
Best Local Similarity 40.0%; Pred. No. 1.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
DB 60 FSAW 64

RESULT 11  
E69268  
hypothetical protein AF0149 - Archaeoglobus fulgidus  
C;Species: Archaeoglobus fulgidus  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C;Accession: E69268  
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F.  
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo  
A;Reference number: A69250; MUID:98049343; PMID:9389475  
A;Accession: E69268  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-84 <KLE>  
A;Cross-references: UNIPROT:O30088; GB:AE001096; NID:g2689419; PIDN:AAB9108

Query Match 73.9%; Score 17; DB 2; Length 84;  
Best Local Similarity 40.0%; Pred. No. 1.8e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
DB 42 FAAW 46

RESULT 12  
B46264  
thioredoxin 2 - slime mold (Dictyostelium discoideum) (fragment)  
C;Species: Dictyostelium discoideum  
C;Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 16-Aug-2004  
C;Accession: B46264  
R;Wetterauer, B.; Jacquot, J.P.; Veron, M.  
J. Biol. Chem. 267, 9895-9904, 1992  
A;Title: Thioredoxins from Dictyostelium discoideum are a developmentally regulated mult  
A;Reference number: A46264; MUID:92250653; PMID:1577820  
A;Accession: B46264  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-88 <WET>  
A;Cross-references: UNIPROT:P29446; GB:M91382; NID:g167930; PIDN:AAA33259.1; PID:g167931  
C;Superfamily: Thioredoxin; thioredoxin homology  
F;8-88/Domain: thioredoxin homology <THR>

Query Match 73.9%; Score 17; DB 2; Length 88;  
Best Local Similarity 40.0%; Pred. No. 1.8e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
DB 26 FSAW 30

RESULT 13  
F47624

Ig heavy chain V-I region - African clawed frog (fragment)  
C;Species: Xenopus laevis (African clawed frog)  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
C;Accession: F47624  
R;Haire, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.  
J. Exp. Med. 171, 1721-1737, 1990

A;Title: Eleven distinct V-H gene families and additional patterns of sequence variation  
A;Reference number: A47624; MUID:90237760; PMID:2110243  
A;Accession: F47624  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-98 <HAI>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.9%; Score 17; DB 2; Length 98;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
DB 29 FSSTW 33

RESULT 14  
S37444

gene E2 protein - human papillomavirus type 5 (fragment)  
C;Species: human papillomavirus type 5  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S37444  
R;Deau, A.C.  
submitted to the EMBL Data Library, August 1993

A;Reference number: S37440  
A;Accession: S37444  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-99 <DEA>  
A;Cross-references: UNIPROT:Q81977; EMBL:X74648  
C;Superfamily: papillomavirus E2 protein

Query Match 73.9%; Score 17; DB 2; Length 99;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
DB 46 FSTTW 50

RESULT 15  
S37447

gene E2 protein - human papillomavirus type 5 (fragment)  
C;Species: human papillomavirus type 5  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S37447  
R;Deau, A.C.  
submitted to the EMBL Data Library, August 1993

A;Reference number: S37440  
A;Accession: S37447  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-99 <DEA>  
A;Cross-references: UNIPROT:Q81979; EMBL:X74651; NID:g404204; PIDN:CAA52715.1; PID:g4042  
C;Superfamily: papillomavirus E2 protein

Query Match 73.9%; Score 17; DB 2; Length 99;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
46 FSTTW 50  
Db

RESULT 16  
S37441  
gene E2 protein - human papillomavirus type 5 (fragment)  
C:Species: human papillomavirus type 5  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S37441  
R:Deau, A.C.  
submitted to the EMBL Data Library, August 1993  
A:Reference number: S37440  
A:Accession: S37441  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-99 <DEA>  
A:Cross-references: UNIPROT:Q81973; EMBL:X74645; NID:g404161; PIDN:CAAS2709.1; PID:g4041  
C:Superfamily: papillomavirus E2 protein

Query Match 73.9%; Score 17; DB 2; Length 99;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
46 FSTTW 50  
Db

RESULT 17  
S37448  
gene E2 protein - human papillomavirus type 5 (fragment)  
C:Species: human papillomavirus type 5  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S37448  
R:Deau, A.C.  
submitted to the EMBL Data Library, August 1993  
A:Reference number: S37440  
A:Accession: S37448  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-99 <DEA>  
A:Cross-references: UNIPROT:Q81981; EMBL:X74652  
C:Superfamily: papillomavirus E2 protein

Query Match 73.9%; Score 17; DB 2; Length 99;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
46 FSTTW 50  
Db

RESULT 18  
S37442  
gene E2 protein - human papillomavirus type 5 (fragment)  
C:Species: human papillomavirus type 5  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S37442  
R:Deau, A.C.  
submitted to the EMBL Data Library, August 1993  
A:Reference number: S37440  
A:Accession: S37442  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-99 <DEA>  
A:Cross-references: UNIPROT:Q81975; EMBL:X74646  
C:Superfamily: papillomavirus E2 protein

Query Match 73.9%; Score 17; DB 2; Length 99;

Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
46 FSTTW 50  
Db

RESULT 19  
G71043  
hypothetical protein PH1639 - Pyrococcus horikoshii  
C:Species: Pyrococcus horikoshii  
C:Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 12-Jul-2004  
C:Accession: G71043  
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin  
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi  
DNA Res. 5, 55-76, 1998  
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a  
A:Reference number: A71000; MUID:98344137; PMID:9679194  
A:Accession: G71043  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-102 <KAW>  
A:Cross-references: UNIPROT:O59305; GB:AP000006; NID:g3236133; PIDN:BAA30751.1; PID:g325  
A:Experimental source: strain OT3  
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank  
C:Genetics:  
A:Gene: PH1639

Query Match 73.9%; Score 17; DB 2; Length 102;  
Best Local Similarity 40.0%; Pred. No. 2.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
34 FASSW 38  
Db

RESULT 20  
B56956  
GTP-binding protein-associated protein (clone c) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Oct-1995 #sequence\_revision 19-Oct-1995 #text\_change 09-Jul-2004  
C:Accession: B56956  
R:Janoueix-Lerosey, I.; Jollivet, F.; Camonis, J.; Marche, P.N.; Goud, B.  
J. Biol. Chem. 270, 14801-14808, 1995  
A:Title: Two-hybrid system screen with the small GTP-binding protein Rab6. Identification  
A:Reference number: A56956; MUID:95301579; PMID:7782346  
A:Accession: B56956  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-102 <JAN>  
A:Cross-references: UNIPROT:Q62145; GB:L40934; NID:g722666; PIDN:AAA78788.1; PID:g722667

Query Match 73.9%; Score 17; DB 2; Length 102;  
Best Local Similarity 40.0%; Pred. No. 2.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
61 FASAW 65  
Db

RESULT 21  
A28086  
thioredoxin - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 30-Jun-1989 #sequence\_revision 26-May-1994 #text\_change 16-Aug-2004  
C:Accession: A28086  
R:Johnson, R.S.; Mathews, W.R.; Biemann, K.; Hopper, S.  
J. Biol. Chem. 263, 9589-9597, 1988  
A:Title: Amino acid sequence of thioredoxin isolated from rabbit bone marrow determined  
A:Reference number: A28086; MUID:88257078; PMID:3164311

A;Accession: A28086  
A;Molecule type: protein  
A;Residues: 1-104 <JOH>  
A;Cross-references: UNIPROT:P08628  
C;Superfamily: Thioredoxin; thioredoxin homology  
C;Keywords: redox-active disulfide  
F;8-91/Domain: thioredoxin homology <THR>  
F;31-34/Disulfide bonds: redox-active #status predicted

Query Match 73.9%; Score 17; DB 1; Length 104;  
Best Local Similarity 40.0%; Pred. No. 2.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5  
| |  
Db 26 FSATW 30

RESULT 22  
A30006  
thioredoxin - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 31-Mar-1989 #sequence\_revision 26-May-1994 #text\_change 16-Aug-2004  
C;Accession: A30006  
R;Jones, S.W.; Luk, K.C.  
J. Biol. Chem. 263, 9607-9611, 1988  
A;Title: Isolation of a chicken thioredoxin cDNA clone: thioredoxin mRNA is differential  
A;Reference number: A30006; MUID:88257080; PMID:2838473  
A;Accession: A30006  
A;Molecule type: mRNA  
A;Residues: 1-105 <JON>  
A;Cross-references: UNIPROT:P08629; GB:J03882; NID:G212765; PIDN:AAA49092.1; PID:G212766  
C;Superfamily: Thioredoxin; thioredoxin homology  
C;Keywords: redox-active disulfide  
F;9-92/Domain: thioredoxin homology <THR>  
F;32-35/Disulfide bonds: redox-active #status predicted

Query Match 73.9%; Score 17; DB 1; Length 105;  
Best Local Similarity 40.0%; Pred. No. 2.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5  
| |  
Db 27 FSATW 31

RESULT 23  
JH0568  
thioredoxin [validated] - human  
N;Alternate names: ATL-derived factor (ADF); eosinophil cytotoxicity-enhancing factor; b  
C;Species: Homo sapiens (man)  
C;Date: 30-Jun-1992 #sequence\_revision 26-May-1994 #text\_change 16-Aug-2004  
C;Accession: JH0568; S04106; S44375; A31993; PT0079; A60749; A38922; S53453; A60870  
R;Tonissen, K.F.; Wells, J.R.E.  
Gene 102, 221-228, 1991  
A;Title: Isolation and characterization of human thioredoxin-encoding genes.  
A;Reference number: JH0568; MUID:91340156; PMID:1874447  
A;Accession: JH0568  
A;Molecule type: DNA  
A;Residues: 1-105 <TON>  
A;Cross-references: UNIPROT:P10599; EMBL:X54539; NID:G37455; PIDN:CAA38410.1; PID:G82572  
R;Tagaya, Y.; Maeda, Y.; Mitsui, A.; Kondo, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai,  
EMBO J. 8, 757-764, 1989  
A;Title: ATL-derived factor (ADF), an IL-2 receptor/Tac inducer homologous to thioredoxi  
A;Reference number: S04106; MUID:89251607; PMID:2785919  
A;Accession: S04106  
A;Molecule type: mRNA  
A;Residues: 1-105 <TAG1>  
A;Cross-references: GB:X77584; NID:G453963; PIDN:CAA54687.1; PID:G453964  
A;Note: this sequence has been revised in reference S44375  
R;Tagaya, Y.; Maeda, Y.; Mitsui, A.; Kando, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai,  
EMBO J. 13, 2244, 1994  
A;Reference number: S44375; MUID:942444626; PMID:8187776

A;Contents: erratum  
A;Accession: S44375  
A;Molecule type: mRNA  
A;Residues: 1-105 <TAG2>  
A;Cross-references: EMBL:X77584; NID:G453963; PIDN:CAA54687.1; PID:G453964  
R;Wollman, E.E.; d'Auriol, L.; Rimsky, L.; Shaw, A.; Jacquot, J.P.; Wingfield, P.; Graber,  
J. Biol. Chem. 263, 15506-15512, 1988  
A;Title: Cloning and expression of a cDNA for human thioredoxin.  
A;Reference number: A31993; MUID:89008454; PMID:3170595  
A;Accession: A31993  
A;Molecule type: mRNA  
A;Residues: 1-38, 'N', '40-73, 'T', '75-105 <WOL>  
A;Cross-references: GB:J04026; NID:G339648; PIDN:AAA74596.1; PID:G339649  
R;Martin, H.; Dean, M.  
Biochem. Biophys. Res. Commun. 175, 123-128, 1991  
A;Title: Identification of a thioredoxin-related protein associated with plasma membranes  
A;Reference number: PT0079; MUID:91151337; PMID:1998498  
A;Accession: PT0079  
A;Molecule type: protein  
A;Residues: 2-13, 'X', '15 <MAR>  
R;Silberstein, D.S.; Ali, M.H.; Baker, S.L.; David, J.R.  
J. Immunol. 143, 979-983, 1989  
A;Title: Human eosinophil cytotoxicity-enhancing factor. Purification, physical character  
A;Reference number: A60749; MUID:89309777; PMID:2745979  
A;Accession: A60749  
A;Molecule type: protein  
A;Residues: 2-12, 'K', '14-15, 'XX', '18-19, 'X', '21-22 <SIL>  
A;Note: the abstract is inconsistent with figure 4 in having one undetermined residue aft  
R;Rimsky, L.; Wakasugi, H.; Ferrara, P.; Robin, P.; Capdevielle, J.; Tursz, T.; Fradelizi,  
J. Immunol. 136, 3304-3310, 1986  
A;Title: Purification to homogeneity and NH-2-terminal amino acid sequence of a novel int  
A;Reference number: A38922; MUID:86169684; PMID:3485686  
A;Accession: A38922  
A;Molecule type: protein  
A;Residues: 2-16 <WAK>  
R;Dean, M.F.; Martin, H.; Sansom, P.A.  
Biochem. J. 304, 861-867, 1994  
A;Title: Characterization of a thioredoxin-related surface protein.  
A;Reference number: S53453; MUID:95118305; PMID:7818492  
A;Accession: S53453  
A;Molecule type: protein  
A;Residues: 1-21;38-57 <DEA>  
A;Note: described to be a surface-associated thioredoxin  
R;Wakasugi, H.; Rimsky, L.; Mahe, Y.; Kamel, A.M.; Fradelizi, D.; Tursz, T.; Bertoglio, L  
Proc. Natl. Acad. Sci. U.S.A. 84, 804-808, 1987  
A;Title: Epstein-Barr virus-containing B-cell line produces an interleukin 1 that it uses  
A;Reference number: A60870; MUID:87118252; PMID:3027706  
A;Contents: annotation  
R;Weichsel, A.; Gasdaska, J.R.; Powis, G.; Montfort, W.R.  
submitted to the Brookhaven Protein Data Bank, February 1996  
A;Reference number: A65533; PDB:1ERT  
A;Contents: annotation; X-ray crystallography, 1.7 angstroms, reduced form, residues 1-1  
R;Weichsel, A.; Gasdaska, J.R.; Powis, G.; Montfort, W.R.  
submitted to the Brookhaven Protein Data Bank, February 1996  
A;Reference number: A65534; PDB:1ERU  
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, oxidized form, residues 1-1  
R;Forman-Kay, J.D.; Clore, G.M.; Gronenborn, A.M.  
submitted to the Brookhaven Protein Data Bank, December 1990  
A;Reference number: A50924; PDB:4TRX  
A;Contents: annotation; conformation by (1)H-NMR, residues 1-73, 'T', '75-105  
R;Forman-Kay, J.D.; Clore, G.M.; Wingfield, P.T.; Gronenborn, A.M.  
Biochemistry 30, 2685-2698, 1991  
A;Title: High-resolution three-dimensional structure of reduced recombinant human thio  
A;Reference number: A38953; MUID:91159399; PMID:2001356  
A;Contents: annotation; conformation by (1)H- and (15)N-NMR  
C;Comment: This small ubiquitous protein functions in many intracellular biological pathwa  
C;Genetics:  
A;Gene: GDB:TXN  
A;Cross-references: GDB:120475; OMIM:187700  
A;Map position: 9q31-9q31  
A;Introns: 8/3; 43/3; 63/3; 85/3  
C;Superfamily: Thioredoxin; thioredoxin homology  
C;Keywords: redox-active disulfide

F;2-105/Product: thioredoxin #status experimental <MAT>  
F;9-92/Domain: thioredoxin homology <THR>  
F;32-35/Disulfide bonds: redox-active #status experimental

Query Match 73.9%; Score 17; DB 1; Length 105;  
Best Local Similarity 40.0%; Pred. No. 2.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 27 FSATW 31

RESULT 24  
JS0667  
thioredoxin - rhesus macaque  
C;Species: Macaca mulatta (rhesus macaque)  
C;Date: 30-Jun-1992 #sequence\_revision 26-May-1994 #text\_change 16-Aug-2004  
C;Accession: JS0667  
R;An, G.; Wu, R.  
Biochem. Biophys. Res. Commun. 183, 170-175, 1992  
A;Title: Thioredoxin gene expression is transcriptionally up-regulated by retinol in monocytes  
A;Reference number: JS0667; MUID:92181438; PMID:1543487  
A;Accession: JS0667  
A;Molecule type: mRNA  
A;Residues: 1-105 <ANG>  
A;Cross-references: UNIPROT:P29451; GB:M84643; NID:G342338; PIDN:AAA36921.1; PID:G342339  
C;Superfamily: Thioredoxin; thioredoxin homology  
C;Keywords: redox-active disulfide  
F;9-92/Domain: thioredoxin homology <THR>  
F;32-35/Disulfide bonds: redox-active #status predicted

Query Match 73.9%; Score 17; DB 1; Length 105;  
Best Local Similarity 40.0%; Pred. No. 2.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 27 FSATW 31

RESULT 25  
S04107  
thioredoxin - mouse  
N;Alternate names: ATL-derived factor (ADF)  
C;Species: Mus musculus (house mouse)  
C;Date: 21-Nov-1993 #sequence\_revision 17-Oct-1997 #text\_change 16-Aug-2004  
C;Accession: JC4068; S44376; S04107  
R;Matsui, M.; Taniguchi, Y.; Hirota, K.; Taketo, M.; Yodoi, J.  
Gene 152, 165-171, 1995  
A;Title: Structure of the mouse thioredoxin-encoding gene and its processed pseudogene.  
A;Reference number: JC4068; MUID:95137382; PMID:7835695  
A;Accession: JC4068  
A;Molecule type: DNA  
A;Residues: 1-105 <MAT>  
A;Cross-references: UNIPROT:P10639; DBJ:D21855; NID:G517128  
R;Tagaya, Y.; Maeda, Y.; Mitsui, A.; Kando, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai, EMBO J. 13, 2244, 1994  
A;Reference number: S44375; MUID:94244626; PMID:8187776  
A;Contents: erratum  
A;Accession: S44376  
A;Molecule type: mRNA  
A;Residues: 1-105 <TAG1>  
A;Cross-references: EMBL:X77585; NID:G453971; PIDN:CAA54688.1; PID:G453972  
R;Tagaya, Y.; Maeda, Y.; Mitsui, A.; Kondo, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai, EMBO J. 8, 757-764, 1989  
A;Title: ATL-derived factor (ADF), an IL-2 receptor/Tac inducer homologous to thioredoxin  
A;Reference number: S04106; MUID:89251607; PMID:2785919  
A;Accession: S04107  
A;Molecule type: mRNA  
A;Residues: 1-93, 'N', '94-96, 'ALT', '100-104, 'S' <TAG2>  
A;Cross-references: GB:X77585  
C;Comment: This small ubiquitous protein functions in many intracellular biological path

C;Genetics:  
A;Gene: MGI:Txn  
A;Cross-references: MGI:36258  
A;Map position: 4:24.6  
A;Introns: 29/2; 44/1; 84/2  
C;Superfamily: Thioredoxin; thioredoxin homology  
C;Keywords: redox-active disulfide  
F;9-92/Domain: thioredoxin homology <THR>  
F;32-35/Disulfide bonds: redox-active #status predicted

Query Match 73.9%; Score 17; DB 1; Length 105;  
Best Local Similarity 40.0%; Pred. No. 2.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 27 FSATW 31

RESULT 26  
S04352  
thioredoxin - rat  
N;Alternate names: thioredoxin-related surface protein SASP  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 31-Mar-1990 #sequence\_revision 26-May-1994 #text\_change 16-Aug-2004  
C;Accession: S04352; S66372  
R;Tonissen, K.F.; Robins, A.J.; Wells, J.R.E.  
Nucleic Acids Res. 17, 3973, 1989  
A;Title: Nucleotide sequence of a cDNA encoding rat thioredoxin.  
A;Reference number: S04352; MUID:89282399; PMID:2734107  
A;Accession: S04352  
A;Molecule type: mRNA  
A;Residues: 1-105 <TON>  
A;Cross-references: UNIPROT:P11232; EMBL:X14878; NID:G57385; PIDN:CAA33019.1; PID:G57386  
R;Dean, M.F.; Martin, H.; Sansom, P.A.  
Biochem. J. 304, 861-867, 1994  
A;Title: Characterization of a thioredoxin-related surface protein.  
A;Reference number: S53453; MUID:95118305; PMID:7818492  
A;Accession: S66372  
A;Molecule type: protein  
A;Residues: 2-21 <DEA>  
A;Note: 12-Lys, 15-Gly, 16-Leu, 17-Gln, and 18-Leu were also found  
A;Note: described to be a surface-associated thioredoxin  
C;Superfamily: Thioredoxin; thioredoxin homology  
C;Keywords: redox-active disulfide  
F;2-105/Product: thioredoxin #status experimental <MAT>  
F;9-92/Domain: thioredoxin homology <THR>  
F;32-35/Disulfide bonds: redox-active #status predicted

Query Match 73.9%; Score 17; DB 1; Length 105;  
Best Local Similarity 40.0%; Pred. No. 2.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 27 FSATW 31

RESULT 27  
T33843  
hypothetical protein Y44E3A.3 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T33843  
R;Woessner, J.; Graves, T.; Keppler, D.  
submitted to the EMBL Data Library, November 1998  
A;Description: The sequence of C. elegans cosmid Y44E3A.  
A;Reference number: Z21422  
A;Accession: T33843  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-107 <WOE>  
A;Cross-references: UNIPROT:Q9TXY8; EMBL:AF106589; PIDN:AAC78230.1; GSPDB:GN00019; CESP:

A;Experimental source: strain Bristol N2; clone Y44E3A

C;Genetics:

A;Gene: CESP:Y44E3A.3

A;Map position: 1

A;Introns: 31/2

C;Superfamily: thioredoxin; thioredoxin homology

Query Match 73.9%; Score 17; DB 2; Length 107;  
Best Local Similarity 40.0%; Pred. No. 2.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5  
| |  
Db 27 FTASW 31

RESULT 28

AH2101

thioredoxin [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 16-Aug-2004

C;Accession: AH2101

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AH2101

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-108 <KUR>

A;Cross-references: UNIPROT:Q8YUH9; GB:BA000019; PIDN:BA000019; PID:g17131459; GSPDB:G

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: all2367

C;Superfamily: Thioredoxin; thioredoxin homology

Query Match 73.9%; Score 17; DB 2; Length 108;  
Best Local Similarity 40.0%; Pred. No. 2.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5  
| |  
Db 28 FTATW 32

RESULT 29

PH0980

Ig heavy chain V region (clone 17s.13) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C;Accession: PH0980

R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A;Title: Both IGM and IGG anti-DNA antibodies are the products of clonally selective B c

A;Reference number: PH0971; MUID:92381444; PMID:1512540

A;Accession: PH0980

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-112 <TIL>

A;Experimental source: B cell, strain [NZB x NZW]F1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F,15-97/Domain: immunoglobulin homology <IMM>

Query Match 73.9%; Score 17; DB 2; Length 112;  
Best Local Similarity 40.0%; Pred. No. 2.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5  
| |  
Db 29 FSSSW 33

RESULT 30

AF2549

hypothetical protein all7681 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120bet

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004

C;Accession: AF2549

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AF2549

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-112 <KUR>

A;Cross-references: UNIPROT:Q8ZS31; GB:AP003602; PIDN:BA003602; PID:g17134766; GSPDB:GN

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: all7681

A;Genome: plasmid

Query Match 73.9%; Score 17; DB 2; Length 112;  
Best Local Similarity 40.0%; Pred. No. 2.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5  
| |  
Db 87 FASAW 91

RESULT 31

S57775

thioredoxin h, cytosolic [validated] - Chlamydomonas reinhardtii

C;Species: Chlamydomonas reinhardtii

C;Date: 27-Oct-1995 #sequence\_revision 21-Jan-1997 #text\_change 16-Aug-2004

C;Accession: S57775; S57799; S54868; S16090; S54870

R;Stein, M.; Jacquot, J.P.; Jeannette, E.; Decottignies, P.; Hodges, M.; Lancelin, J.M.;

Plant Mol. Biol. 28, 487-503, 1995

A;Title: Chlamydomonas reinhardtii thioredoxins: structure of the genes coding for the ch

on and biochemical properties.

A;Reference number: S57774; MUID:95359406; PMID:7632918

A;Accession: S57775

A;Molecule type: DNA

A;Residues: 1-113 <STE>

A;Cross-references: UNIPROT:P80028; EMBL:X80887; NID:g840742; PIDN:CAA56850.1; PID:g84074

A;Accession: S57799

A;Molecule type: protein

A;Residues: 2-15 <STW>

R;Stein, M.; Hodges, M.; Jeanette, E.; Lancelin, J.M.; Jacquot, J.P.

submitted to the EMBL Data Library, April 1994

A;Description: Chlamydomonas reinhardtii thioredoxins I : cDNA and amino acid deduced seq

A;Reference number: S54844

A;Accession: S54868

A;Molecule type: mRNA

A;Residues: 1-113 <STF>

A;Cross-references: EMBL:X78822; NID:g840740; PIDN:CAA55399.1; PID:g840741

R;Decottignies, P.; Schmitter, J.M.; Dutka, S.; Jacquot, J.P.; Miginiac-Maslou, M.

Eur. J. Biochem. 198, 505-512, 1991

A;Title: Characterization and primary structure of a second thioredoxin from the green a

A;Reference number: S16090; MUID:91249849; PMID:2040309

A;Accession: S16090

A;Molecule type: protein

A;Residues: 2-112 <MIG>

R;Mittard, V.; Blackledge, M.J.; Stein, M.; Jacquot, J.P.; Marion, D.; Lancelin, J.M.

submitted to the Brookhaven Protein Data Bank, May 1996

A;Reference number: A66748; PDB:1TOF

A;Contents: annotation; conformation by (1)H, (13)C, (15)N-NMR, residues 2-113

R;Mittard, V.; Morelle, N.; Brutscher, B.; Simorre, J.P.; Marion, D.; Stein, M.; Jacquot,

Eur. J. Biochem. 229, 473-485, 1995

A;Title: (1)H, (13)C, (15)N-NMR resonance assignments of oxidized thioredoxin h from the



R spectroscopy and computer-assisted backbone assignment.  
A:Reference number: A58618; MUID:95262711; PMID:7744070  
A:Contents: annotation; conformation by (1)H, (13)C, (15)N-NMR  
C:Genetics:  
A:Introns: 27/3; 35/3; 69/3  
C:Superfamily: Thioresdoxin; thioresdoxin homology  
C:Keywords: redox-active disulfide  
F:2-113/Product: thioresdoxin h #status experimental <MAT>  
F:15-98/Domain: thioresdoxin homology <THR>  
F:37-40/Disulfide bonds: redox-active #status experimental

Query Match 73.9%; Score 17; DB 1; Length 113;  
Best Local Similarity 40.0%; Pred. No. 2.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 32 FTATW 36

## RESULT 32

JQ2242  
thioredoxin h - Arabidopsis thaliana  
N:Alternate names: protein F24M12.70  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 19-May-1994 #sequence revision 26-May-1994 #text\_change 16-Aug-2004  
C:Accession: JQ2242; T45734; S29905  
R:Rivera-Madrid, R.; Marinho, P.; Brugidou, C.; Chartier, Y.; Meyer, Y.  
Plant Physiol. 102, 327-328, 1993  
A:Title: Nucleotide sequence of a cDNA clone encoding an Arabidopsis thaliana thioredoxin  
A:Reference number: JQ2242; MUID:94151431; PMID:8108503  
A:Accession: JQ2242  
A:Molecule type: mRNA  
A:Residues: 1-114 <RIV>  
A:Cross-references: UNIPROT:P29448; EMBL:Z14084; NID:g16551; PIDN:CAA78462.1; PID:g16552  
R:Vitale, D.; Liguori, R.; Flores, M.; Argiriou, A.; De Simone, V.; Mewes, H.W.; Lemcke, S.  
submitted to the Protein Sequence Database, December 1999  
A:Reference number: Z23012  
A:Accession: T45734  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-114 <VIT>  
A:Cross-references: EMBL:AL132980  
A:Experimental source: cultivar Columbia; BAC clone F24M12  
C:Genetics:  
A:Gene: F24M12.70  
A:Map position: 3  
A:Introns: 30/3; 71/3  
C:Superfamily: Thioresdoxin; thioresdoxin homology  
C:Keywords: redox-active disulfide  
F:18-100/Domain: thioresdoxin homology <THR>  
F:40-43/Disulfide bonds: redox-active #status predicted

Query Match 73.9%; Score 17; DB 1; Length 114;  
Best Local Similarity 40.0%; Pred. No. 2.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 35 FTASW 39

## RESULT 33

G3HJUN  
Ig heavy chain V-III region (Jon) - human (tentative sequence)  
C:Species: Homo sapiens (man)  
C:Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 09-Jul-2004  
C:Accession: A02063  
R:Capra, J.D.; Kehoe, J.M.  
Proc. Natl. Acad. Sci. U.S.A. 71, 845-848, 1974  
A:Title: Variable region sequences of five human immunoglobulin heavy chains of the V-H1  
A:Reference number: A93794; MUID:74142702; PMID:4522793  
A:Accession: A02063

A:Molecule type: protein  
A:Residues: 1-115 <CAP>  
A:Cross-references: UNIPROT:P01780  
C:Comment: This chain was isolated from an IgG3 myeloma protein.  
C:Genetics:  
A:Gene: GDB:IGHV@  
A:Cross-references: GDB:128528; OMIM:147070  
A:Map position: 14q32.33-14q32.33  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>  
F:22-96/Disulfide bonds: #status predicted

Query Match 73.9%; Score 17; DB 1; Length 115;  
Best Local Similarity 40.0%; Pred. No. 2.3e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 29 FSTAW 33

## RESULT 34

PL0238  
Ig heavy chain V region (anti-DNA, 6NVH and 6QVH) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996  
C:Accession: PL0238  
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.  
J. Exp. Med. 171, 265-297, 1990  
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic  
A:Reference number: PL0231; MUID:90111618; PMID:2104919  
A:Accession: PL0238  
A:Molecule type: mRNA  
A:Residues: 1-115 <SHL>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-30/Region: framework 1  
F:15-98/Domain: immunoglobulin homology <IMM>  
F:31-35/Region: complementarity-determining 1  
F:36-49/Region: framework 2  
F:50-66/Region: complementarity-determining 2  
F:67-98/Region: framework 3  
F:99-107/Region: complementarity-determining 3  
F:108-115/Region: framework 4

Query Match 73.9%; Score 17; DB 2; Length 115;  
Best Local Similarity 40.0%; Pred. No. 2.3e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 29 FSSSW 33

## RESULT 35

G72642  
probable surface protein-1 APE0575 - Aeropyrum pernix (strain K1)  
C:Species: Aeropyrum pernix  
C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
C:Accession: G72642  
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah  
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K  
DNA Res. 6, 83-101, 1999  
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr  
A:Reference number: A72450; MUID:99310339; PMID:10382966  
A:Accession: G72642  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-115 <KAW>  
A:Cross-references: UNIPROT:Q9YEK3; DDBJ:AP000060; NID:g5104188; PIDN:BAA79543.1; PID:d1  
A:Experimental source: strain K1  
C:Genetics:



A;Gene: APE0575

Query Match 73.9%; Score 17; DB 2; Length 115;  
Best Local Similarity 40.0%; Pred. No. 2.3e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 2 FSAW 6

RESULT 36

T10739  
thioredoxin - common buckwheat  
C;Species: Fagopyrum esculentum (common buckwheat)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C;Accession: T10739

R;Fujino, K.  
submitted to the EMBL Data Library, September 1996

A;Reference number: Z17109

A;Accession: T10739

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-116 <FUJ>

A;Cross-references: UNIPROT:Q96419; EMBL:D87984

A;Experimental source: cv. Kitayuki

C;Function:

A;Description: participates, by the reversible oxidation of an active center disulfide b

C;Superfamily: thioredoxin; thioredoxin homology

C;Keywords: redox-active disulfide

F;17-99/Domain: thioredoxin homology <TXN>

Query Match

Best Local Similarity 73.9%; Score 17; DB 2; Length 116;  
Matches 2; Conservative 0; Pred. No. 2.3e+03;  
Matches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 34 FTASW 38

RESULT 37

PL0237  
Ig heavy chain V region (anti-DNA, 1A11VH) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996  
C;Accession: PL0237

R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A

J. Exp. Med. 171, 265-297, 1990

A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic

A;Reference number: PL0231; MUID:90111618; PMID:2104919

A;Accession: PL0237

A;Molecule type: mRNA

A;Residues: 1-117 <SHL>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-30/Region: framework 1

F;15-98/Domain: immunoglobulin homology <IMM>

F;31-35/Region: complementarity-determining 1

F;36-49/Region: framework 2

F;50-66/Region: complementarity-determining 2

F;67-98/Region: framework 3

F;99-109/Region: complementarity-determining 3

F;110-117/Region: framework 4

Query Match

Best Local Similarity 73.9%; Score 17; DB 2; Length 117;  
Matches 2; Conservative 0; Pred. No. 2.3e+03;  
Matches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 29 FSSSW 33

RESULT 38

PL0234

Ig heavy chain V region (anti-DNA, 3H9VH) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996

C;Accession: PL0234

R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.

J. Exp. Med. 171, 265-297, 1990

A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n

A;Reference number: PL0231; MUID:90111618; PMID:2104919

A;Accession: PL0234

A;Molecule type: mRNA

A;Residues: 1-117 <SHL>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-30/Region: framework 1

F;15-98/Domain: immunoglobulin homology <IMM>

F;31-35/Region: complementarity-determining 1

F;36-49/Region: framework 2

F;50-66/Region: complementarity-determining 2

F;67-98/Region: framework 3

F;99-109/Region: complementarity-determining 3

F;110-117/Region: framework 4

Query Match

Best Local Similarity 73.9%; Score 17; DB 2; Length 117;  
Matches 2; Conservative 0; Pred. No. 2.3e+03;  
Matches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 29 FSSSW 33

RESULT 39

PL0235

Ig heavy chain V region (anti-DNA, 2F2VH and 4H8VH) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996

C;Accession: PL0235

R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.

J. Exp. Med. 171, 265-297, 1990

A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n

A;Reference number: PL0231; MUID:90111618; PMID:2104919

A;Accession: PL0235

A;Molecule type: mRNA

A;Residues: 1-117 <SHL>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-30/Region: framework 1

F;15-98/Domain: immunoglobulin homology <IMM>

F;31-35/Region: complementarity-determining 1

F;36-49/Region: framework 2

F;50-66/Region: complementarity-determining 2

F;67-98/Region: framework 3

F;99-109/Region: complementarity-determining 3

F;110-117/Region: framework 4

Query Match

Best Local Similarity 73.9%; Score 17; DB 2; Length 117;  
Matches 2; Conservative 0; Pred. No. 2.3e+03;  
Matches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 29 FSSSW 33

RESULT 40

S34812

thioredoxin h2 - common tobacco

C;Species: Nicotiana tabacum (common tobacco)

C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 16-Aug-2004

C;Accession: S34812

R;Brugidou, C.; Marty, I.; Chartier, Y.; Meyer, Y.  
Mol. Gen. Genet. 238, 285-293, 1993  
A;Title: The Nicotiana tabacum genome encodes two cytoplasmic thioredoxin genes which are  
A;Reference number: S34812; MUID:93241165; PMID:8479434  
A;Accession: S34812  
A;Molecule type: DNA  
A;Residues: 1-118 <BRU>  
A;Cross-references: UNIPROT:Q07090; EMBL:Z11803; NID:g297518; PIDN:CAA77847.1; PID:g297518  
C;Genetics:  
A;Introns: 29/3; 70/3  
C;Superfamily: Thioredoxin; thioredoxin homology  
F;17-99/Domain: thioredoxin homology <THR>

Query Match 73.9%; Score 17; DB 1; Length 118;  
Best Local Similarity 40.0%; Pred. No. 2.3e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5

Db 34 FTASW 38

Search completed: October 18, 2005, 15:31:03  
Job time : 25.0588 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:30:23 ; Search time 107.294 Seconds  
(without alignments)  
31.079 Million cell updates/sec

Title: US-09-214-371-10  
Perfect score: 23  
Sequence: 1 FXXXWXXX 8

Scoring table: BLOSUM62  
Gapop 10.0 ; Gapext 0.5

Searched: 1860064 seqs, 416830855 residues

Total number of hits satisfying chosen parameters: 1860064

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications, AA.\*  
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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
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21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	73.9	8	18	US-10-818-036-24 Sequence 24, Appl
2	17	73.9	8	18	US-10-818-036-27 Sequence 27, Appl
3	17	73.9	8	18	US-10-818-036-28 Sequence 28, Appl
4	17	73.9	8	18	US-10-818-036-30 Sequence 30, Appl
5	17	73.9	9	14	US-10-072-419-3 Sequence 3, Appl1
6	17	73.9	9	16	US-10-072-419-8 Sequence 8, Appl1
7	17	73.9	9	16	US-10-869-768-3 Sequence 3, Appl1
8	17	73.9	9	16	US-10-869-768-8 Sequence 8, Appl1
9	17	73.9	9	18	US-10-818-036-14 Sequence 14, Appl
10	17	73.9	9	18	US-10-818-036-15 Sequence 15, Appl
11	17	73.9	9	18	US-10-818-036-23 Sequence 23, Appl

85 17 73.9 66 15 US-10-424-599-181984 Sequence 181984,  
86 17 73.9 67 16 US-10-425-115-222248 Sequence 222248,  
87 17 73.9 68 16 US-10-425-115-308662 Sequence 308662,  
88 17 73.9 69 14 US-10-029-386-29425 Sequence 29425, A  
89 17 73.9 69 15 US-10-412-699B-1967 Sequence 1967, Ap  
90 17 73.9 69 18 US-10-450-763-41422 Sequence 41422, A  
91 17 73.9 70 16 US-10-437-963-172557 Sequence 172557,  
92 17 73.9 71 9 US-09-864-761-45867 Sequence 45867, A  
93 17 73.9 71 16 US-10-425-115-204522 Sequence 204522,  
94 17 73.9 71 16 US-10-425-115-268403 Sequence 268403,  
95 17 73.9 72 16 US-10-425-115-286869 Sequence 286869,  
96 17 73.9 73 16 US-10-425-115-236925 Sequence 236925,  
97 17 73.9 74 16 US-10-425-115-200161 Sequence 200161,  
98 17 73.9 75 9 US-09-867-550-510 Sequence 510, App  
99 17 73.9 77 13 US-10-001-843-186 Sequence 186, App  
100 17 73.9 77 16 US-10-437-963-150690 Sequence 150690,

ALIGNMENTS

RESULT 1  
US-10-818-036-24  
; Sequence 24, Application US/10818036  
; Publication No. US20050222040A1  
; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice Z  
; APPLICANT: Schacter, Lee P.  
; APPLICANT: Zeldin, Michael H.  
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM  
; FILE REFERENCE: 303544.3000-100  
; CURRENT APPLICATION NUMBER: US/10/818,036  
; CURRENT FILING DATE: 2004-04-05  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-818-036-24

Query Match 73.9%; Score 17; DB 18; Length 8;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
| |  
Db 4 FTASW 8

RESULT 2  
US-10-818-036-27  
; Sequence 27, Application US/10818036  
; Publication No. US20050222040A1  
; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice Z  
; APPLICANT: Schacter, Lee P.  
; APPLICANT: Zeldin, Michael H.  
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM  
; FILE REFERENCE: 303544.3000-100  
; CURRENT APPLICATION NUMBER: US/10/818,036  
; CURRENT FILING DATE: 2004-04-05  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 27  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
; FEATURE:

; NAME/KEY: MOD RES  
; LOCATION: (8)..(8)  
; OTHER INFORMATION: AMIDATION  
US-10-818-036-27  
Query Match 73.9%; Score 17; DB 18; Length 8;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
| |  
Db 4 FTASW 8

RESULT 3  
US-10-818-036-28  
; Sequence 28, Application US/10818036  
; Publication No. US20050222040A1  
; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice Z  
; APPLICANT: Schacter, Lee P.  
; APPLICANT: Zeldin, Michael H.  
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM  
; FILE REFERENCE: 303544.3000-100  
; CURRENT APPLICATION NUMBER: US/10/818,036  
; CURRENT FILING DATE: 2004-04-05  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 28  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (8)..(8)  
; OTHER INFORMATION: AMIDATION  
US-10-818-036-28

Query Match 73.9%; Score 17; DB 18; Length 8;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
| |  
Db 4 FTASW 8

RESULT 4  
US-10-818-036-30  
; Sequence 30, Application US/10818036  
; Publication No. US20050222040A1  
; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice Z  
; APPLICANT: Schacter, Lee P.  
; APPLICANT: Zeldin, Michael H.  
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM  
; FILE REFERENCE: 303544.3000-100  
; CURRENT APPLICATION NUMBER: US/10/818,036  
; CURRENT FILING DATE: 2004-04-05  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 30  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID  
US-10-818-036-30

Query Match 73.9%; Score 17; DB 18; Length 8;  
Best Local Similarity 40.0%; Pred. No. 1.6e+06;

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Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 FXXW 5
Db 4 FTASW 8

RESULT 5
US-10-072-419-3
; Sequence 3, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Apis mellifera
US-10-072-419-3

Query Match 73.9%; Score 17; DB 14; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 FXXW 5
Db 4 FTSSW 8

RESULT 6
US-10-072-419-8
; Sequence 8, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Vanessa cardui
US-10-072-419-8

Query Match 73.9%; Score 17; DB 14; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 FXXW 5
Db 4 FTSSW 8

RESULT 7
US-10-072-419-3
; Sequence 3, Application US/10869768
; Publication No. US20040224898A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/869,768
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; CURRENT FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: US 10/072,419
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Apis mellifera
US-10-869-768-3

Query Match 73.9%; Score 17; DB 16; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 FXXW 5
Db 4 FTSSW 8

RESULT 8
US-10-869-768-8
; Sequence 8, Application US/10869768
; Publication No. US20040224898A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/869,768
; CURRENT FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: US 10/072,419
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Vanessa cardui
US-10-869-768-8

Query Match 73.9%; Score 17; DB 16; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 FXXW 5
Db 4 FTSSW 8

RESULT 9
US-10-818-036-14
; Sequence 14, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-818-036-14

Query Match 73.9%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY      1 FXXXW 5
Db      4 FTASW 8

RESULT 10
US-10-818-036-15
; Sequence 15, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-818-036-15
Query Match      73.9%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
Db      4 FTASW 8

RESULT 11
US-10-818-036-23
; Sequence 23, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Manduca sexta
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: AMIDATION
US-10-818-036-23
Query Match      73.9%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
Db      4 FTSSW 8

RESULT 12
Query Match      73.9%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
US-10-818-036-25
; Sequence 25, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
US-10-818-036-25
Query Match      73.9%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
Db      4 FTASW 8

RESULT 13
US-10-818-036-26
; Sequence 26, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: AMIDATION
US-10-818-036-26
Query Match      73.9%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
Db      4 FTASW 8

RESULT 14
US-10-818-036-29
; Sequence 29, Application US/10818036
; Publication No. US20050222040A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice Z
; APPLICANT: Schacter, Lee P.
; APPLICANT: Zeldin, Michael H.
```



```

; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM
; FILE REFERENCE: 303544.3000-100
; CURRENT APPLICATION NUMBER: US/10/818,036
; CURRENT FILING DATE: 2004-04-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: PYRROLIDONE CARBOXYLIC ACID
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (9)..(9)
; OTHER INFORMATION: AMIDATION
; US-10-818-036-29

Query Match          73.9%; Score 17; DB 18; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
Db      4 FTASW 8

RESULT 15
US-09-842-776A-28
; Sequence 28, Application US/09842776A
; Publication No. US20040023316A1
; GENERAL INFORMATION:
; APPLICANT: CONNEX GMBH
; TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS
; FILE REFERENCE: 41735
; CURRENT APPLICATION NUMBER: US/09/842,776A
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/EP99/08212
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Complementarity determining region (CDR1) of an
; OTHER INFORMATION: antibody heavy chain directed to a beta-urease
; OTHER INFORMATION: epitope (alternative sequence)
US-09-842-776A-28

Query Match          73.9%; Score 17; DB 11; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
Db      4 FSTSW 8

RESULT 16
US-10-996-316-139
; Sequence 139, Application US/10996316
; Publication No. US20050129690A1
; GENERAL INFORMATION:
; APPLICANT: Alexion Pharmaceuticals, Inc.
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: McWhirter, John
; APPLICANT: Kretz-Rommel, Anke
```

```

; TITLE OF INVENTION: POLYPEPTIDES AND ANTIBODIES DERIVED FROM CHRONIC LYMPHOCYTIC
; TITLE OF INVENTION: LEUKEMIA CELLS AND USES THEREOF
; FILE REFERENCE: 60 CIP IV (1087-43 CIP IV)
; CURRENT APPLICATION NUMBER: US/10/996,316
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: US 10/894,672
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 10/736,188
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/379,151
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: PCT/US01/47931
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/254,113
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 139
; LENGTH: 10
; TYPE: PRT
; ORGANISM: murine
; US-10-996-316-139

Query Match          73.9%; Score 17; DB 18; Length 10;
Best Local Similarity 40.0%; Pred. No. 6.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
Db      4 FSAAW 8

RESULT 17
US-10-072-419-37
; Sequence 37, Application US/10072419
; Publication No. US20030162717A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Vanessa cardui
; US-10-072-419-37

Query Match          73.9%; Score 17; DB 14; Length 11;
Best Local Similarity 40.0%; Pred. No. 6.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
Db      4 FTSSW 8

RESULT 18
US-10-869-768-37
; Sequence 37, Application US/10869768
; Publication No. US20040224898A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/869,768
; CURRENT FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: US 10/072,419
; PRIOR FILING DATE: 2002-02-07
```

```
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Vanuessa cardui
US-10-869 768-77

Query Match      73.9%; Score 17; DB 16; Length 11;
Best Local Similarity 40.0%; Pred. No. 6.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXW 5
DB      4 FTSSW 8

RESULT 19
US-10-354-240-87
; Sequence 87, Application US/10354240
; Publication No. US20030185847A1
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Iwama, Akiko
; APPLICANT: Kino, Kohsuke
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease
; FILE REFERENCE: SPO-103D1
; CURRENT APPLICATION NUMBER: US/10/354,240
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: PCT/JP97/00740
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 09/142,524
; PRIOR FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria japonica
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(15)
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 4
US-10-354-240-87

Query Match      73.9%; Score 17; DB 14; Length 15;
Best Local Similarity 40.0%; Pred. No. 8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXW 5
DB      9 FSTAW 13

RESULT 20
US-10-354-240-88
; Sequence 88, Application US/10354240
; Publication No. US20030185847A1
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Iwama, Akiko
; APPLICANT: Kino, Kohsuke
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease
; FILE REFERENCE: SPO-103D1
; CURRENT APPLICATION NUMBER: US/10/354,240
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: PCT/JP97/00740
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 09/142,524
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; PRIOR FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria japonica
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(15)
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 5
US-10-354-240-88

Query Match      73.9%; Score 17; DB 14; Length 15;
Best Local Similarity 40.0%; Pred. No. 8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXW 5
DB      4 FSTAW 8

RESULT 21
US-09-963-339-10
; Sequence 10, Application US/09963339
; Publication No. US20030049700A1
; GENERAL INFORMATION:
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: 22108 AND 47916, NOVEL HUMAN THIOREDOXIN
; TITLE OF INVENTION: FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-090001
; CURRENT APPLICATION NUMBER: US/09/963,339
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/235,049
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-963-339-10

Query Match      73.9%; Score 17; DB 10; Length 19;
Best Local Similarity 40.0%; Pred. No. 9.3e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXW 5
DB      4 FSATW 8

RESULT 22
US-10-145-586-59
; Sequence 59, Application US/10145586
; Publication No. US20030138890A1
; GENERAL INFORMATION:
; APPLICANT: Alexandra Glucksmann, Maria
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: M. Galvin, Katherine
; APPLICANT: Weich, Nadine
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Bandaru, Rajasekhar
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS,
; TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LEUCINE-RICH
; TITLE OF INVENTION: REPEAT FAMILY MEMBERS, AND HUMAN RINGFINGER FAMILY MEMBER
; FILE REFERENCE: 10448-188001
; CURRENT APPLICATION NUMBER: US/10/145,586
; CURRENT FILING DATE: 2002-05-14
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 59  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-145-586-59

Query Match 73.9%; Score 17; DB 14; Length 19;  
Best Local Similarity 40.0%; Pred. No. 9.3e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5  
|  
Db 4 FSATW 8

RESULT 23  
US-10-931-260-265  
; Sequence 265, Application US/10931260  
; Publication No. US20050152927A1  
; GENERAL INFORMATION:  
; APPLICANT: Griffith, Irwin J.;  
; Pollock, Joanne;  
; Bond, Julian F.;  
; Garman, Richard D;  
; Kuo, Mei-Chang;  
; Powers, Stephen P.;  
; Exley, Mark A.;  
; Chen, Xian;  
; Shaked, Ze'ev  
; TITLE OF INVENTION: Allergenic Proteins And Peptides From  
; Japanese Cedar Pollen  
; NUMBER OF SEQUENCES: 283  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lahive & Cockfield, LLP  
; STREET: 28 State St  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/931,260  
; FILING DATE: 30-Aug-2004  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/240,203  
; FILING DATE: 29-Jan-1999  
; APPLICATION NUMBER: 08/467,023  
; FILING DATE: 1995-JUN-06  
; APPLICATION NUMBER: 08/350,225  
; FILING DATE: 1994-DEC-06  
; APPLICATION NUMBER: 08/226,248  
; FILING DATE: 1994-APR-08  
; APPLICATION NUMBER: PCT/US93/00139  
; FILING DATE: 1993-JAN-15  
; APPLICATION NUMBER: 07/938,990  
; FILING DATE: 1992-SEP-01  
; APPLICATION NUMBER: 07/730,452  
; FILING DATE: 1991-JUL-15  
; APPLICATION NUMBER: 07/729,134  
; FILING DATE: 1991-JUL-12  
; APPLICATION NUMBER: 07/975,179  
; APPLICATION NUMBER: PCT/US92/05661  
; FILING DATE: 1992-JUL-10  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Amy E. Mandragouras, Esq.  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: IMI-028CD2CCPA2

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 742-4214  
; INFORMATION FOR SEQ ID NO: 265:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
; SEQUENCE DESCRIPTION: SEQ ID NO: 265:  
US-10-931-260-265

Query Match 73.9%; Score 17; DB 18; Length 20;  
Best Local Similarity 40.0%; Pred. No. 9.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5  
|  
Db 12 FSTAW 16

RESULT 24  
US-10-931-260-264  
; Sequence 264, Application US/10931260  
; Publication No. US20050152927A1  
; GENERAL INFORMATION:  
; APPLICANT: Griffith, Irwin J.;  
; Pollock, Joanne;  
; Bond, Julian F.;  
; Garman, Richard D;  
; Kuo, Mei-Chang;  
; Powers, Stephen P.;  
; Exley, Mark A.;  
; Chen, Xian;  
; Shaked, Ze'ev  
; TITLE OF INVENTION: Allergenic Proteins And Peptides From  
; Japanese Cedar Pollen  
; NUMBER OF SEQUENCES: 283  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lahive & Cockfield, LLP  
; STREET: 28 State St  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/931,260  
; FILING DATE: 30-Aug-2004  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/240,203  
; FILING DATE: 29-Jan-1999  
; APPLICATION NUMBER: 08/467,023  
; FILING DATE: 1995-JUN-06  
; APPLICATION NUMBER: 08/350,225  
; FILING DATE: 1994-DEC-06  
; APPLICATION NUMBER: 08/226,248  
; FILING DATE: 1994-APR-08  
; APPLICATION NUMBER: PCT/US93/00139  
; FILING DATE: 1993-JAN-15  
; APPLICATION NUMBER: 07/938,990  
; FILING DATE: 1992-SEP-01  
; APPLICATION NUMBER: 07/730,452  
; FILING DATE: 1991-JUL-15  
; APPLICATION NUMBER: 07/729,134  
; FILING DATE: 1991-JUL-12  
; APPLICATION NUMBER: 07/975,179

; FILING DATE: 1992-NOV-12
; APPLICATION NUMBER: PCT/US92/05661
; FILING DATE: 1992 JUL 10
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras, Esq.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-028CD2CCPA2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 264:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 264:
US-10-931-260-264

Query Match 73.9%; Score 17; DB 18; Length 24;
Best Local Similarity 40.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 12 FSTAW 16

RESULT 25
US-10-338-777-404
; Sequence 404, Application US/10338777
; Publication No. US20030188343A1
; GENERAL INFORMATION:
; APPLICANT: Lynx Therapeutics, Inc.
; APPLICANT: United States Department of Agriculture
; APPLICANT: Bowen, Benjamin A
; APPLICANT: Haudenschild, Christian D
; APPLICANT: Hukler, Edward S
; TITLE OF INVENTION: Identification of Genes Associated with Growth in Plants
; FILE REFERENCE: 37-000510US
; CURRENT APPLICATION NUMBER: US/10/338,777
; CURRENT FILING DATE: 2003-01-07
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 404
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: example conservative variation of residues 2-26 of SEQ ID NO:31
US-10-338-777-404

Query Match 73.9%; Score 17; DB 14; Length 25;
Best Local Similarity 40.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 20 FAASW 24

RESULT 26
US-09-864-761-46828
; Sequence 46828, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 46828
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007739.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.62
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.66
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.68
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.61
US-09-864-761-46828

Query Match 73.9%; Score 17; DB 9; Length 27;
Best Local Similarity 40.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 4 FSATW 8

RESULT 27
US-08-424-550B-428
; Sequence 428, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY

APPLICANT: ANTHONY SCOTT MUERHOFF  
APPLICANT: JAMES C. ERKER  
APPLICANT: SHERI L. BUIJK  
APPLICANT: ISA K. MUSHAWAR  
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
NUMBER OF SEQUENCES: 716  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
STREET: 100 ABBOTT PARK ROAD  
CITY: ABBOTT PARK  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/424,550B  
FILING DATE:  
CLASSIFICATION: 435435  
ATTORNEY/AGENT INFORMATION:  
NAME: POREMSKI, PRISCILLA E.  
REGISTRATION NUMBER: 33,207  
REFERENCE/DOCKET NUMBER: 5527.PC.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 428:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-424-550B-428

Query Match 73.9%; Score 17; DB 8; Length 29;  
Best Local Similarity 40.0%; Pred. No. 1.2e+04;  
Matches 2; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 1 FXXXW 5  
|  
Db 12 FASAW 16

RESULT 28  
US-10-424-599-160512  
; Sequence 160512, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 160512  
; LENGTH: 32  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_115960C.1.pap  
US-10-424-599-160512

Query Match 73.9%; Score 17; DB 15; Length 32;  
Best Local Similarity 40.0%; Pred. No. 1.3e+04;  
Matches 2; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 1 FXXXW 5  
|  
Db 18 FTASW 22  
RESULT 29  
US-10-032-201B-157  
; Sequence 157, Application US/10032201B  
; Publication No. US20030167524A1  
; GENERAL INFORMATION:  
; APPLICANT: Van Rooijen, Gijb  
; APPLICANT: Deckers, Harm  
; APPLICANT: Heifetz, Peter Bernard  
; APPLICANT: Briggs, Steven  
; APPLICANT: Dalmia, Bipin Kumar  
; APPLICANT: Del Val, Greg  
; APPLICANT: Zaplachinski, Steve  
; APPLICANT: Moloney, Maurice  
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED  
; TITLE OF INVENTION: COMPOSITIONS  
; FILE REFERENCE: 38814 351B  
; CURRENT APPLICATION NUMBER: US/10/032,201B  
; CURRENT FILING DATE: 2001-12-19  
; NUMBER OF SEQ ID NOS: 313  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 157  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Sus scrofa  
US-10-032-201B-157

Query Match 73.9%; Score 17; DB 14; Length 33;  
Best Local Similarity 40.0%; Pred. No. 1.3e+04;  
Matches 2; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 1 FXXXW 5  
|  
Db 26 FSATW 30

RESULT 30  
US-10-029-386-28347  
; Sequence 28347, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G  
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 28347  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO ALL33499.1  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.45  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.55  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.46  
; OTHER INFORMATION: SWISSPROT HIT: Q03368, EVALUE 8.60e+00  
US-10-029-386-28347

Query Match 73.9%; Score 17; DB 14; Length 33;  
Best Local Similarity 40.0%; Pred. No. 1.3e+04;  
Matches 2; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 1 FXXXW 5

Db 14 FSASW 18

RESULT 31

US-10-307-817-584

; Sequence 584, Application US/10307817

; Publication No. US20040058338A1

; GENERAL INFORMATION:

; APPLICANT: Agee et al.

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: 21402-502C

; CURRENT APPLICATION NUMBER: US/10/307,817

; CURRENT FILING DATE: 2002-12-02

; NUMBER OF SEQ ID NOS: 682

; SOFTWARE: CuraSeqList version 0.1

; SEQ ID NO 584

; LENGTH: 35

; TYPE: PRT

; ORGANISM: Mus musculus

US-10-307-817-584

Query Match 73.9%; Score 17; DB 15; Length 35;

Best Local Similarity 40.0%; Pred. No. 1.3e+04;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db 22 FSATW 26

RESULT 32

US-10-931-260-137

; Sequence 137, Application US/10931260

; Publication No. US20050152927A1

; GENERAL INFORMATION:

; APPLICANT: Griffith, Irwin J.;

; Pollock, Joanne;

; Bond, Julian F.;

; Garman, Richard D.;

; Kuo, Mei-Chang;

; Powers, Stephen P.;

; Exley, Mark A.;

; Chen, Xian;

; Shaked, Ze'ev

; TITLE OF INVENTION: Allergenic Proteins And Peptides From

; Japanese Cedar Pollen

; NUMBER OF SEQUENCES: 283

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lahive & Cockfield, LLP

; STREET: 28 State St

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/931,260

; FILING DATE: 30-Aug-2004

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/240,203

; FILING DATE: 29-Jan-1999

; APPLICATION NUMBER: 08/467,023

; FILING DATE: 1995-JUN-06

; APPLICATION NUMBER: 08/350,225

; FILING DATE: 1994-DEC-06

; APPLICATION NUMBER: 08/226,248

; FILING DATE: 1994-APR-08

; APPLICATION NUMBER: PCT/US93/00139

; FILING DATE: 1993-JAN-15

; APPLICATION NUMBER: 07/938,990

; FILING DATE: 1992-SEP-01

; APPLICATION NUMBER: 07/730,452

; FILING DATE: 1991-JUL-15

; APPLICATION NUMBER: 07/729,134

; FILING DATE: 1991-JUL-12

; APPLICATION NUMBER: 07/975,179

; FILING DATE: 1992-NOV-12

; APPLICATION NUMBER: PCT/US92/05661

; FILING DATE: 1992-JUL-10

; ATTORNEY/AGENT INFORMATION:

; NAME: Amy E. Mandragouras, Esq.

; REGISTRATION NUMBER: 36,207

; REFERENCE/DOCKET NUMBER: IMI-028CD2CCPA2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 742-4214

; INFORMATION FOR SEQ ID NO: 137:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 36 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal

; SEQUENCE DESCRIPTION: SEQ ID NO: 137:

US-10-931-260-137

Query Match 73.9%; Score 17; DB 18; Length 36;

Best Local Similarity 40.0%; Pred. No. 1.4e+04;

Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5

Db 28 FSTAW 32

RESULT 33

US-10-193-795-10

; Sequence 10, Application US/10193795

; Publication No. US20030082202A1

; GENERAL INFORMATION:

; APPLICANT: Flohe, Leopold

; No. US20030082202Aleceke, Everson

; Kalisz, Henryk

; Montemartini, Marisa

; TITLE OF INVENTION: TRYPAEDOXIN, EXPRESSION PLASMID, PROCESS OF

; PRODUCTION, METHOD OF USE, TEST KIT, AND

; PHARMACEUTICAL COMPOSITION

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Broun

; STREET: 233 South Wacker Drive/6300 Sears Tower

; CITY: Chicago

; STATE: Illinois

; COUNTRY: Unites States of America

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/193,795

; FILING DATE: 12-Jul-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/330,914

; FILING DATE: 11-Jun-1999

; APPLICATION NUMBER: WO PCT/EP97/06983

; FILING DATE: 12-DEC-1997

; ATTORNEY/AGENT INFORMATION:

NAME: Zeller, James P.  
REGISTRATION NUMBER: 28,491  
REFERENCE/DOCKET NUMBER: 29473/35678  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-10-193-795-10  
Query Match 73.9%; Score 17; DB 14; Length 37;  
Best Local Similarity 40.0%; Pred. No. 1.4e+04;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 FXXW 5  
Db 11 FSASW 15  
RESULT 34  
US-10-962-760-10  
; Sequence 10, Application US/10962760  
; Publication No. US20050143559A1  
; GENERAL INFORMATION:  
; APPLICANT: Flohe, Leopold  
; Nogeceke, Everson  
; Kalisz, Henryk  
; Montemartini, Marisa  
; TITLE OF INVENTION: TRYPAEDOXIN, EXPRESSION PLASMID, PROCESS OF  
; PRODUCTION, METHOD OF USE, TEST KIT, AND  
; PHARMACEUTICAL COMPOSITION  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Broun  
; STREET: 233 South Wacker Drive/6300 Sears Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: Unites States of America  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/962,760  
; FILING DATE: 12-Oct-2004  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP97/06983  
; FILING DATE: 12-DEC-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, James P.  
; REGISTRATION NUMBER: 28,491  
; REFERENCE/DOCKET NUMBER: 29473/35678  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 37 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-10-962-760-10  
Query Match 73.9%; Score 17; DB 18; Length 37;  
Best Local Similarity 40.0%; Pred. No. 1.4e+04;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 FXXW 5  
Db 11 FSASW 15  
RESULT 35  
US-10-818-036-1  
; Sequence 1, Application US/10818036  
; Publication No. US20050222040A1  
; GENERAL INFORMATION:  
; APPLICANT: Schacter, Bernice Z  
; APPLICANT: Schacter, Lee P.  
; APPLICANT: Zeldin, Michael H.  
; TITLE OF INVENTION: VERTEBRATE PEPTIDE MODULATORS OF LIPID METABOLISM  
; FILE REFERENCE: 303544.3000-100  
; CURRENT APPLICATION NUMBER: US/10/818,036  
; CURRENT FILING DATE: 2004-04-05  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 37  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Search sequence  
US-10-818-036-1  
Query Match 73.9%; Score 17; DB 18; Length 37;  
Best Local Similarity 40.0%; Pred. No. 1.4e+04;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 FXXW 5  
Db 32 FTASW 36  
RESULT 36  
US-09-892-877-347  
; Sequence 347, Application US/09892877  
; Publication No. US20030077809A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et. al.  
; TITLE OF INVENTION: 97 Human secreted proteins  
; FILE REFERENCE: P2028P1  
; CURRENT APPLICATION NUMBER: US/09/892,877  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/437,658  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-10  
; NUMBER OF SEQ ID NOS: 461  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 347  
; LENGTH: 38  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-892-877-347  
Query Match 73.9%; Score 17; DB 10; Length 38;  
Best Local Similarity 40.0%; Pred. No. 1.4e+04;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 FXXW 5  
Db 19 FAAAW 23



RESULT 37  
US-09-948-783-287  
; Sequence 287, Application US/09948783  
; Publication No. US20030100051A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et. al.  
; TITLE OF INVENTION: 97 Human secreted proteins  
; FILE REFERENCE: P2028P2  
; CURRENT APPLICATION NUMBER: US/09/948,783  
; CURRENT FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: 60/231,846  
; PRIOR FILING DATE: 2000-09-11  
; PRIOR APPLICATION NUMBER: 09/892,877  
; PRIOR FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: 09/437,658  
; PRIOR FILING DATE: 1999-11-10  
; PRIOR APPLICATION NUMBER: PCT/US99/09847  
; PRIOR FILING DATE: 1999-05-06  
; PRIOR APPLICATION NUMBER: 60/085,093  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: 60/085,094  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: 60/085,105  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: 60/085,180  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: 60/085,927  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,906  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,924  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,922  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,921  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,923  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,925  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,928  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,920  
; PRIOR FILING DATE: 1998-05-18  
; NUMBER OF SEQ ID NOS: 465  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 287  
; LENGTH: 38  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-948-783-287

Query Match 73.9%; Score 17; DB 10; Length 38;  
Best Local Similarity 40.0%; Pred. No. 1.4e+04;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5  
|  
Db 19 FAAW 23

RESULT 38  
US-09-057-951-6  
; Sequence 6, Application US/09057951  
; Patent No. US2002025551A1  
; GENERAL INFORMATION:  
; APPLICANT: Holtzman, Douglas  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE T129-RELATED  
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/057,951  
; FILING DATE: 09-APR-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D., Anita L.  
; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 09404/046001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 40 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-057-951-6

Query Match 73.9%; Score 17; DB 9; Length 40;  
Best Local Similarity 40.0%; Pred. No. 1.5e+04;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5  
|  
Db 6 FSAW 10

RESULT 39  
US-09-864-761-46093  
; Sequence 46093, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aeomica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30

;; PRIOR APPLICATION NUMBER: PCT/US01/00668  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00663  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00662  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00661  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00670  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: US 60/234,687  
;; PRIOR FILING DATE: 2000-09-21  
;; PRIOR APPLICATION NUMBER: US 09/608,408  
;; PRIOR FILING DATE: 2000-06-30  
;; PRIOR APPLICATION NUMBER: US 09/774,203  
;; PRIOR FILING DATE: 2001-01-29  
;; NUMBER OF SEQ ID NOS: 49117  
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
;; SEQ ID NO 46093  
;; LENGTH: 40  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; OTHER INFORMATION: MAP TO AF233390.1  
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7  
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5  
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4  
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.3  
US-09-864-761-46093

Query Match 73.9%; Score 17; DB 9; Length 40;  
Best Local Similarity 40.0%; Pred. No. 1.5e+04;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5  
|  
Db 23 FTSSW 27

RESULT 40  
US-10-105-150-6  
; Sequence 6, Application US/10105150  
; Publication No. US20020119524A1  
; GENERAL INFORMATION:  
; APPLICANT: Holtzman, Douglas  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE T129-RELATED  
; PROTEIN FAMILY AND USES THEREOF  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/105,150  
; FILING DATE: 25-Mar-2002  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/057,951  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meiklejohn, Ph.D., Anita L.  
; REGISTRATION NUMBER: 35,283  
; REFERENCE/DOCKET NUMBER: 09404/046001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906

;; TELEX: 200154  
;; INFORMATION FOR SEQ ID NO: 6:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 40 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-105-150-6

Query Match 73.9%; Score 17; DB 13; Length 40;  
Best Local Similarity 40.0%; Pred. No. 1.5e+04;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXXW 5  
|  
Db 6 FSAAW 10

Search completed: October 18, 2005, 15:50:34  
Job time : 109.294 secs

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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:19:12 ; Search time 28.7059 Seconds  
(without alignments)  
20.804 Million cell updates/sec

Title: US-09-214-371-10  
Perfect score: 23  
Sequence: 1 FXXXWXXX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Issued Patents AA: \*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	17	73.9	15	4	US-09-142-524D-87
3	17	73.9	15	4	US-09-142-524D-88
4	17	73.9	29	4	US-08-469-260A-428
5	17	73.9	29	4	US-08-488-446-428
6	17	73.9	29	4	US-08-467-344A-428
7	17	73.9	29	4	US-08-424-550B-428
8	17	73.9	34	1	US-08-118-270-134
9	17	73.9	34	1	US-08-118-270-172
10	17	73.9	34	5	PCT-US93-08528-134
11	17	73.9	34	5	PCT-US93-08528-172
12	17	73.9	36	3	US-08-467-023-137
13	17	73.9	37	4	US-09-330-914A-10
14	17	73.9	41	3	US-08-467-023-136
15	17	73.9	45	3	US-08-467-023-135
16	17	73.9	45	4	US-09-149-476-475
17	17	73.9	47	4	US-09-369-247-129
18	17	73.9	49	1	US-08-118-270-209
19	17	73.9	49	5	PCT-US93-08528-209
20	17	73.9	54	4	US-09-434-840-73
21	17	73.9	54	4	US-09-733-643B-21
22	17	73.9	56	4	US-09-621-976-6592
23	17	73.9	60	4	US-09-270-767-35869
24	17	73.9	60	4	US-09-270-767-51086
25	17	73.9	61	3	US-09-134-001C-4258
26	17	73.9	62	4	US-09-252-991A-28658
27	17	73.9	62	4	US-09-621-976-5704

28	17	73.9	62	4	US-09-248-796A-26247	Sequence 26247, A
29	17	73.9	63	4	US-09-902-540-11838	Sequence 11838, A
30	17	73.9	69	4	US-09-621-976-6715	Sequence 6715, Ap
31	17	73.9	69	4	US-09-248-796A-24056	Sequence 24056, A
32	17	73.9	80	4	US-09-330-914A-4	Sequence 4, Appli
33	17	73.9	80	4	US-09-270-767-37303	Sequence 37303, A
34	17	73.9	80	4	US-09-270-767-52520	Sequence 52520, A
35	17	73.9	80	4	US-09-248-796A-24759	Sequence 24759, A
36	17	73.9	82	4	US-09-248-796A-19864	Sequence 19864, A
37	17	73.9	84	2	US-08-353-476-78	Sequence 78, Appl
38	17	73.9	84	3	US-08-679-493A-97	Sequence 97, Appl
39	17	73.9	86	4	US-09-583-110-3199	Sequence 3199, Ap
40	17	73.9	89	4	US-09-621-976-6168	Sequence 6168, Ap
41	17	73.9	91	2	US-08-598-873-19	Sequence 19, Appl
42	17	73.9	91	3	US-08-605-430-19	Sequence 19, Appl
43	17	73.9	91	4	US-09-717-054-19	Sequence 19, Appl
44	17	73.9	93	4	US-09-621-976-6449	Sequence 6449, Ap
45	17	73.9	93	4	US-09-248-796A-16647	Sequence 16647, A
46	17	73.9	95	4	US-09-949-016-9308	Sequence 9308, Ap
47	17	73.9	98	4	US-09-252-991A-22311	Sequence 22311, A
48	17	73.9	102	3	US-08-984-295-3	Sequence 3, Appli
49	17	73.9	102	3	US-08-741-411-12	Sequence 12, Appl
50	17	73.9	104	6	5210073-1	Patent No. 5210073
51	17	73.9	104	6	5210073-1	Patent No. 5210073
52	17	73.9	105	2	US-08-826-910-3	Sequence 3, Appli
53	17	73.9	105	2	US-08-826-910-4	Sequence 4, Appli
54	17	73.9	105	4	US-09-601-144-68	Sequence 68, Appl
55	17	73.9	105	4	US-09-513-999C-8037	Sequence 8037, Ap
56	17	73.9	105	4	US-09-107-433-2856	Sequence 2856, Ap
57	17	73.9	109	4	US-09-902-540-13327	Sequence 13327, A
58	17	73.9	114	3	US-09-450-520A-9	Sequence 9, Appli
59	17	73.9	114	3	US-09-450-520A-10	Sequence 10, Appl
60	17	73.9	114	3	US-09-450-520A-11	Sequence 11, Appl
61	17	73.9	114	4	US-09-897-425-41	Sequence 41, Appl
62	17	73.9	116	3	US-09-065-059-9	Sequence 9, Appli
63	17	73.9	116	3	US-08-545-809A-134	Sequence 134, App
64	17	73.9	116	4	US-09-134-000C-6570	Sequence 6570, Ap
65	17	73.9	116	4	US-09-949-016-10735	Sequence 10735, A
66	17	73.9	117	1	US-07-634-278-105	Sequence 105, App
67	17	73.9	117	1	US-08-477-728-105	Sequence 105, App
68	17	73.9	117	1	US-08-474-040-105	Sequence 105, App
69	17	73.9	117	1	US-08-487-200-105	Sequence 105, App
70	17	73.9	117	3	US-08-484-537-105	Sequence 105, App
71	17	73.9	120	3	US-09-065-059-1	Sequence 1, Appli
72	17	73.9	121	4	US-09-107-532A-5275	Sequence 5275, Ap
73	17	73.9	122	3	US-09-540-014-2	Sequence 2, Appli
74	17	73.9	122	4	US-09-538-864-25	Sequence 25, Appl
75	17	73.9	122	4	US-10-091-841A-2	Sequence 2, Appli
76	17	73.9	125	4	US-09-949-016-9663	Sequence 9663, Ap
77	17	73.9	127	3	US-09-540-014-4	Sequence 4, Appli
78	17	73.9	127	4	US-09-252-991A-17639	Sequence 17639, A
79	17	73.9	127	4	US-09-252-991A-24186	Sequence 24186, A
80	17	73.9	127	4	US-10-091-841A-4	Sequence 4, Appli
81	17	73.9	128	3	US-08-467-023-187	Sequence 187, App
82	17	73.9	130	1	US-08-276-852-69	Sequence 69, Appl
83	17	73.9	130	1	US-08-276-852-70	Sequence 70, Appl
84	17	73.9	130	1	US-08-276-852-71	Sequence 71, Appl
85	17	73.9	130	1	US-08-899-575-69	Sequence 69, Appl
86	17	73.9	130	1	US-08-899-575-70	Sequence 70, Appl
87	17	73.9	130	1	US-08-899-575-71	Sequence 71, Appl
88	17	73.9	130	1	US-08-899-575-69	Sequence 69, Appl
89	17	73.9	130	1	US-08-899-575-70	Sequence 70, Appl
90	17	73.9	130	1	US-08-899-575-71	Sequence 71, Appl
91	17	73.9	130	3	US-09-540-014-6	Sequence 6, Appli
92	17	73.9	130	4	US-10-091-841A-6	Sequence 6, Appli
93	17	73.9	130	5	PCT-US95-08743-69	Sequence 69, Appl
94	17	73.9	130	5	PCT-US95-08743-70	Sequence 70, Appl
95	17	73.9	130	5	PCT-US95-08743-71	Sequence 71, Appl
96	17	73.9	131	4	US-09-248-796A-15325	Sequence 15325, A
97	17	73.9	132	4	US-09-386-658A-2	Sequence 2, Appli
98	17	73.9	136	3	US-09-450-520A-4	Sequence 4, Appli
99	17	73.9	136	3	US-09-252-991A-26095	Sequence 26095, A
100	17	73.9	138	4		

ALIGNMENTS

RESULT 1  
US-09-085-072-7  
; Sequence 7, Application US/09085072  
; Patent No. 6265150  
; GENERAL INFORMATION:  
; APPLICANT: L. Terstappen et al.  
; TITLE OF INVENTION: PHAGE ANTIBODIES  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hoffmann & Baron, LLP  
; STREET: 350 Jericho Turnpike  
; CITY: Jericho  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 11753  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/085,072  
; FILING DATE: 26-MAY-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Felt, Irving N.  
; REGISTRATION NUMBER: 28,601  
; REFERENCE/DOCKET NUMBER: 890-2 PWC/CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 822-3550  
; TELEFAX: (516) 822-3582  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-085-072-7

Query Match 73.9%; Score 17; DB 3; Length 13;  
Best Local Similarity 40.0%; Pred. No. 1.9e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 6 FASSW 10

RESULT 2  
US-09-142-524D-87  
; Sequence 87, Application US/09142524D  
; Patent No. 6719976  
; GENERAL INFORMATION:  
; APPLICANT: Sone, Toshio  
; APPLICANT: Kume, Akinori  
; APPLICANT: Dairiki, Kazuo  
; APPLICANT: Iwama, Akiko  
; APPLICANT: Kino, Kohsuke  
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease  
; FILE REFERENCE: SPO-103  
; CURRENT APPLICATION NUMBER: US/09/142,524D  
; CURRENT FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: PCT/JP97/00740  
; PRIOR FILING DATE: 1997-03-10  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 87

; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Cryptomeria japonica  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(15)  
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 4  
US-09-142-524D-87

Query Match 73.9%; Score 17; DB 4; Length 15;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 9 FSTAW 13

RESULT 3  
US-09-142-524D-88  
; Sequence 88, Application US/09142524D  
; Patent No. 6719976  
; GENERAL INFORMATION:  
; APPLICANT: Sone, Toshio  
; APPLICANT: Kume, Akinori  
; APPLICANT: Dairiki, Kazuo  
; APPLICANT: Iwama, Akiko  
; APPLICANT: Kino, Kohsuke  
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease  
; FILE REFERENCE: SPO-103  
; CURRENT APPLICATION NUMBER: US/09/142,524D  
; CURRENT FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: PCT/JP97/00740  
; PRIOR FILING DATE: 1997-03-10  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 88  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Cryptomeria japonica  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(15)  
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 5  
US-09-142-524D-88

Query Match 73.9%; Score 17; DB 4; Length 15;  
Best Local Similarity 40.0%; Pred. No. 2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 4 FSTAW 8

RESULT 4  
US-08-469-260A-428  
; Sequence 428, Application US/08469260A  
; Patent No. 6451578  
; GENERAL INFORMATION:  
; APPLICANT: JOHN N. SIMONS  
; APPLICANT: TAMI J. PILOT-MATIAS  
; APPLICANT: GEORGE J. DAWSON  
; APPLICANT: GEORGE G. SCHLAUDER  
; APPLICANT: SURESH M. DESAI  
; APPLICANT: THOMAS P. LEARY  
; APPLICANT: ANTHONY SCOTT MUERHOFF  
; APPLICANT: JAMES C. ERKER  
; APPLICANT: SHERI L. BUIJK  
; APPLICANT: ISA K. MUSHAWAR  
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS REAGENTS AND METHODS FOR THEIR USE  
; NUMBER OF SEQUENCES: 716

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
; STREET: 100 ABBOTT PARK ROAD  
; CITY: ABBOTT PARK  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/469,260A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/424,550  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: POREMBSKI, PRISCILLA E.  
; REGISTRATION NUMBER: 33,207  
; REFERENCE/DOCKET NUMBER: 5527.PC.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 708-937-6365  
; TELEFAX: 708-938-2623  
; INFORMATION FOR SEQ ID NO: 428:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 29 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-469-260A-428  
  
Query Match 73.9%; Score 17; DB 4; Length 29;  
Best Local Similarity 40.0%; Pred. No. 3.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 FXXW 5  
Db 12 FASAW 16  
  
RESULT 5  
US-08-488-446-428  
; Sequence 428, Application US/08488446  
; Patent No. 655898  
; GENERAL INFORMATION:  
; APPLICANT: JOHN N. SIMONS  
; APPLICANT: TAMI J. PILOT-MATIAS  
; APPLICANT: GEORGE J. DAWSON  
; APPLICANT: GEORGE G. SCHLAUDER  
; APPLICANT: SURESH M. DESAI  
; APPLICANT: THOMAS P. LEARY  
; APPLICANT: ANTHONY SCOTT MUERHOFF  
; APPLICANT: JAMES C. ERKER  
; APPLICANT: SHERI L. BUIJK  
; APPLICANT: ISA K. MUSHAWAR  
; TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS  
; REAGENTS AND METHODS FOR THEIR USE  
; NUMBER OF SEQUENCES: 716  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
; STREET: 100 ABBOTT PARK ROAD  
; CITY: ABBOTT PARK  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,446  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/424,550  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: POREMBSKI, PRISCILLA E.  
; REGISTRATION NUMBER: 33,207  
; REFERENCE/DOCKET NUMBER: 5527.PC.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 708-937-6365  
; TELEFAX: 708-938-2623  
; INFORMATION FOR SEQ ID NO: 428:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 29 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-488-446-428  
  
Query Match 73.9%; Score 17; DB 4; Length 29;  
Best Local Similarity 40.0%; Pred. No. 3.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 FXXW 5  
Db 12 FASAW 16  
  
RESULT 6  
US-08-467-344A-428  
; Sequence 428, Application US/08467344A  
; Patent No. 6586568  
; GENERAL INFORMATION:  
; APPLICANT: JOHN N. SIMONS  
; APPLICANT: TAMI J. PILOT-MATIAS  
; APPLICANT: GEORGE J. DAWSON  
; APPLICANT: GEORGE G. SCHLAUDER  
; APPLICANT: SURESH M. DESAI  
; APPLICANT: THOMAS P. LEARY  
; APPLICANT: ANTHONY SCOTT MUERHOFF  
; APPLICANT: JAMES C. ERKER  
; APPLICANT: SHERI L. BUIJK  
; APPLICANT: ISA K. MUSHAWAR  
; TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS  
; REAGENTS AND METHODS FOR THEIR USE  
; NUMBER OF SEQUENCES: 716  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
; STREET: 100 ABBOTT PARK ROAD  
; CITY: ABBOTT PARK  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,344A  
; FILING DATE: 07-Jun-1995  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/424,550  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: POREMBSKI, PRISCILLA E.  
; REGISTRATION NUMBER: 33,207  
; REFERENCE/DOCKET NUMBER: 5527.PC.01  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 708-937-6365  
TELEFAX: 708-938-2623  
INFORMATION FOR SEQ ID NO: 428:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 428:  
US-08-467-344A-428

Query Match 73.9%; Score 17; DB 4; Length 29;  
Best Local Similarity 40.0%; Pred. No. 3.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 12 FASAW 16

RESULT 7  
US-08-424-550B-428  
; Sequence 428, Application US/08424550B  
; Patent No. 6720166  
; GENERAL INFORMATION:  
; APPLICANT: JOHN N. SIMONS  
; APPLICANT: TAMI J. PILOT-MATIAS  
; APPLICANT: GEORGE J. DAWSON  
; APPLICANT: GEORGE G. SCHLAUDER  
; APPLICANT: SURESH M. DESAI  
; APPLICANT: THOMAS P. LEARY  
; APPLICANT: ANTHONY SCOTT MUERHOFF  
; APPLICANT: JAMES C. ERKER  
; APPLICANT: SHERI L. BUIJK  
; APPLICANT: ISA K. MUSHAWAR  
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
; NUMBER OF SEQUENCES: 716  
; CORRESPONDENCE ADDRESS: 716  
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
; STREET: 100 ABBOTT PARK ROAD  
; CITY: ABBOTT PARK  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/424,550B  
; FILING DATE:  
; CLASSIFICATION: 435435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: POREBSKI, PRISCILLA E.  
; REGISTRATION NUMBER: 33,207  
; REFERENCE/DOCKET NUMBER: 5527.PC.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 708-937-6365  
; TELEFAX: 708-938-2623  
; INFORMATION FOR SEQ ID NO: 428:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 29 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-424-550B-428

Query Match 73.9%; Score 17; DB 4; Length 29;  
Best Local Similarity 40.0%; Pred. No. 3.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 12 FASAW 16

RESULT 8  
US-08-118-270-134  
; Sequence 134, Application US/08118270  
; Patent No. 5508384  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Randall B.  
; APPLICANT: Schuster, David I.  
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
; NUMBER OF SEQUENCES: 348  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004

Query Match 73.9%; Score 17; DB 1; Length 34;  
Best Local Similarity 40.0%; Pred. No. 3.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 16 FTSAW 20

US-08-118-270-134  
; Sequence 134, Application US/08118270  
; Patent No. 5508384  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Randall B.  
; APPLICANT: Schuster, David I.  
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
; NUMBER OF SEQUENCES: 348  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/118,270  
; FILING DATE: 09-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/943,236  
; FILING DATE: 10-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Townsend, Kevin G.  
; REGISTRATION NUMBER: 34,033  
; REFERENCE/DOCKET NUMBER: MURPHY=2A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 134:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 34 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-118-270-134

Query Match 73.9%; Score 17; DB 1; Length 34;  
Best Local Similarity 40.0%; Pred. No. 3.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 16 FTSAW 20

RESULT 9  
US-08-118-270-172  
; Sequence 172, Application US/08118270  
; Patent No. 5508384  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Randall B.  
; APPLICANT: Schuster, David I.  
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
; NUMBER OF SEQUENCES: 348  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington



STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/118,270  
FILING DATE: 09-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/943,236  
FILING DATE: 10-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, Kevin G.  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: MURPHY=2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 172:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-118-270-172

Query Match 73.9%; Score 17; DB 1; Length 34;  
Best Local Similarity 40.0%; Pred. No. 3.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5  
Db 16 FTTAW 20

RESULT 10  
PCT-US93-08528-134  
Sequence 134, Application PC/TUS9308528  
GENERAL INFORMATION:  
APPLICANT: New York University  
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
NUMBER OF SEQUENCES: 348  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/08528  
FILING DATE: 09-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/943,236  
FILING DATE: 10-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, Kevin G.  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528

TELEX: 248633  
INFORMATION FOR SEQ ID NO: 134:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US93-08528-134

Query Match 73.9%; Score 17; DB 5; Length 34;  
Best Local Similarity 40.0%; Pred. No. 3.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5  
Db 16 FTTAW 20

RESULT 11  
PCT-US93-08528-172  
Sequence 172, Application PC/TUS9308528  
GENERAL INFORMATION:  
APPLICANT: New York University  
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
NUMBER OF SEQUENCES: 348  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/08528  
FILING DATE: 09-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/943,236  
FILING DATE: 10-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, Kevin G.  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 172:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US93-08528-172

Query Match 73.9%; Score 17; DB 5; Length 34;  
Best Local Similarity 40.0%; Pred. No. 3.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5  
Db 16 FTTAW 20

RESULT 12  
US-08-467-023-137

; Sequence 137, Application US/08467023  
; Patent No. 6090386  
; GENERAL INFORMATION:  
; APPLICANT: Griffith, Irwin J.;  
; APPLICANT: Pollock, Joanne;  
; APPLICANT: Bond, Julian F.;  
; APPLICANT: Garman, Richard D;  
; APPLICANT: Kuo, Mei-Chang;  
; APPLICANT: Yeung, Siu-mei H.;  
; APPLICANT: Brauer, Andrew;  
; APPLICANT: Exley, Mark A.;  
; APPLICANT: Powers, Steven P.  
; TITLE OF INVENTION: Allergenic Proteins And Peptides From  
; TITLE OF INVENTION: Japanese Cedar Pollen  
; NUMBER OF SEQUENCES: 261  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ImmuLogic Pharmaceutical Corporation, Inc.  
; STREET: 610 Lincoln St  
; CITY: Waltham  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,023  
; FILING DATE: June 6, 1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/350,225  
; FILING DATE: December 6, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jane E. Remillard  
; REGISTRATION NUMBER: 38,872  
; REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 137:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-08-467-023-137

Query Match 73.9%; Score 17; DB 3; Length 36;  
Best Local Similarity 40.0%; Pred. No. 3.8e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 28 FSTAW 32

RESULT 13  
US-09-330-914A-10  
; Sequence 10, Application US/09330914A  
; Patent No. 6432671  
; GENERAL INFORMATION:  
; APPLICANT: Flohe, Leopold  
; No. 6432671ecke, Everson  
; Kalisz, Henryk  
; Montemartini, Marisa  
; TITLE OF INVENTION: TRYPAEDOXIN, EXPRESSION PLASMID, PROCESS OF  
; PRODUCTION, METHOD OF USE, TEST KIT, AND  
; PHARMACEUTICAL COMPOSITION  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Broun  
; STREET: 233 South Wacker Drive/6300 Sears Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: Unites States of America  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/330,914A  
; FILING DATE: 11-Jun-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/EP97/06983  
; FILING DATE: 12-DEC-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, James P.  
; REGISTRATION NUMBER: 28,491  
; REFERENCE/DOCKET NUMBER: 29473/35678  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 37 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-09-330-914A-10

Query Match 73.9%; Score 17; DB 4; Length 37;  
Best Local Similarity 40.0%; Pred. No. 3.8e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 11 FSASW 15

RESULT 14  
US-08-467-023-136  
; Sequence 136, Application US/08467023  
; Patent No. 6090386  
; GENERAL INFORMATION:  
; APPLICANT: Griffith, Irwin J.;  
; APPLICANT: Pollock, Joanne;  
; APPLICANT: Bond, Julian F.;  
; APPLICANT: Garman, Richard D;  
; APPLICANT: Kuo, Mei-Chang;  
; APPLICANT: Brauer, Andrew;  
; APPLICANT: Exley, Mark A.;  
; APPLICANT: Powers, Steven P.  
; TITLE OF INVENTION: Allergenic Proteins And Peptides From  
; TITLE OF INVENTION: Japanese Cedar Pollen  
; NUMBER OF SEQUENCES: 261  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ImmuLogic Pharmaceutical Corporation, Inc.  
; STREET: 610 Lincoln St  
; CITY: Waltham  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,023  
FILING DATE: June 6, 1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/350,225  
FILING DATE: December 6, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane E. Remillard  
REGISTRATION NUMBER: 38,872  
REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 136:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 41 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-467-023-136

Query Match 73.9%; Score 17; DB 3; Length 41;  
Best Local Similarity 40.0%; Pred. No. 4.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5  
|  
Db 33 FSTAW 37

RESULT 15  
US-08-467-023-135  
Sequence 135, Application US/08467023  
Patent No. 6090386  
GENERAL INFORMATION:  
APPLICANT: Griffith, Irwin J.;  
APPLICANT: Pollock, Joanne;  
APPLICANT: Bond, Julian F.;  
APPLICANT: Garman, Richard D;  
APPLICANT: Kuo, Mei-Chang;  
APPLICANT: Yeung, Siu-mei H.;  
APPLICANT: Brauer, Andrew;  
APPLICANT: Exley, Mark A.;  
APPLICANT: Powers, Steven P.  
TITLE OF INVENTION: Allergenic Proteins And Peptides From  
TITLE OF INVENTION: Japanese Cedar Pollen  
NUMBER OF SEQUENCES: 261  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.  
STREET: 610 Lincoln St  
CITY: Waltham  
STATE: MA  
COUNTRY: USA  
ZIP: 02154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,023  
FILING DATE: June 6, 1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/350,225  
FILING DATE: December 6, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane E. Remillard  
REGISTRATION NUMBER: 38,872

REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 135:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-467-023-135

Query Match 73.9%; Score 17; DB 3; Length 45;  
Best Local Similarity 40.0%; Pred. No. 4.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5  
|  
Db 33 FSTAW 37

RESULT 16  
US-09-149-476-475  
Sequence 475, Application US/09149476  
Patent No. 6420526  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: PZ002P1  
CURRENT APPLICATION NUMBER: US/09/149,476  
CURRENT FILING DATE: 1998-09-08  
EARLIER APPLICATION NUMBER: PCT/US98/04493  
EARLIER FILING DATE: 1998-03-06  
EARLIER APPLICATION NUMBER: 60/040,162  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,333  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/038,621  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,626  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,334  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,336  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,163  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/047,600  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,615  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,597  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,502  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,633  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,583  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,617  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,618  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,503  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,592  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,581  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,584  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,500

[illegible]

;	EARLIER	APPLICATION	NUMBER: 60/056, 899
;	EARLIER	FILING DATE: 1997-08-22	
;	EARLIER	APPLICATION NUMBER: 60/056, 911	
;	EARLIER	FILING DATE: 1997-08-22	
;	EARLIER	APPLICATION NUMBER: 60/056, 636	
;	EARLIER	FILING DATE: 1997-08-22	
;	EARLIER	APPLICATION NUMBER: 60/056, 874	
;	EARLIER	FILING DATE: 1997-08-22	
;	EARLIER	APPLICATION NUMBER: 60/056, 910	
;	EARLIER	FILING DATE: 1997-08-22	
;	EARLIER	APPLICATION NUMBER: 60/056, 864	
;	EARLIER	FILING DATE: 1997-08-22	
;	EARLIER	APPLICATION NUMBER: 60/056, 631	
;	EARLIER	FILING DATE: 1997-08-22	
;	EARLIER	APPLICATION NUMBER: 60/056, 845	
;	EARLIER	FILING DATE: 1997-08-22	
;	EARLIER	APPLICATION NUMBER: 60/056, 892	
;	EARLIER	FILING DATE: 1997-08-22	
;	EARLIER	APPLICATION NUMBER: 60/057, 761	
;	EARLIER	FILING DATE: 1997-08-22	
;	EARLIER	APPLICATION NUMBER: 60/047, 595	
;	EARLIER	FILING DATE: 1997-05-23	
;	EARLIER	APPLICATION NUMBER: 60/047, 599	
;	EARLIER	FILING DATE: 1997-05-23	
;	EARLIER	APPLICATION NUMBER: 60/047, 588	
;	EARLIER	FILING DATE: 1997-05-23	
;	EARLIER	APPLICATION NUMBER: 60/047, 585	
;	EARLIER	FILING DATE: 1997-05-23	
;	EARLIER	APPLICATION NUMBER: 60/047, 586	
;	EARLIER	FILING DATE: 1997-05-23	
;	EARLIER	APPLICATION NUMBER: 60/047, 590	
;	EARLIER	FILING DATE: 1997-05-23	
;	EARLIER	APPLICATION NUMBER: 60/047, 594	
;	EARLIER	FILING DATE: 1997-05-23	
;	EARLIER	APPLICATION NUMBER: 60/047, 589	
;	EARLIER	FILING DATE: 1997-05-23	
;	EARLIER	APPLICATION NUMBER: 60/047, 593	
;	EARLIER	FILING DATE: 1997-05-23	
;	EARLIER	APPLICATION NUMBER: 60/047, 614	
;	EARLIER	FILING DATE: 1997-05-23	
;	EARLIER	APPLICATION NUMBER: 60/043, 578	
;	EARLIER	FILING DATE: 1997-04-11	
;	EARLIER	APPLICATION NUMBER: 60/043, 576	
;	EARLIER	FILING DATE: 1997-04-11	
;	EARLIER	APPLICATION NUMBER: 60/047, 501	
;	EARLIER	FILING DATE: 1997-05-23	
;	EARLIER	APPLICATION NUMBER: 60/043, 670	
;	EARLIER	FILING DATE: 1997-04-11	
;	EARLIER	APPLICATION NUMBER: 60/056, 632	
;	EARLIER	FILING DATE: 1997-08-22	
;	EARLIER	APPLICATION NUMBER: 60/056, 664	
;	EARLIER	FILING DATE: 1997-08-22	
;	EARLIER	APPLICATION NUMBER: 60/056, 876	
;	EARLIER	FILING DATE: 1997-08-22	
;	EARLIER	APPLICATION NUMBER: 60/056, 881	
;	EARLIER	FILING DATE: 1997-08-22	
;	EARLIER	APPLICATION NUMBER: 60/056, 909	
;	EARLIER	FILING DATE: 1997-08-22	
;	EARLIER	APPLICATION NUMBER: 60/056, 875	
;	EARLIER	FILING DATE: 1997-08-22	
;	EARLIER	APPLICATION NUMBER: 60/056, 862	
;	EARLIER	FILING DATE: 1997-08-22	
;	EARLIER	APPLICATION NUMBER: 60/056, 887	
;	EARLIER	FILING DATE: 1997-08-22	
;	EARLIER	APPLICATION NUMBER: 60/056, 908	
;	EARLIER	FILING DATE: 1997-08-22	
;	EARLIER	APPLICATION NUMBER: 60/048, 964	
;	EARLIER	FILING DATE: 1997-06-06	
;	EARLIER	APPLICATION NUMBER: 60/057, 650	
;	EARLIER	FILING DATE: 1997-09-05	
;	EARLIER	APPLICATION NUMBER: 60/056, 884	
;	EARLIER	FILING DATE: 1997-08-22	
;	EARLIER	APPLICATION NUMBER: 60/057, 669	

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; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match      73.9%; Score 17; DB 4; Length 45;
Best Local Similarity 40.0%; Pred. No. 4.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 FXXXW 5
Db      31 FSAW 35

RESULT 17
US-09-369-247-129
; Sequence 129, Application US/09369247
; Patent No. 656992
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 44 Human Secreted Proteins
; FILE REFERENCE: P2024P1
; CURRENT APPLICATION NUMBER: US/09/369,247
; CURRENT FILING DATE: 1999-08-05
; EARLIER APPLICATION NUMBER: 60/074,118
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,157
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,137
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,341
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/074,141
; EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 129
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-369-247-129

Query Match      73.9%; Score 17; DB 4; Length 47;
Best Local Similarity 40.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 FXXXW 5
Db      39 FSSW 43

RESULT 18
US-08-118-270-209
; Sequence 209, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
US-08-118-270-209
```

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,270
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY=2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 209:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-118-270-209

Query Match      73.9%; Score 17; DB 1; Length 49;
Best Local Similarity 40.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 FXXXW 5
Db      36 FTSW 40

RESULT 19
PCT-US93-08528-209
; Sequence 209, Application PC/TUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08528
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 209:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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```
; MOLECULE TYPE: peptide
PCT-US93-08528-209

Query Match      73.9%; Score 17; DB 5; Length 49;
Best Local Similarity 40.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
Db      36 FTSAW 40

RESULT 20
US-09-434-840-73
; Sequence 73, Application US/09434840
; Patent No. 6620985
; GENERAL INFORMATION:
; APPLICANT: Glazebrook, Jane
; APPLICANT: Jirage, Dayadevi
; APPLICANT: Tootle, Tina L
; APPLICANT: Zhou, Nan
; APPLICANT: Feys, Bart
; TITLE OF INVENTION: PAD4 COMPOSITIONS AND METHODS THEREFOR
; FILE REFERENCE: 043503.0009
; CURRENT APPLICATION NUMBER: US/09/434,840
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: 09/190,733
; EARLIER FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Thermomyces lanuginosus
US-09-434-840-73

Query Match      73.9%; Score 17; DB 4; Length 54;
Best Local Similarity 40.0%; Pred. No. 4.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
Db      7 FTSSW 11

RESULT 21
US-09-733-643B-21
; Sequence 21, Application US/09733643B
; Patent No. 6734344
; GENERAL INFORMATION:
; APPLICANT: Laroche, Andre J.
; APPLICANT: Huang, Timothy Y
; APPLICANT: Lu, Zhen-Xiang
; APPLICANT: Frick, Michele M.
; APPLICANT: Huang, Hung Chang
; APPLICANT: Cheng, Kuo Joan
; TITLE OF INVENTION: Coniothyrium minitans beta-(1,3) exoglucanase gene
; FILE REFERENCE: 24014US1
; CURRENT APPLICATION NUMBER: US/09/733,643B
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/170,168
; PRIOR FILING DATE: 1999-12-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: Exopg
US-09-733-643B-21

Query Match      73.9%; Score 17; DB 4; Length 54;
Best Local Similarity 40.0%; Pred. No. 4.9e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
Db      23 FAAAW 27

RESULT 22
US-09-621-976-6592
; Sequence 6592, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6592
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6592

Query Match      73.9%; Score 17; DB 4; Length 56;
Best Local Similarity 40.0%; Pred. No. 5.1e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
Db      8 FTSSW 12

RESULT 23
US-09-270-767-35869
; Sequence 35869, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35869
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-35869

Query Match      73.9%; Score 17; DB 4; Length 60;
Best Local Similarity 40.0%; Pred. No. 5.3e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
Db      13 FTSSW 17

RESULT 24
US-09-270-767-51086
; Sequence 51086, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
```

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; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51086
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-51086

Query Match          73.9%; Score 17; DB 4; Length 60;
Best Local Similarity 40.0%; Pred. No. 5.3e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 FXXW 5
Db      13 FTSSW 17

RESULT 25
US-09-134-001C-4258
; Sequence 4258, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4258
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4258

Query Match          73.9%; Score 17; DB 3; Length 61;
Best Local Similarity 40.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 FXXW 5
Db      14 FSTSW 18

RESULT 26
US-09-252-991A-28658
; Sequence 28658, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28658
; LENGTH: 62
; TYPE: PRT
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28658

Query Match          73.9%; Score 17; DB 4; Length 62;
Best Local Similarity 40.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 FXXW 5
Db      58 FAASW 62

RESULT 27
US-09-621-976-5704
; Sequence 5704, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5704
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -43..-1
US-09-621-976-5704

Query Match          73.9%; Score 17; DB 4; Length 62;
Best Local Similarity 40.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 FXXW 5
Db      35 FTAAW 39

RESULT 28
US-09-248-796A-26247
; Sequence 26247, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 26247
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-26247

Query Match          73.9%; Score 17; DB 4; Length 62;
Best Local Similarity 40.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 FXXW 5
Db      27 FSTSW 31
```



```
RESULT 29
US-09-902-540-11838
; Sequence 11838, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11838
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11838

Query Match      73.9%; Score 17; DB 4; Length 63;
Best Local Similarity 40.0%; Pred. No. 5.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
Db      27 FATAW 31

RESULT 30
US-09-621-976-6715
; Sequence 6715, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6715
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6715

Query Match      73.9%; Score 17; DB 4; Length 69;
Best Local Similarity 40.0%; Pred. No. 5.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
Db      62 FATTW 66

RESULT 31
US-09-248-796A-24056
; Sequence 24056, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
```

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; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 24056
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-24056

Query Match      73.9%; Score 17; DB 4; Length 69;
Best Local Similarity 40.0%; Pred. No. 5.8e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 FXXXW 5
Db      62 FTTAW 66

RESULT 32
US-09-330-914A-4
; Sequence 4, Application US/09330914A
; Patent No. 6432671
; GENERAL INFORMATION:
; APPLICANT: Flohe, Leopold
; APPLICANT: Kalisz, Henryk
; APPLICANT: Montemartini, Marisa
; TITLE OF INVENTION: TRYPARADOXIN, EXPRESSION PLASMID, PROCESS OF
; PRODUCTION, METHOD OF USE, TEST KIT, AND
; PHARMACEUTICAL COMPOSITION
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Broun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: Unites States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/330,914A
; FILING DATE: 11-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP97/06983
; FILING DATE: 12-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, James P.
; REGISTRATION NUMBER: 28,491
; REFERENCE/DOCKET NUMBER: 29473/35678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-330-914A-4

Query Match      73.9%; Score 17; DB 4; Length 80;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
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Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 FXXW 5
Db 8 FSASW 12
RESULT 33
US-09-270-767-37303
; Sequence 37303, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37303
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-37303
Query Match 73.9%; Score 17; DB 4; Length 80;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 FXXW 5
Db 41 FTASW 45
RESULT 34
US-09-270-767-52520
; Sequence 52520, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52520
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-52520
Query Match 73.9%; Score 17; DB 4; Length 80;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 FXXW 5
Db 41 FTASW 45
RESULT 35
US-09-248-796A-24759
; Sequence 24759, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 24759
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-24759
Query Match 73.9%; Score 17; DB 4; Length 80;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 FXXW 5
Db 72 FTTAW 76
RESULT 36
US-09-248-796A-19864
; Sequence 19864, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19864
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19864
Query Match 73.9%; Score 17; DB 4; Length 82;
Best Local Similarity 40.0%; Pred. No. 6.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 FXXW 5
Db 74 FTTAW 78
RESULT 37
US-08-353-476-78
; Sequence 78, Application US/08353476
; Patent No. 5871902
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

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US-09-214-371-10.rai
Query Match 73.9%; Score 17; DB 4; Length 80;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 FXXW 5
Db 41 FTASW 45
RESULT 35
US-09-248-796A-24759
; Sequence 24759, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 24759
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-24759
Query Match 73.9%; Score 17; DB 4; Length 80;
Best Local Similarity 40.0%; Pred. No. 6.5e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 FXXW 5
Db 72 FTTAW 76
RESULT 36
US-09-248-796A-19864
; Sequence 19864, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19864
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19864
Query Match 73.9%; Score 17; DB 4; Length 82;
Best Local Similarity 40.0%; Pred. No. 6.6e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 FXXW 5
Db 74 FTTAW 78
RESULT 37
US-08-353-476-78
; Sequence 78, Application US/08353476
; Patent No. 5871902
; GENERAL INFORMATION:
; APPLICANT: Weininger, Susan
; APPLICANT: Weininger, Arthur M
; TITLE OF INVENTION: METHOD OF DETECTION OF DNA WITH A
; TITLE OF INVENTION: SPECIFIC SEQUENCE COMPOSITION
; NUMBER OF SEQUENCES: 117
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st St., Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/353,476  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Bencen, Gerard H  
REGISTRATION NUMBER: 35,746  
REFERENCE/DOCKET NUMBER: GP-100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (904) 375-8100  
TELEFAX: (904) 372-5800  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 84 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
US-08-353-476-78

Query Match 73.9%; Score 17; DB 2; Length 84;  
Best Local Similarity 40.0%; Pred. No. 6.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 31 FSTTW 35

## RESULT 38

US-08-679-493A-97  
Sequence 97, Application US/08679493A  
Patent No. 6303295

GENERAL INFORMATION:  
APPLICANT: Taylor, Ethan W.  
TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS  
FILE REFERENCE: 55-95  
CURRENT APPLICATION NUMBER: US/08/679,493A  
CURRENT FILING DATE: 1996-07-12  
PRIOR APPLICATION NUMBER: 60/001203  
PRIOR FILING DATE: 1995-07-14  
PRIOR APPLICATION NUMBER: 60/003,112  
PRIOR FILING DATE: 1995-09-01  
NUMBER OF SEQ ID NOS: 216  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 97  
LENGTH: 84  
TYPE: PRT  
ORGANISM: bovine papillomavirus type 8  
US-08-679-493A-97

Query Match 73.9%; Score 17; DB 3; Length 84;  
Best Local Similarity 40.0%; Pred. No. 6.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 31 FSTTW 35

## RESULT 39

US-09-583-110-3199  
Sequence 3199, Application US/09583110  
Patent No. 6699703

GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al.  
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus  
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

FILE REFERENCE: PATH00-07A  
CURRENT APPLICATION NUMBER: US/09/583,110  
CURRENT FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/107,433  
PRIOR FILING DATE: 1998-06-30  
PRIOR APPLICATION NUMBER: US 60/085,131  
PRIOR FILING DATE: 1998-05-12  
PRIOR APPLICATION NUMBER: US 60/051,553  
PRIOR FILING DATE: 1997-07-02  
NUMBER OF SEQ ID NOS: 5322  
SEQ ID NO 3199  
LENGTH: 86  
TYPE: PRT  
ORGANISM: Streptococcus pneumoniae  
US-09-583-110-3199

Query Match 73.9%; Score 17; DB 4; Length 86;  
Best Local Similarity 40.0%; Pred. No. 6.8e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 4 FSSAW 8

## RESULT 40

US-09-621-976-6168  
Sequence 6168, Application US/09621976  
Patent No. 6639063

GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Jobert, S.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
FILE REFERENCE: GENSET.054PR2  
CURRENT APPLICATION NUMBER: US/09/621,976  
CURRENT FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm  
SEQ ID NO 6168  
LENGTH: 89  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-621-976-6168

Query Match 73.9%; Score 17; DB 4; Length 89;  
Best Local Similarity 40.0%; Pred. No. 7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
|  
Db 58 FSASW 62

Search completed: October 18, 2005, 15:32:10  
Job time : 30.7059 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 18, 2005, 15:14:39 ; Search time 111.529 Seconds  
(without alignments)  
27.742 Million cell updates/sec

Title: US-09-214-371-10

Perfect score: 23

Sequence: 1 FXXXWXXX 8

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	73.9	9	7	ADC07129 Honeybee
2	17	73.9	9	7	ADC07134 Painted 1
3	17	73.9	10	3	AAB10010
4	17	73.9	10	4	AAB86090 H. pylori
5	17	73.9	10	4	AAB86058
6	17	73.9	11	7	ADC07163 Painted 1
7	17	73.9	13	4	AAE05735
8	17	73.9	13	6	ABG75574
9	17	73.9	14	4	AAM98088
10	17	73.9	15	2	AAR97874
11	17	73.9	15	2	AAR97875
12	17	73.9	15	2	AAW57758
13	17	73.9	19	5	AAE23038
14	17	73.9	20	2	AAW42165
15	17	73.9	20	4	AAG62999
16	17	73.9	25	7	ADE25429
17	17	73.9	27	4	AAM18617
18	17	73.9	27	4	AAM31077
19	17	73.9	27	4	ABG52487
20	17	73.9	27	5	ABG40522
21	17	73.9	29	3	AAB09301
22	17	73.9	32	4	AAG71365
23	17	73.9	33	5	ABP60808
24	17	73.9	33	8	ABO54713
25	17	73.9	34	2	AAR50631

99 17 73.9 61 4 AA04154 Human gen  
100 17 73.9 61 4 AA45906 Propionib

ALIGNMENTS

RESULT 1  
ADC07129  
ID ADC07129 standard; peptide; 9 AA.  
XX  
AC ADC07129;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Honeybee AKH peptide.  
XX  
KW lipid mobilisation; insect; adipokinetic hormone; AKH; anorectic;  
KW antidiabetic; hypotensive; cardiant; antiarthritic; cytostatic;  
KW nephrotropic; hepatotropic; analgesic; cerebroprotective; uropathic;  
KW obesity; type II diabetes; cholelithiasis; hypertension;  
KW coronary heart disease; atherosclerosis; glycosenosis; arthritis; cancer;  
KW renal failure; liver; chronic pain; sleep apnea; stroke;  
KW urinary incontinence; honeybee.

OS Synthetic.  
OS Apis mellifera.  
XX  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /label= OTHER  
FT /note= "OTHER = Pyroglutamic acid"  
FT Misc-difference 9  
FT /note= "Preferably C-terminal amide"

XX WO2003066080-A1.  
XX  
PD 14-AUG-2003.  
XX  
PF 07-FEB-2003; 2003WO-US003800.  
XX  
PR 07-FEB-2002; 2002US-00072419.  
XX  
PA (BLMB-) BLM GROUP.  
XX  
PI Schacter BZ, Schacter LP;  
XX  
DR WPI; 2003-712542/67.  
XX  
PT Pharmaceutical composition useful for promoting weight loss, comprises an  
PT insect adipokinetic hormone, having a pyroglutamate residue at its amino  
PT terminus.

XX Claim 29; Page 20; 82pp; English.  
XX  
CC The invention relates to a novel method of promoting lipid mobilisation  
CC in a human which comprises administering an insect adipokinetic hormone  
CC (AKH). The hormone of the invention demonstrates anorectic, antidiabetic,  
CC hypotensive, cardiant, antiarthritic, cytostatic, nephrotropic,  
CC hepatotropic, analgesic, cerebroprotective and uropathic activities. The  
CC method of the invention may be useful for treating obesity, type II  
CC diabetes, cholelithiasis, hypertension, coronary heart disease,  
CC atherosclerosis, types I to VI glycosenosis, arthritis, cancer, renal  
CC failure, liver disease, chronic pain, sleep apnea, stroke and urinary  
CC incontinence. The current sequence is that of the honeybee AKH peptide of  
CC the invention.

XX Sequence 9 AA;  
SQ  
Query Match 73.9%; Score 17; DB 7; Length 9;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
| |  
Db 4 FTSSW 8  
RESULT 2  
ADC07134  
ID ADC07134 standard; peptide; 9 AA.  
XX  
AC ADC07134;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Painted lady AKH peptide.  
XX  
KW lipid mobilisation; insect; adipokinetic hormone; AKH; anorectic;  
KW antidiabetic; hypotensive; cardiant; antiarthritic; cytostatic;  
KW nephrotropic; hepatotropic; analgesic; cerebroprotective; uropathic;  
KW obesity; type II diabetes; cholelithiasis; hypertension;  
KW coronary heart disease; atherosclerosis; glycosenosis; arthritis; cancer;  
KW renal failure; liver; chronic pain; sleep apnea; stroke;  
KW urinary incontinence; painted lady.  
XX  
OS Synthetic.  
OS Vanessa cardui.  
XX  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /label= OTHER  
FT /note= "OTHER = Pyroglutamic acid"  
FT Misc-difference 9  
FT /note= "Preferably C-terminal amide"

XX WO2003066080-A1.  
XX  
PD 14-AUG-2003.  
XX  
PF 07-FEB-2003; 2003WO-US003800.  
XX  
PR 07-FEB-2002; 2002US-00072419.  
XX  
PA (BLMB-) BLM GROUP.  
XX  
PI Schacter BZ, Schacter LP;  
XX  
DR WPI; 2003-712542/67.  
XX  
PT Pharmaceutical composition useful for promoting weight loss, comprises an  
PT insect adipokinetic hormone, having a pyroglutamate residue at its amino  
PT terminus.  
XX  
PS Claim 29; Page 20; 82pp; English.  
XX  
CC The invention relates to a novel method of promoting lipid mobilisation  
CC in a human which comprises administering an insect adipokinetic hormone  
CC (AKH). The hormone of the invention demonstrates anorectic, antidiabetic,  
CC hypotensive, cardiant, antiarthritic, cytostatic, nephrotropic,  
CC hepatotropic, analgesic, cerebroprotective and uropathic activities. The  
CC method of the invention may be useful for treating obesity, type II  
CC diabetes, cholelithiasis, hypertension, coronary heart disease,  
CC atherosclerosis, types I to VI glycosenosis, arthritis, cancer, renal  
CC failure, liver disease, chronic pain, sleep apnea, stroke and urinary  
CC incontinence. The current sequence is that of the painted lady AKH  
CC peptide of the invention.

XX Sequence 9 AA;  
SQ  
Query Match 73.9%; Score 17; DB 7; Length 9;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 FXXXW 5  
| |

```
Db          4 FTSSW 8

RESULT 3
AAB10010
ID  AAB10010 standard; protein; 10 AA.
XX
AC  AAB10010;
XX
DT  01-NOV-2000 (first entry)
XX
DE  H. pylori beta-urease-binding antibody heavy chain CDR1 protein #2.
XX
KW  Acid-resistant microorganism; detection; faecal; intestine; infection;
KW  monoclonal antibody; heavy chain; complementarity determining region;
KW  CDR; beta-urease.
XX
OS  Unidentified.
XX
PN  WO200026671-A1.
XX
PD  11-MAY-2000.
XX
PF  29-OCT-1999; 99WO-EP008212.
XX
PR  29-OCT-1998; 98EP-00120517.
PR  06-NOV-1998; 98EP-00120687.
XX
PA  (CONN-) CONNEX GMBH.
XX
PI  Reiter C, Cullmann G, Friedrichs U, Heppner P, Lakner M;
PI  Ringeis A;
XX
DR  WPI; 2000-365747/31.
DR  N-PSDB; AAA40166.
XX
PT  Detecting infection by acid-fast microbes for diagnosis of Helicobacter
PT  pylori, comprises reacting a fecal sample with two binding reagents for
PT  antigens that survive intestinal passage.
XX
PS  Claim 26; Page 22; 84pp; German.
XX
CC  This invention describes a novel method for the detection of a mammalian
CC  infection by an acid-resistant microorganism (A) by treating a faecal
CC  sample with at least two different monoclonal antibodies (Mab) (or their
CC  fragments or derivatives) or aptamers (collectively (I)) and detecting
CC  formation of a complex (C) between (I) and the corresponding antigens of
CC  (A). The first and second (I) bind to epitopes of different antigens
CC  (Ag). These epitopes are present, after passage through the intestines,
CC  in at least some mammals, and have either: (i) their native structure; or
CC  (ii) a structure against which an antibody is produced by an animal
CC  infected or immunized with (A), or its extract, lysate, derived protein
CC  or fragment, or with a synthetic peptide. Practically all mammals display
CC  at least one of the specified epitopes. The method is used to detect
CC  infection by acid-fast bacteria, particularly of the genera Helicobacter,
CC  Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus, M.
CC  tuberculosis, C. jejuni and C. pylori. (i) may also be used
CC  therapeutically. The method is direct and non-invasive, and provides an
CC  inexpensive and easily standardizable diagnosis, despite possible
CC  degradation of antigens during passage through the intestines. This
CC  sequence represents a fragment of a H. pylori beta-urease-binding
CC  antibody heavy chain complementarity determining region CDR1 which is
CC  used to illustrate the method of the invention
XX
SQ  Sequence 10 AA;

Query Match      73.9%; Score 17; DB 3; Length 10;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 4 FSTSW 8

RESULT 5
AAB86058
ID  AAB86058 standard; peptide; 10 AA.
XX
```

```
RESULT 4
AAB86090
ID  AAB86090 standard; peptide; 10 AA.
XX
AC  AAB86090;
XX
DT  17-JUL-2001 (first entry)
XX
DE  H. pylori beta-urease derived antibody light chain CDR1 #1.
XX
KW  Catalase; beta-urease; antibody; antigen; detection; infection; epitope;
KW  acid-resistant microorganism; complementarity determining region; CDR;
KW  feces; heavy chain; light chain.
XX
OS  Unidentified.
XX
PN  WO200127612-A2.
XX
PD  19-APR-2001.
XX
PF  12-OCT-2000; 2000WO-EP010057.
XX
PR  12-OCT-1999; 99EP-00120351.
PR  16-MAR-2000; 2000EP-00105592.
PR  31-MAR-2000; 2000EP-00107028.
PR  10-MAY-2000; 2000EP-00110110.
XX
PA  (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.
XX
PI  Reiter C, Cullmann G, Lakner M, Truee A, Dehnert S, Schwartz G;
XX
DR  WPI; 2001-282086/29.
DR  N-PSDB; AAF88117.
XX
PT  Detecting infections by acid-resistant microorganisms, particularly for
PT  diagnosing Helicobacter pylori, comprises immunochromatographic detection
PT  of antigen in feces.
XX
PS  Claim 27; Page 27; 90pp; German.
XX
CC  This invention describes a novel method for detecting infection by an
CC  acid-resistant microorganism (A), in a mammal, using
CC  immunochromatography. The method is used to diagnose infection by an acid
CC  -resistant microorganism (A), in a mammal, such as Helicobacter,
CC  Campylobacter or Mycobacterium, particularly H. pylori (most preferred),
CC  H. hepatica, C. jejuni and M. tuberculosis. The method is rapid, simple,
CC  inexpensive and non-invasive, and may indicate the stage of infection. A
CC  test strip used in the method may include a filter to eliminate particles
CC  present in the sample and only a single receptor provides a reasonably
CC  secure diagnosis, with specificity and selectivity improved by detecting
CC  several epitopes (of catalase) or different antigens (catalase and beta-
CC  urease). The method can be automated. This sequence represents a
CC  complementarity determining region (CDR) from an antibody raised against
CC  the H. pylori catalase or beta-urease antigen which is used to illustrate
CC  the method of the invention
XX
SQ  Sequence 10 AA;

Query Match      73.9%; Score 17; DB 4; Length 10;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5
Db 4 FSTSW 8

RESULT 5
AAB86058
ID  AAB86058 standard; peptide; 10 AA.
XX
```

AC AAB86058;  
XX  
DT 17-JUL-2001 (first entry)  
XX  
DE H. pylori beta-urease derived antibody light chain CDR1 #1.  
XX  
KW Heavy chain; light chain; catalase; beta-urease; detection; CDR; antigen;  
KW infection; acid-resistant microorganism; fecal; antibody; diagnosis;  
KW antibacterial; complementarity determining region.  
XX  
OS Unidentified.  
XX  
PN WO200127613-A2.  
XX  
PD 19-APR-2001.  
XX  
PF 12-OCT-2000; 2000WO-EP010058.  
XX  
PR 12-OCT-1999; 99EP-00120351.  
PR 16-MAR-2000; 2000EP-00105592.  
PR 31-MAR-2000; 2000EP-00107028.  
PR 10-MAY-2000; 2000EP-00110110.  
XX  
PA (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.  
XX  
PI Reiter C, Cullmann G, Heppner P, Ringeis A, Mueller H, Haindl E;  
XX WPI; 2001-282087/29.  
DR N-PSDB; AAF88060.  
XX  
PT Detecting infections by acid-resistant microorganisms, particularly for  
PT diagnosing Helicobacter pylori, comprises an immunoassay on a fecal  
PT sample.  
XX  
PS Claim 23; Page 17; 89pp; German.  
XX  
CC This invention describes a novel method for detecting, in a mammal,  
CC infection by an acid-resistant microorganism (A) which comprises reacting  
CC a fecal sample with: (i) a receptor (R) such that a complex is formed  
CC with an antigen (Ag) of (A); or (ii) two different R so that a three-part  
CC complex is formed with Ag, and the formation of a complex detected. R are  
CC specific for an Ag which, after passage through the intestines, at least  
CC in some mammals, retains a native (or corresponding) structure against  
CC which the mammal produces antibodies (when immunized or infected with  
CC (A), or its extracts, lysates or derived proteins (or fragments) or  
CC synthetic peptides). The products of the invention have antibacterial  
CC activity. The method is used to diagnose infection by Helicobacter,  
CC Campylobacter or Mycobacterium, particularly H. pylori (most preferred),  
CC H. hepatica, C. jejuni and M. tuberculosis, and also to monitor the  
CC progress of treatment. Receptors, particularly antibodies, directed  
CC against Ag can be used therapeutically for treatment of infections. The  
CC method requires only one R to provide a reasonably secure diagnosis  
CC (although use of two R improves sensitivity), so is relatively  
CC inexpensive and more easily standardized. Also it is direct, non-  
CC invasive, suitable for automation and may indicate the stage of an  
CC infection. This sequence represents a complementarity determining region  
CC (CDR) from an antibody generated against a Helicobacter pylori antigen  
CC (catalase or beta-urease) which is used to illustrate the method of the  
CC invention  
XX  
SQ Sequence 10 AA;  
  
Query Match 73.9%; Score 17; DB 4; Length 10;  
Best Local Similarity 40.0%; Pred. No. 3.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 FXXXW 5  
| |  
Db 4 FTSSW 8  
  
RESULT 6  
ADC07163

ID ADC07163 standard; peptide; 11 AA.  
XX  
AC ADC07163;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Painted lady AKH peptide 2.  
XX  
KW lipid mobilisation; insect; adipokinetic hormone; AKH; anorectic;  
KW antidiabetic; hypotensive; cardiant; antiarthritic; cytostatic;  
KW nephrotropic; hepatotropic; analgesic; cerebroprotective; uropathic;  
KW obesity; type II diabetes; cholelithiasis; hypertension;  
KW coronary heart disease; atherosclerosis; glycosenosis; arthritis; cancer;  
KW renal failure; liver; chronic pain; sleep apnea; stroke;  
KW urinary incontinence; painted lady.  
XX  
OS Synthetic.  
OS Vanessa cardui.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /label= OTHER  
FT /note= "OTHER = Pyroglutamic acid"  
FT Misc-difference 11  
FT /note= "Preferably C-terminal amide"  
XX  
PN WO2003066080-A1.  
XX  
PD 14-AUG-2003.  
XX  
PF 07-FEB-2003; 2003WO-US003800.  
XX  
PR 07-FEB-2002; 2002US-00072419.  
XX  
PA (BLMB-) BLM GROUP.  
XX  
PI Schacter BZ, Schacter LP;  
XX WPI; 2003-712542/67.  
XX  
PT Pharmaceutical composition useful for promoting weight loss, comprises an  
PT insect adipokinetic hormone, having a pyroglutamate residue at its amino  
PT terminus.  
XX  
PS Claim 29; Page 20; 82pp; English.  
XX  
CC The invention relates to a novel method of promoting lipid mobilisation  
CC in a human which comprises administering an insect adipokinetic hormone  
CC (AKH). The hormone of the invention demonstrates anorectic, antidiabetic,  
CC hypotensive, cardiant, antiarthritic, cytostatic, nephrotropic,  
CC hepatotropic, analgesic, cerebroprotective and uropathic activities. The  
CC method of the invention may be useful for treating obesity, type II  
CC diabetes, cholelithiasis, hypertension, coronary heart disease,  
CC atherosclerosis, types I to VI glycosenosis, arthritis, cancer, renal  
CC failure, liver disease, chronic pain, sleep apnea, stroke and urinary  
CC incontinence. The current sequence is that of the painted lady AKH  
CC peptide 2 of the invention.  
XX  
SQ Sequence 11 AA;  
  
Query Match 73.9%; Score 17; DB 7; Length 11;  
Best Local Similarity 40.0%; Pred. No. 3.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 FXXXW 5  
| |  
Db 4 FTSSW 8  
  
RESULT 7  
AAE05735  
ID AAE05735 standard; peptide; 13 AA.  
XX



AC AAE05735;  
XX  
DT 24-SEP-2001 (first entry)  
XX  
DE Complementarity-determining region 3 (CDR3) of MoPhabs #7.  
XX  
KW CDR3; complementarity-determining region 3; monoclonal phage antibody;  
KW MoPhabs; antigen.  
XX  
OS Synthetic.  
XX  
PN US6265150-B1.  
XX  
PD 24-JUL-2001.  
XX  
PF 26-MAY-1998; 98US-00085072.  
XX  
PR 07-JUN-1995; 95US-00483633.  
PR 18-SEP-1997; 97US-00932892.  
XX  
PA (BECT ) BECTON DICKINSON & CO.  
PA (CRUC-) CRUCELL HOLLAND BV.  
XX  
PI Terstappen LW, Logtenberg T;  
XX  
DR WPI; 2001-463929/50.  
XX  
PT Obtaining a phage particle, useful for obtaining human antibodies against  
PT known and novel surface antigens, by incubating a phage library with  
PT target cells to allow binding of the antibody fragment to the antigen.  
XX  
PS Example 6; Col 6; 6pp; English.  
XX  
CC The invention relates to a method of obtaining a phage particle which has  
CC an antibody fragment directed against an antigen associated with the  
CC surface of target cells in a heterogeneous cell population. The method  
CC involves incubating a library of phage particles with the target cells to  
CC allow binding of the antibody fragment expressed on the surface of the  
CC phage particles to the antigen associated with the target cells. The  
CC method is useful for obtaining human antibodies against known and novel  
CC surface antigens in their native configuration, expressed on  
CC phenotypically defined subpopulations of cells. The present sequence is  
CC complementarity-determining region 3 (CDR3) of monoclonal phage  
CC antibodies (MoPhabs) used in the exemplification of the invention  
XX  
SQ Sequence 13 AA;  
  
Query Match 73.9%; Score 17; DB 4; Length 13;  
Best Local Similarity 40.0%; Pred. No. 4.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 FXXXW 5  
Db 6 FASSW 10  
  
RESULT 8  
ABG75574  
ID ABG75574 standard; peptide; 13 AA.  
XX  
AC ABG75574;  
XX  
DT 22-APR-2003 (first entry)  
XX  
DE CDR3 peptide sequence, #7, used in phage antibody construction.  
XX  
KW Phage; antibody; antigen; target cell; phage particle;  
KW cell-type specific phage antibody library; phage antibody; Phab;  
KW monoclonal phage antibody; MoPhab; blood cell; foetal bone marrow cell;  
KW complementarity determining region 3; CDR3; human.  
XX  
OS Homo sapiens.  
OS Synthetic.

XX US2002132228-A1.  
PN  
XX 19-SEP-2002.  
PD  
XX  
PF 24-MAY-2001; 2001US-00865048.  
XX  
PR 07-JUN-1995; 95US-00483633.  
PR 18-SEP-1997; 97US-00932892.  
PR 26-MAY-1998; 98US-00085072.  
XX  
PA (TERS/) TERSTAPPEN L W M M.  
PA (LOGT/) LOGTENBERG T.  
XX  
PI Terstappen LWM, Logtenberg T;  
XX  
DR WPI; 2003-174076/17.  
XX  
PT Obtaining phage having antibody specific for cell surface antigen of  
PT target cells in heterogeneous cell population, by incubating phage  
PT antibody library with target cells, and separating phage particles bound  
PT target cells.  
XX  
PS Example 6; Page 4; 5pp; English.  
XX  
CC The invention discloses a method for obtaining a phage comprising an  
CC antibody, or its fragment, directed against antigens associated with a  
CC target cells surface in a heterogeneous cell population. The method  
CC comprises providing a library of antibodies, or their fragments,  
CC expressed on the surface of phage particles, incubating the phage  
CC antibody library with the target cells, separating the target cells and  
CC phage particles associated with them from the phage particles not  
CC associated with the target cells and then recovering the phage particles.  
CC Also disclosed is a cell-type specific phage antibody library and an  
CC antibody, or antibody fragment, obtained using the method. The method is  
CC useful for obtaining a selection of phage antibodies (Phabs) and  
CC monoclonal phage antibodies (MoPhabs). The method is also useful for  
CC detecting known and novel structures on various populations of blood and  
CC foetal bone marrow cells. The sequence presented is an example of the  
CC partly randomised human complementarity determining region 3 (CDR3) used  
CC in the construction of the antibodies  
XX  
SQ Sequence 13 AA;  
  
Query Match 73.9%; Score 17; DB 6; Length 13;  
Best Local Similarity 40.0%; Pred. No. 4.2e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 FXXXW 5  
Db 6 FASSW 10  
  
RESULT 9  
AAM98088  
ID AAM98088 standard; peptide; 14 AA.  
XX  
AC AAM98088;  
XX  
DT 24-JAN-2002 (first entry)  
XX  
DE Human peptide #1363 encoded by a SNP oligonucleotide.  
XX  
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;  
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease.  
XX  
OS Homo sapiens.

XX WO200147944-A2.  
PN  
XX  
PD 05-JUL-2001.  
XX  
XX  
PF 28-DEC-2000; 2000WO-US035498.  
XX  
XX 28-DEC-1999; 99US-0173419P.  
PR 27-DEC-2000; 2000US-00173419.  
XX  
XX (CURA-) CURAGEN CORP.  
PA  
XX Shimkets RA, Leach M;  
PI  
XX WPI; 2001-465210/50.  
XX  
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
PT autoimmune diseases and infections.  
XX  
XX Disclosure; Page 3967; 4143pp; English.  
PS  
XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)  
CC encoding polymorphic variants of proteins related to amylases, amyloid  
CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,  
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,  
CC complement related proteins, cytochromes, kinesins, cytokines,  
CC interferons, interleukins, G-protein coupled receptors and thioesterases.  
CC The present sequence is a peptide encoded by one such oligonucleotide.  
CC The oligonucleotides and the peptide encoded by them may be used in the  
CC prevention, diagnosis and treatment of diseases associated with  
CC inappropriate expression of the proteins listed above. Disorders that may  
CC be prevented, diagnosed and/or treated include multifactorial diseases  
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus  
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous  
CC system and an infection of pathogenic organisms  
XX  
XX Sequence 14 AA;  
SQ  
Query Match 73.9%; Score 17; DB 4; Length 14;  
Best Local Similarity 40.0%; Pred. No. 4.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 FXXXW 5  
Db |  
6 FASTW 10  
RESULT 10  
AAR97874  
ID AAR97874 standard; peptide; 15 AA.  
XX  
XX AAR97874;  
AC  
XX 16-AUG-1996 (first entry)  
DT  
XX Japan cedar pollen mature allergen Cry j II amino acids 16-30.  
DE Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;  
XX Sugi pollinosis; diagnosis; treatment.  
KW  
XX Cryptomeria japonica.  
OS  
XX JP08047392-A.  
PN  
XX 20-FEB-1996.  
PD  
XX 07-NOV-1994; 94JP-00297840.  
PF  
XX 05-NOV-1993; 93JP-00276773.  
PR 26-MAY-1994; 94JP-00134868.  
XX  
XX (MEIP ) MEIJI MILK PROD CO LTD.  
PA  
XX WPI; 1996-166249/17.  
DR  
XX Japan cedar pollen allergen Cry j II epitope - comprises at least part of  
DE specified 460 aminoacid protein.  
XX Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;  
KW Sugi pollinosis; diagnosis; treatment.  
XX  
XX Cryptomeria japonica.  
OS  
XX JP08047392-A.  
PN  
XX 20-FEB-1996.  
PD  
XX 07-NOV-1994; 94JP-00297840.  
PF  
XX 05-NOV-1993; 93JP-00276773.  
PR 26-MAY-1994; 94JP-00134868.  
XX

XX (MEIP ) MEIJI MILK PROD CO LTD.  
PA  
XX WPI; 1996-166249/17.  
DR  
XX Japan cedar pollen allergen Cry j II epitope - comprises at least part of  
PT specified 460 aminoacid protein.  
PT  
XX Claim 8; Fig 3; 17pp; Japanese.  
PS  
XX AAR97871-R97960 are overlapping peptides used for the epitope mapping of  
CC the Japan cedar pollen allergen Cry j II. Cry j II and allergenic  
CC peptides of it are useful in the diagnosis, prevention and treatment of  
CC Sugi pollinosis, the allergic reaction to Japan cedar pollen. Significant  
CC regions of the allergen were identified using the overlapping peptides of  
CC the full epitope derived from a Cry j II antigen-specific T cell line.  
CC Amino acids 66-80 (AAR97884) and 186-200 (R978908) of the full mature 460  
CC amino acid allergen are the most allergenic of the 90 peptides tested  
XX  
XX Sequence 15 AA;  
SQ  
Query Match 73.9%; Score 17; DB 2; Length 15;  
Best Local Similarity 40.0%; Pred. No. 4.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 FXXXW 5  
Db |  
9 FSTAW 13  
RESULT 11  
AAR97875  
ID AAR97875 standard; peptide; 15 AA.  
XX  
XX AAR97875;  
AC  
XX 16-AUG-1996 (first entry)  
DT  
XX Japan cedar pollen mature allergen Cry j II amino acids 21-35.  
DE Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;  
XX Sugi pollinosis; diagnosis; treatment.  
KW  
XX Cryptomeria japonica.  
OS  
XX JP08047392-A.  
PN  
XX 20-FEB-1996.  
PD  
XX 07-NOV-1994; 94JP-00297840.  
PF  
XX 05-NOV-1993; 93JP-00276773.  
PR 26-MAY-1994; 94JP-00134868.  
XX  
XX (MEIP ) MEIJI MILK PROD CO LTD.  
PA  
XX WPI; 1996-166249/17.  
DR  
XX Japan cedar pollen allergen Cry j II epitope - comprises at least part of  
PT specified 460 aminoacid protein.  
PT  
XX Claim 8; Fig 3; 17pp; Japanese.  
PS  
XX AAR97871-R97960 are overlapping peptides used for the epitope mapping of  
CC the Japan cedar pollen allergen Cry j II. Cry j II and allergenic  
CC peptides of it are useful in the diagnosis, prevention and treatment of  
CC Sugi pollinosis, the allergic reaction to Japan cedar pollen. Significant  
CC regions of the allergen were identified using the overlapping peptides of  
CC the full epitope derived from a Cry j II antigen-specific T cell line.  
CC Amino acids 66-80 (AAR97884) and 186-200 (R978908) of the full mature 460  
CC amino acid allergen are the most allergenic of the 90 peptides tested  
XX  
XX Sequence 15 AA;  
SQ

Query Match 73.9%; Score 17; DB 2; Length 15;  
Best Local Similarity 40.0%; Pred. No. 4.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
| |  
Db 4 FSTAW 8

RESULT 12  
AAW57758  
ID AAW57758 standard; peptide; 15 AA.  
XX  
AC AAW57758;  
XX  
DT 17-SEP-1998 (first entry)  
DE Residues 16-30 of Cry j 2.  
XX  
KW Cry j 2; Japanese cedar pollen antigen; allergy; immunotherapy;  
KW HLA class II molecule.  
XX  
OS Cryptomeria japonica.  
XX  
PN WO9820902-A1.  
XX  
PD 22-MAY-1998.  
XX  
PF 12-NOV-1997; 97WO-JP004129.  
XX  
PR 13-NOV-1996; 96JP-00302053.  
XX  
PA (MEIP ) MEIJI MILK PROD CO LTD.  
XX  
PI Sone T, Kume A, Dairiki K, Kino K;  
XX  
DR WPI; 1998-297617/26.  
XX  
PT Peptides derived from Japanese cedar pollen antigens are  
PT immunotherapeutic agents - useful for allergy treatment and typing HLA  
PT class II molecules in allergy sufferers.  
XX  
PS Claim 12; Page 29; 50pp; Japanese.  
XX  
CC This sequence represents residues 16-30 of the Cry j 2 protein, and is a  
CC peptide of the invention. The peptides are derived from Japanese cedar  
CC pollen antigens, and are used as immunotherapeutic agents in the  
CC treatment of allergy. The peptides can be used for identification and  
CC typing of the particular HLA class II molecules in an allergy sufferer,  
CC and also for peptide immunotherapy of an allergy. Using these peptides  
CC the immunotherapy can be targeted more specifically to the requirements  
CC of the individual patient, allowing more effective treatment of an  
CC allergy, including those patients for whom treatment with a conventional  
CC immunotherapeutic agent is ineffective  
XX  
SQ Sequence 15 AA;

Query Match 73.9%; Score 17; DB 2; Length 15;  
Best Local Similarity 40.0%; Pred. No. 4.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
| |  
Db 9 FSTAW 13

RESULT 13  
AAE23038  
ID AAE23038 standard; peptide; 19 AA.  
XX  
AC AAE23038;  
XX

DT 21-AUG-2002 (first entry)  
XX  
DE Human thioredoxin, 47916 peptide.  
XX  
KW Human; thioredoxin; 22108; 47916; haematopoietic disorder; leukaemia;  
KW cancer; lung; breast; thyroid; head; neck; prostate; genitourinary tract;  
KW cardiovascular disease; angina pectoris; arteriosclerosis; heart failure;  
KW brain disorder; brain abscess; meningitis; Alzheimer's disease; sarcoma;  
KW cytostatic; carcinoma; cardiant; neuroprotective; antiinflammatory;  
KW gene therapy; nootropic.  
XX  
OS Homo sapiens.  
XX  
PN WO200226803-A2.  
XX  
PD 04-APR-2002.  
XX  
PF 25-SEP-2001; 2001WO-US029967.  
XX  
PR 25-SEP-2000; 2000US-0235049P.  
XX  
PA (MILL-) MILLENIUM PHARM INC.  
XX  
PI Bandaru R, Kapeller-Libermann R;  
XX  
DR WPI; 2002-416475/44.  
XX  
PT New human thioredoxin nucleic acid and polypeptide molecules, designated  
PT 22108 and 47916, useful for diagnosing, preventing or treating cancer  
PT (e.g. carcinoma), cardiovascular diseases (e.g. heart failure) or brain  
PT disorders.  
XX  
PS Disclosure; Page 11; 124pp; English.  
XX  
CC The invention relates to human thioredoxin nucleic acid and polypeptide  
CC molecules, designated 22108 and 47916. The compound that modulates the  
CC activity or expression of 22108 and 47916 nucleic acid is useful for  
CC treating or preventing a disorder characterised by aberrant activity of  
CC 22108 and 47916-expressing cell, specifically for reducing or inhibiting  
CC the aberrant activity of the 22108 and 47916-expressing cancer cell. The  
CC 22108 and 47916 nucleic acid and polypeptide are useful for diagnosing,  
CC preventing or treating cancer in a subject (e.g. carcinoma, sarcoma,  
CC metastatic or haematopoietic disorders (e.g. leukaemia), or cancers of the  
CC lung, breast, thyroid, head neck, prostate or genito-urinary tract),  
CC cardiovascular diseases (e.g. angina pectoris, arteriosclerosis or heart  
CC failure) or brain disorders (e.g. brain abscess, meningitis, Alzheimer's  
CC diseases). The thioredoxin DNA is also useful in gene therapy. The  
CC present sequence is human thioredoxin, 47916 peptide  
XX  
SQ Sequence 19 AA;

Query Match 73.9%; Score 17; DB 5; Length 19;  
Best Local Similarity 40.0%; Pred. No. 5.6e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
| |  
Db 4 FSATW 8

RESULT 14  
AAW42165  
ID AAW42165 standard; peptide; 20 AA.  
XX  
AC AAW42165;  
XX  
DT 27-AUG-2003 (revised)  
DT 25-MAR-2003 (revised)  
DT 16-JUN-1998 (first entry)  
XX  
DE T-cell epitope peptide 45 from Japanese cypress pollen antigen Chao2.  
XX  
KW Japanese cypress pollen; antigen; T-cell epitope; Chao1; Chao2;



XX Disclosure; Page 16; 81pp; English.

PS The invention describes an isolated or recombinant polypeptide (I)

XX comprising a sequence: (a) comprising 1 of 30 sequences (S1), as given in

CC the specification, or a conservative variant; (b) encoded by 1 of 30

CC sequences (S2), as given in the specification, or a conservative variant;

CC (c) encoded by a sequence that hybridizes under stringent conditions to

CC S2; and (d) encoded by a sequence 70 % identical to S2. The expression or

CC activity of (I) is modulated to modulate a plant growth trait in a

CC flowering plant, of the family Brassicaceae, preferably in a plant that

CC is Arabidopsis, Brassica, Zea, Oryza, Triticum, Hordeum, Lolium, Sorghum,

CC Glycine, Medicago, Helianthus, Lactuca, Beta, Vitis, Solanum,

CC Lycopersicon, Capsicum, Gossypium, Hevea, Linum, Prunus, Citrus, Populus,

CC Pinus, or Quercus. A new method is used to detect genes for a plant

CC growth trait. This is the amino acid sequence of region of ADE25056 used

CC to demonstrate conservative substitutions occurring in the protein.

XX Sequence 25 AA;

SQ

Query Match 73.9%; Score 17; DB 7; Length 25;  
Best Local Similarity 40.0%; Pred. No. 7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5  
|  
20 FAASW 24

Db

RESULT 17  
AAM18617

ID AAM18617 standard; protein; 27 AA.

XX

AC AAM18617;

XX

DT 12-OCT-2001 (first entry)

XX

DE Peptide #5051 encoded by probe for measuring cervical gene expression.

XX

KW Probe; human; microarray; gene expression; cervical epithelial cell;

KW cervical cancer.

XX

OS Homo sapiens.

XX

PN WO200157278-A2.

XX

PD 09-AUG-2001.

XX

PF 30-JAN-2001; 2001WO-US000670.

XX

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX

PA (MOLE-) MOLECULAR DYNAMICS INC.

XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX

DR WPI; 2001-488901/53.

XX

PT Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human cervical epithelial cells.

XX

PS Claim 27; SEQ ID NO 23443; 487pp; English.

XX

XX The present invention relates to human single exon nucleic acid probes

CC (SENPs: see AAI10068-AAI28459). The present sequence is a peptide encoded

CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs

CC can be used to produce a single exon microarray, which can be used for

CC measuring human gene expression in a sample derived from human cervical

CC epithelial cells. By measuring gene expression, the probes are therefore

CC useful in grading and/or staging of diseases of the cervix, notably

CC cervical cancer. Note: The sequence data for this patent did not form

CC part of the printed specification, but was obtained in electronic format

CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 27 AA;

Query Match 73.9%; Score 17; DB 4; Length 27;  
Best Local Similarity 40.0%; Pred. No. 7.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5  
|  
4 FSATW 8

Db

RESULT 18  
AAM31077

ID AAM31077 standard; protein; 27 AA.

XX

AC AAM31077;

XX

DT 17-OCT-2001 (first entry)

XX

DE Peptide #5114 encoded by probe for measuring placental gene expression.

XX

KW Probe; microarray; human; placenta; antenatal diagnosis;

KW genetic disorder.

XX

OS Homo sapiens.

XX

PN WO200157272-A2.

XX

PD 09-AUG-2001.

XX

PF 30-JAN-2001; 2001WO-US000663.

XX

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX

PA (MOLE-) MOLECULAR DYNAMICS INC.

XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX

DR WPI; 2001-48897/53.

XX

PT Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human placenta.

XX

PS Claim 27; SEQ ID NO 31346; 654pp; English.

XX

XX The present invention relates to single exon nucleic acid probes (SENPs:

CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one

CC such probe. The probes are useful for producing a microarray for

CC predicting, measuring and displaying gene expression in samples derived

CC from human placenta. The probes are useful for antenatal diagnosis of

CC human genetic disorders

XX

SQ Sequence 27 AA;

Query Match 73.9%; Score 17; DB 4; Length 27;  
Best Local Similarity 40.0%; Pred. No. 7.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5  
|  
4 FSATW 8





CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary  
CC histiocytosis, lymphangiomyomatosis, pulmonary alveolar proteinosis,  
CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
CC present sequence is a peptide/protein encoded by a single exon probe of  
CC the invention. Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 27 AA;  
  
Query Match 73.9%; Score 17; DB 5; Length 27;  
Best Local Similarity 40.0%; Pred. No. 7.4e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 FXXW 5  
| |  
Db 4 FSATW 8  
  
RESULT 21  
AAB09301  
ID AAB09301 standard; protein; 29 AA.  
XX  
AC AAB09301;  
XX  
DT 06-AUG-2003 (revised)  
DT 30-AUG-2000 (first entry)  
XX  
DE Hepatitis GB virus protein sequence SEQ ID NO:428.  
XX  
KW Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic; infection;  
KW detection; characterisation; hepatitis.  
XX  
OS Hepatitis GB virus.  
XX  
PN US6051374-A.  
XX  
PD 18-APR-2000.  
XX  
PF 07-JUN-1995; 95US-00488445.  
XX  
PR 14-FEB-1994; 94US-00196030.  
PR 13-MAY-1994; 94US-00242654.  
PR 29-JUL-1994; 94US-00283314.  
PR 23-NOV-1994; 94US-00344185.  
PR 23-NOV-1994; 94US-00344190.  
PR 30-JAN-1995; 95US-00377557.  
XX  
PA (ABBO ) ABBOTT LAB.  
XX  
PI Dawson GJ, Leary TP, Muerhoff AS, Pilot-Matias TJ, Buijk SL;  
PI Mushahwar IK, Simons JN, Desai SM, Erker JC, Schlauder GG;  
XX  
DR WPI; 2000-338307/29.  
XX  
PT Detecting target hepatitis GB virus nucleic acid in a test sample  
PT suspected of containing HGBV comprises reacting the test sample the HGBV  
PT polynucleotide probe and detecting the complex that contains target HGBV.  
XX  
PS Example 18; Col 491-492; 369pp; English.  
XX  
CC The present invention describe a method for detecting target hepatitis GB  
CC virus (HGBV) nucleic acid (THN) in a test sample (T) suspected of  
CC containing HGBV. The method involves reacting (T) with a HGBV  
CC polynucleotide probe (I) containing 15 contiguous nucleotides, and which  
CC selectively hybridises to the HGBV genome or its full complement, and  
CC detecting the complex that contains THN, indicating the presence of  
CC target HGBV. The method is used for detecting target HGBV nucleic acid in  
CC the test sample suspected of containing HGBV and for characterisation of  
CC newly ascertained etiological agent of non-A, non-B, non-C, non-D and non  
CC -E hepatitis causing agents collectively termed as hepatitis GB virus.  
CC AAA55270 to AAA55489 and AAB08985 to AAB09480 represent nucleotide and

CC protein sequences used in the exemplification of the present invention.  
CC (Updated on 06-AUG-2003 to correct OS field.)  
XX  
SQ Sequence 29 AA;  
  
Query Match 73.9%; Score 17; DB 3; Length 29;  
Best Local Similarity 40.0%; Pred. No. 7.8e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 FXXW 5  
| |  
Db 12 FASAW 16  
  
RESULT 22  
AAG71365  
ID AAG71365 standard; peptide; 32 AA.  
XX  
AC AAG71365;  
XX  
DT 30-JUL-2001 (first entry)  
XX  
DE Human gene 10-encoded secreted protein fragment, SEQ ID NO:216.  
XX  
KW Human; secreted protein; proliferative disorder; cancer; chromosome 1;  
KW foetal abnormality; developmental abnormality; haematopoietic disorder;  
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
KW inflammation; allergy; neurological disorder; Alzheimer's disease;  
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;  
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;  
KW cardiovascular disorder; angiogenic disorder; kidney disorder;  
KW gastrointestinal disorder; pregnancy-related disorder; tumour;  
KW endocrine disorder; infection; wound healing; vulnerary; cell culture;  
KW chemotaxis; food additive; binding partner identification.  
XX  
OS Homo sapiens.  
XX  
PN WO200132674-A1.  
XX  
PD 10-MAY-2001.  
XX  
PF 25-OCT-2000; 2000WO-US029360.  
XX  
PR 29-OCT-1999; 99US-0162211P.  
PR 30-JUN-2000; 2000US-0215138P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, Komatsoulis GA, Young PE, Moore PA;  
XX  
DR WPI; 2001-291051/30.  
XX  
PT New nucleic acid molecule encoding a human secreted protein, useful for  
PT preventing, treating or ameliorating medical conditions such as  
PT rheumatoid arthritis, Alzheimer's disease and microbial infections.  
XX  
PS Disclosure; Page 27; 581pp; English.  
XX  
CC AAH31349-AAH31428 represent cDNAs corresponding to 26 human secreted  
CC protein genes, and AAG71243-AAG71319 represent the proteins they encode.  
CC AAG71320-AAG71403 represent human secreted protein fragments. The genes  
CC and their corresponding secreted proteins are useful for preventing,  
CC treating or ameliorating medical conditions, e.g., by protein or gene  
CC therapy. Pathological conditions can be diagnosed by determining the  
CC amount of the new protein in a sample or by determining the presence of  
CC mutations in the new genes. Specific uses are described for each of the  
CC 52 genes, based on the tissues in which they are most highly expressed,  
CC and include developing products for the diagnosis or treatment of  
CC proliferative disorders, cancer, tumours, foetal and developmental  
CC abnormalities, haematopoietic disorders, diseases of the immune system,  
CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,  
CC allergies, neurological disorders (e.g., Alzheimer's disease,  
CC Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin



CC disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,  
 CC cardiovascular disorders, angiogenic disorders, kidney disorders,  
 CC gastrointestinal disorders, pregnancy-related disorders, endocrine  
 CC disorders, and infections. The proteins can also be used to aid wound  
 CC healing and epithelial cell proliferation, to prevent skin aging due to  
 CC sunburn, to maintain organs before transplantation, for supporting cell  
 CC culture of primary tissues, to regenerate tissues, to identify their  
 CC cognate ligands or binding partners, and in chemotaxis, and can be used  
 CC as a food additive or preservative to modify storage properties.  
 CC Antibodies specific for a protein of the invention can be used in  
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked  
 CC immunosorbent assay (ELISA). The present sequence represents a human  
 CC secreted protein fragment referred to in the disclosure of the invention  
 XX  
 SQ Sequence 32 AA;  
 Query Match 73.9%; Score 17; DB 4; Length 32;  
 Best Local Similarity 40.0%; Pred. No. 8.5e+03;  
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 FXXXW 5  
 Db 15 FAATW 19  
 RESULT 23  
 ABP60808  
 ID ABP60808 standard; protein; 33 AA.  
 XX  
 AC ABP60808;  
 XX  
 DT 06-SEP-2002 (first entry)  
 XX  
 DE Sus scrofa thioresoxin SEQ ID NO:157.  
 XX  
 KW Multimeric protein; redox protein; thioresoxin; thioresoxin reductase;  
 KW oil body; ophthalmological; antidiabetic; cytostatic; antipsoriatic;  
 KW vasotropic; vulnerary; antibacterial; immunosuppressive; antiulcer;  
 KW food product; milk; wheat; oxidative stress; cataract; diabetes;  
 KW chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;  
 KW bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;  
 KW gastro intestinal bleeding; intestinal bowel disease; ulcer;  
 KW gastro oesophageal reflux disease.  
 XX  
 OS Sus scrofa.  
 XX  
 PN WO200250289-A1.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 19-DEC-2001; 2001WO-US050240.  
 XX  
 PR 19-DEC-2000; 2000US-00742900.  
 PR 05-JUL-2001; 2001US-0302885P.  
 PR 04-DEC-2001; 2001US-00006038.  
 XX  
 PA (SEMB-) SEMBIOSYS GENETICS INC.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 XX  
 PI Van Rooijen G, Deckers H, Heifetz PB, Briggs SP, Dalmia BK;  
 PI Del Val G, Zaplachinski S, Moloney M;  
 XX  
 DR WPI; 2002-508806/54.  
 XX  
 PT Producing oil body associated with recombinant multimeric protein complex  
 PT e.g. redox proteins and immunoglobulins comprises producing recombinant  
 PT polypeptides capable of forming the complex in cells comprising oil  
 PT bodies.  
 XX  
 PS Claim 81; Page 248; 362pp; English.  
 XX  
 CC The present invention describes a method (M1) for producing an oil body

CC associated with a recombinant multimeric protein complex (MPC). M1  
 CC comprises producing in a cell comprising oil bodies a first and second  
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with  
 CC P2 to form the MPC and associating the complex with an occlusion body  
 CC (OB) through an OB-targeting-protein capable of associating with OB and  
 CC P1. M1 is useful for producing an oil body associated with a recombinant  
 CC MPC. The oil bodies are further formulated for use in the preparation of  
 CC a food product such as milk or wheat based food product, personal care  
 CC product which reduces the oxidative stress on the surface area of the  
 CC human body or used to lighten the skin, or a pharmaceutical composition  
 CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,  
 CC diabetes, envenomation, bronchiopulmonary disease, psoriasis,  
 CC malignancies, reperfusion injury, wound healing, sepsis, gastro  
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD  
 CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to  
 CC ABP60964 represent sequence given in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 33 AA;  
 Query Match 73.9%; Score 17; DB 5; Length 33;  
 Best Local Similarity 40.0%; Pred. No. 8.7e+03;  
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 FXXXW 5  
 Db 26 FSATW 30  
 RESULT 24  
 ABO54713  
 ID ABO54713 standard; protein; 33 AA.  
 XX  
 AC ABO54713;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Human genome derived single exon protein #947.  
 XX  
 KW Human; gene expression; single exon probe; microarray;  
 KW alternative splicing event; genomic alteration.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003194704-A1.  
 XX  
 PD 16-OCT-2003.  
 XX  
 PF 03-APR-2002; 2002US-00029386.  
 XX  
 PR 03-APR-2002; 2002US-00029386.  
 XX  
 PA (PENN/) PENN S G.  
 PA (RANK/) RANK D R.  
 PA (HANZ/) HANZEL D K.  
 XX  
 PI Penn SG, Rank DR, Hanzel DK;  
 XX  
 DR WPI; 2004-119264/12.  
 XX  
 PT New human genome-derived single exon nucleic acid probes useful for human  
 PT gene expression analysis, for identifying or characterizing alternative  
 PT splicing events, for assessing genomic alterations or as tools for  
 PT surveying tissues.  
 XX  
 PS Claim 45; SEQ ID NO 28347; 80pp; English.  
 XX  
 CC The invention relates to a nucleic acid probe for measuring human gene  
 CC expression, comprising any of the 27,400 fully defined nucleotide  
 CC sequences in the specification, or their complements or fragments, and  
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences  
 CC fully defined in the specification. The probe is a single exon probe that  
 CC hybridises under high stringency conditions to a nucleic acid molecule

expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a vector comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above-mentioned amino acid sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising alternative splicing events, in detecting and characterising gross alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at [seqdata.uspto.gov/sequence.html?DocID=20030194704](http://seqdata.uspto.gov/sequence.html?DocID=20030194704)

Sequence 33 AA;

Query Match 73.9%; Score 17; DB 8; Length 33;  
Best Local Similarity 40.0%; Pred. No. 8.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5  
| |  
Db 14 FSASW 18

RESULT 25

AAR50631  
ID AAR50631 standard; peptide; 34 AA.

XX AC AAR50631;

XX DT 08-MAY-1996 (first entry)

XX DE G-protein coupled receptor TM3 consensus polypeptide #77.

XX KW G-protein coupled receptor; ligand binding assay; transmembrane domain; psychotic disorder; schizophrenia; dopamine; cAMP; adenosine; thrombin; muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine; rhodopsin; opsin; odorant; cytomegalovirus; serotonergic.

XX OS Synthetic.

XX PN WO9405695-A1.

XX PD 17-MAR-1994.

XX PF 09-SEP-1993; 93WO-US008528.

XX PR 10-SEP-1992; 92US-00943236.

XX PA (UUNY ) UNIV NEW YORK STATE.

XX PI Murphy RB, Schuster DI;

XX DR WPI; 1994-101120/12.

XX PT Polypeptides of G-coupled receptor proteins (GPRs) - useful for binding

PT GPR ligands or modulating GPR binding.

XX Claim 9; Page 28; 160pp; English.

XX Polypeptides AAR48768-81 and AAR50569-R50718 are based on the consensus transmembrane domain III sequence from G-protein coupled receptor (GPR) proteins, and can be used in G-protein coupled receptor ligand binding assays. The assay can be used to identify fragments pref. transmembrane fragments, from GPR proteins (see AAR48686-R48758 for examples) which retain biological activity such as binding a GPR ligand or modulating GPR ligand binding to a GPR (see AAR48759-R48758, AAR50569-R50807 and AAR89189-R89195 for examples of polypeptide fragments). The polypeptide fragments can be used in compositions for treating subjects suffering from a pathology related to a GPR abnormality e.g. a psychotic disorder such as schizophrenia

XX Sequence 34 AA;

Query Match 73.9%; Score 17; DB 2; Length 34;  
Best Local Similarity 40.0%; Pred. No. 8.9e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5  
| |  
Db 16 FTTAW 20

RESULT 26

AAR50593  
ID AAR50593 standard; peptide; 34 AA.

XX AC AAR50593;

XX DT 03-MAY-1996 (first entry)

XX DE G-protein coupled receptor TM3 consensus polypeptide #39.

XX KW G-protein coupled receptor; ligand binding assay; transmembrane domain; psychotic disorder; schizophrenia; dopamine; cAMP; adenosine; thrombin; muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine; rhodopsin; opsin; odorant; cytomegalovirus; serotonergic.

XX OS Synthetic.

XX PN WO9405695-A1.

XX PD 17-MAR-1994.

XX PF 09-SEP-1993; 93WO-US008528.

XX PR 10-SEP-1992; 92US-00943236.

XX PA (UUNY ) UNIV NEW YORK STATE.

XX PI Murphy RB, Schuster DI;

XX DR WPI; 1994-101120/12.

XX PT Polypeptides of G-coupled receptor proteins (GPRs) - useful for binding GPR ligands or modulating GPR binding.

XX Claim 9; Page 27; 160pp; English.

XX Polypeptides AAR48768-81 and AAR50569-R50718 are based on the consensus transmembrane domain III sequence from G-protein coupled receptor (GPR) proteins, and can be used in G-protein coupled receptor ligand binding assays. The assay can be used to identify fragments pref. transmembrane fragments, from GPR proteins (see AAR48686-R48758 for examples) which retain biological activity such as binding a GPR ligand or modulating GPR ligand binding to a GPR (see AAR48759-R48758, AAR50569-R50807 and AAR89189-R89195 for examples of polypeptide fragments). The polypeptide fragments can be used in compositions for treating subjects suffering from a pathology related to a GPR abnormality e.g. a psychotic disorder

CC	such as schizophrenia									
XX										
SQ	Sequence 34 AA;									
Query Match										
Best Local Similarity 73.9%; Score 17; DB 2; Length 34;										
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;										
QY	1 FXXW 5									
Db	16 FTSW 20									
RESULT 27										
ID	AAW02823 standard; peptide; 34 AA.									
XX										
AC	AAW02823;									
XX										
DT	25-MAR-2003 (revised)									
DT	20-SEP-1996 (first entry)									
XX										
DE	G-protein coupled receptor TM3 consensus polypeptide #78.									
XX										
KW	G-protein coupled receptor; ligand binding assay; transmembrane domain;									
KW	schizophrenia; dopamine; CAMP; adenosine; thrombin; adrenergic; opsin;									
KW	muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin;									
KW	odorant; cytomegalovirus; serotonergic.									
XX										
OS	Synthetic.									
XX										
PN	US5508384-A.									
XX										
PD	16-APR-1996.									
XX										
PF	09-SEP-1993; 93US-00118270.									
XX										
PR	10-SEP-1992; 92US-00943236.									
XX										
PA	(UYNV ) UNIV NEW YORK STATE.									
XX										
PI	Schuster DI, Murphy RB;									
XX										
DR	WPI; 1996-208785/21.									
XX										
PT	New dopamine receptor peptide - useful as antipsychotic agent, e.g. for									
PT	treating schizophrenia.									
XX										
PS	Disclosure; Col 227-228; 184pp; English.									
XX										
CC	Polypeptides AAW02747-W02910 are based on the consensus transmembrane									
CC	domain III sequence from G-protein coupled receptor (GPR) proteins and									
CC	can be used in GPR ligand binding assays. The assays can be used to									
CC	identify fragments, pref. transmembrane fragments, from GPR proteins (see									
CC	AAW02657-W02635) which retain biological activity such as binding a GPR									
CC	ligand or modulating a GPR ligand binding to a GPR (see W02747-AAW02999									
CC	for examples of polypeptide fragments). The polypeptide fragments can be									
CC	used in comps. for treating subjects suffering from a pathology related									
CC	to a GPR abnormality e.g. schizophrenia. (Updated on 25-MAR-2003 to									
CC	correct PF field.)									
XX										
SQ	Sequence 34 AA;									
Query Match										
Best Local Similarity 73.9%; Score 17; DB 2; Length 34;										
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;										
QY	1 FXXW 5									
Db	16 FTTW 20									
RESULT 28										

AAW02785	
ID	AAW02785 standard; peptide; 34 AA.
XX	
AC	AAW02785;
XX	
DT	25-MAR-2003 (revised)
DT	20-SEP-1996 (first entry)
XX	
DE	G-protein coupled receptor TM3 consensus polypeptide #39.
XX	
KW	G-protein coupled receptor; ligand binding assay; transmembrane domain;
KW	schizophrenia; dopamine; CAMP; adenosine; thrombin; adrenergic; opsin;
KW	muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin;
KW	odorant; cytomegalovirus; serotonergic.
XX	
OS	Synthetic.
XX	
PN	US5508384-A.
XX	
PD	16-APR-1996.
XX	
PF	09-SEP-1993; 93US-00118270.
XX	
PR	10-SEP-1992; 92US-00943236.
XX	
PA	(UYNV ) UNIV NEW YORK STATE.
XX	
PI	Schuster DI, Murphy RB;
XX	
DR	WPI; 1996-208785/21.
XX	
PT	New dopamine receptor peptide - useful as antipsychotic agent, e.g. for
PT	treating schizophrenia.
XX	
PS	Disclosure; Col 207-208; 184pp; English.
XX	
CC	Polypeptides AAW02747-W02910 are based on the consensus transmembrane
CC	domain III sequence from G-protein coupled receptor (GPR) proteins and
CC	can be used in GPR ligand binding assays. The assays can be used to
CC	identify fragments, pref. transmembrane fragments, from GPR proteins (see
CC	AAW02657-W02635) which retain biological activity such as binding a GPR
CC	ligand or modulating a GPR ligand binding to a GPR (see W02747-AAW02999
CC	for examples of polypeptide fragments). The polypeptide fragments can be
CC	used in comps. for treating subjects suffering from a pathology related
CC	to a GPR abnormality e.g. schizophrenia. (Updated on 25-MAR-2003 to
CC	correct PF field.)
XX	
SQ	Sequence 34 AA;
Query Match	
Best Local Similarity 73.9%; Score 17; DB 2; Length 34;	
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
QY	1 FXXW 5
Db	16 FTSW 20
RESULT 29	
ID	AAW028042
XX	
AC	AAW028042;
XX	
DT	06-NOV-2001 (first entry)
XX	
DE	Human polypeptide SEQ ID NO 21934.
XX	
KW	Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW	tissue growth factor; immunomodulatory; cancer; leukaemia;
KW	nervous system disorders; arthritis; inflammation.
XX	

Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
tissue growth factor; immunomodulatory; cancer; leukaemia;  
nervous system disorders; arthritis; inflammation.

Query Match 73.9%; Score 17; DB 2; Length 34;  
Best Local Similarity 40.0%; Pred. No. 8.9e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FXXW 5  
Db 16 FTSW 20

RESULT 29  
AAO08042  
ID AAO08042 standard; protein; 35 AA.

XX AAO08042;

XX 06-NOV-2001 (first entry)

XX Human polypeptide SEQ ID NO 21934.

OS Homo sapiens.  
XX WO200164835-A2.  
PN  
XX  
PD 07-SEP-2001.  
PF  
XX 26-FEB-2001; 2001WO-US004927.  
XX  
PR 28-FEB-2000; 2000US-00515126.  
PR 18-MAY-2000; 2000US-00577409.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Drmanac RT;  
XX  
DR WPI; 2001-514838/56.  
DR N-PSDB; AAI87973.  
XX  
PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing  
PT and treating e.g. leukemia, inflammation and immune disorders.  
XX  
PS Claim 20; SEQ ID NO 21934; 1399pp + Sequence Listing; English.  
XX  
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and  
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, haematopoiesis regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activin/inhibin activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation. Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 35 AA;  
  
Query Match 73.9%; Score 17; DB 4; Length 35;  
Best Local Similarity 40.0%; Pred. No. 9.1e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 FXXW 5  
Db 3 FAATW 7  
  
RESULT 30  
AAR53693  
ID AAR53693 standard; protein; 36 AA.  
XX  
AC AAR53693;  
XX  
DT 25-MAR-2003 (revised)  
DT 01-FEB-1995 (first entry)  
XX  
DE Japanese cedar pollen allergen Cry j II fragment.  
XX  
KW Cedar pollinosis; diagnostic.  
XX  
OS Cryptomeria japonica.  
PN WO9411512-A2.  
XX  
PD 26-MAY-1994.  
XX  
PF 12-NOV-1993; 93WO-US011000.  
XX  
PR 12-NOV-1992; 92US-00975179.  
XX  
PA (IMMU-) IMMULOGIC PHARM CORP.  
XX

PI Kuo M, Yeung S, Brauer A, Pollock J;  
XX WPI; 1994-183513/22.  
DR  
XX  
PT Allergenic Cry j II protein and fragments from Japanese cedar pollen -  
PT used to diagnose, treat and prevent Japanese cedar pollinosis.  
XX  
PS Disclosure; Page 47; 89pp; English.  
XX  
CC The sequence is of a Japanese cedar pollen allergen Cry j II fragment.  
CC The protein and fragments can be used for diagnosis and treatment of  
CC Japanese cedar pollinosis and to identify similar sequences in other  
CC plants. See also AAR53690-6. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX  
SQ Sequence 36 AA;  
  
Query Match 73.9%; Score 17; DB 2; Length 36;  
Best Local Similarity 40.0%; Pred. No. 9.3e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 FXXW 5  
Db 28 FSTAW 32  
  
RESULT 31  
AAO08979  
ID AAO08979 standard; protein; 37 AA.  
XX  
AC AAO08979;  
XX  
DT 06-NOV-2001 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 22871.  
XX  
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
KW nervous system disorders; arthritis; inflammation.  
XX  
OS Homo sapiens.  
XX  
PN WO200164835-A2.  
XX  
PD 07-SEP-2001.  
XX  
PF 26-FEB-2001; 2001WO-US004927.  
XX  
PR 28-FEB-2000; 2000US-00515126.  
PR 18-MAY-2000; 2000US-00577409.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Drmanac RT;  
XX  
DR WPI; 2001-514838/56.  
DR N-PSDB; AAI88910.  
XX  
PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing  
PT and treating e.g. leukemia, inflammation and immune disorders.  
XX  
PS Claim 20; SEQ ID NO 22871; 1399pp + Sequence Listing; English.  
XX  
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and  
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, haematopoiesis regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activin/inhibin activity and may be useful in the diagnosis and/or

CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation. Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 37 AA;  
  
Query Match 73.9%; Score 17; DB 4; Length 37;  
Best Local Similarity 40.0%; Pred. No. 9.5e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 FXXXW 5  
| |  
Db 6 FAATW 10  
  
RESULT 32  
AAY76339  
ID AAY76339 standard; protein; 38 AA.  
XX  
AC AAY76339;  
XX  
DT 23-MAR-2000 (first entry)  
DE Fragment of human secreted protein encoded by gene 38.  
XX  
KW Human; secreted protein; cancer; tumour; developmental abnormality;  
KW foetal deficiency; blood disorder; immune system disorder; inflammation;  
KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;  
KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;  
KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;  
KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;  
KW therapy.  
XX  
OS Homo sapiens.  
XX  
FN WO9958660-A1.  
XX  
PD 18-NOV-1999.  
XX  
PF 06-MAY-1999; 99WO-US009847.  
XX  
PR 12-MAY-1998; 98US-0085093P.  
PR 12-MAY-1998; 98US-0085094P.  
PR 12-MAY-1998; 98US-0085105P.  
PR 12-MAY-1998; 98US-0085180P.  
PR 18-MAY-1998; 98US-0085906P.  
PR 18-MAY-1998; 98US-0085920P.  
PR 18-MAY-1998; 98US-0085921P.  
PR 18-MAY-1998; 98US-0085922P.  
PR 18-MAY-1998; 98US-0085923P.  
PR 18-MAY-1998; 98US-0085924P.  
PR 18-MAY-1998; 98US-0085925P.  
PR 18-MAY-1998; 98US-0085927P.  
PR 18-MAY-1998; 98US-0085928P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA;  
PI Olsen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR, Lafleur DW;  
PI Endress GA, Ebner R;  
XX  
DR WPI; 2000-062296/05.  
XX  
PT New isolated human genes and the secreted polypeptides they encode,  
PT useful for diagnosis and treatment of e.g. cancers, neurological  
PT disorders, immune diseases, inflammation or blood disorders.  
XX  
PS Disclonuro; Page 450; 475pp; English.  
XX  
CC AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes.  
CC AAY76124 to AAY76223 are the secreted proteins encoded by the 97 human  
CC genes. This sequence represents a fragment of one of the human secreted

CC proteins. The genes and their corresponding secreted polypeptides are  
CC useful for preventing, treating or ameliorating medical conditions, e.g.  
CC by protein or gene therapy. Also pathological conditions can be diagnosed  
CC by determining the amount of the new polypeptides in a sample or by  
CC determining the presence of mutations in the new genes. Specific uses are  
CC described for each of the 97 genes, based on which tissues they are most  
CC highly expressed in, and include developing products for the diagnosis or  
CC treatment of cancer, tumours, developmental abnormalities and foetal  
CC deficiencies, blood disorders, diseases of the immune system, autoimmune  
CC diseases, inflammation, allergies, Alzheimer's and cognitive disorders,  
CC schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,  
CC atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,  
CC digestive/endocrine disorders, infections and AIDS. The polypeptides are  
CC also useful for identifying their binding partners. The sequences shown  
CC in AAY76224 to AAY76424 represent fragments of the secreted proteins  
XX  
SQ Sequence 38 AA;  
  
Query Match 73.9%; Score 17; DB 3; Length 38;  
Best Local Similarity 40.0%; Pred. No. 9.7e+03;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 FXXXW 5  
| |  
Db 19 FAAAAW 23  
  
RESULT 33  
AAG10451  
ID AAG10451 standard; protein; 38 AA.  
XX  
AC AAG10451;  
XX  
DT 17-OCT-2000 (first entry)  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 8778.  
XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-00301439.  
XX  
PR 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
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PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
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PR 28-APR-1999; 99US-0130891P.  
PR 30-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 30-APR-1999; 99US-0132407P.  
PR 04-MAY-1999; 99US-0132484P.  
PR 05-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
PR 06-MAY-1999; 99US-0132487P.  
PR 07-MAY-1999; 99US-0132863P.  
PR 11-MAY-1999; 99US-0134256P.  
PR 14-MAY-1999; 99US-0134218P.

PR 14-MAY-1999; 99US-0134219P.  
PR 14-MAY-1999; 99US-0134221P.  
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PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
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PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
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PR 17-JUN-1999; 99US-0139492P.  
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PR 18-JUN-1999; 99US-0139455P.  
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PR 21-JUN-1999; 99US-0139817P.  
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PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
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PR 15-JUL-1999; 99US-0144005P.  
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PR 19-JUL-1999; 99US-0144325P.  
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PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
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PR 20-JUL-1999; 99US-0144632P.  
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PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
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PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.

PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.  
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PR 11-AUG-1999; 99US-0148319P.  
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PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
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PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
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PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
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PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.

PA	(ENDR/) ENDRESS G A.
PA	(EBNE/) EBNER R.
PA	(BIRS/) BIRSE C E.
XX	
PI	Ruben SM, Florence KA, Ni J, Rosen CA, Carter KC, Moore PA;
PI	Olsen HS, Shi Y, Young PE, Wei Y, Brewer LA, Soppet DR, Lafleur DW;
PI	Endress GA, Ebner R, Birse CE;
XX	
DR	WPI; 2003-801210/75.
XX	
PT	New nucleic acid molecule, useful for preparing a medicament for
PT	preventing, treating or ameliorating a medical condition e.g. cancer,
PT	liver disorders or neural disorders.
XX	
PS	Claim 11; SEQ ID NO 287; 453pp; English.
XX	
CC	The invention relates to human secreted polypeptides and the
CC	polynucleotides encoding them. The sequences are useful for preparing
CC	medicaments for preventing, treating or ameliorating medical conditions
CC	e.g., cancer, liver disorders such as hepatitis or neural disorders such
CC	as Alzheimer's disease. This sequence represents a human secreted
CC	polypeptide of the invention.
XX	
SQ	Sequence 38 AA;
	Query Match 73.9%; Score 17; DB 7; Length 38;
	Best Local Similarity 40.0%; Pred. No. 9.7e+03;
	Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	1 FXXXW 5
Db	19 FAAAW 23
RESULT 35	
AAAY41113	
ID	AAAY41113 standard; peptide; 40 AA.
XX	
AC	AAAY41113;
XX	
DT	17-JAN-2000 (first entry)
XX	
DE	TNFR/NGFR cysteine-rich domain of T129 polypeptide.
XX	
KW	Tumor necrosis factor receptor; TNF; T129 protein; TANGO 129; human;
KW	cellular process; immunological disorder; abnormal lymphoid development;
KW	thymic development; T-cell mediated immune response; humoral B cell;
KW	skeletal muscle disorder; drug screening.
XX	
OS	Homo sapiens.
XX	
PN	WO9952924-A1.
XX	
PD	21-OCT-1999.
XX	
PF	08-APR-1999; 99WO-US007832.
XX	
PR	09-APR-1998; 98US-00057951.
XX	
PA	(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX	
PI	Holtzman D;
XX	
DR	WPI; 1999-620368/53.
XX	
PT	New isolated tumor necrosis factor receptor member used to develop
PT	products for treating, e.g. immunological disorders or disorders of the
PT	skeletal muscle.
XX	
PS	Example 3; Fig 2; 118pp; English.
XX	
CC	The invention provides an isolated human tumor necrosis factor (TNF)
CC	receptor member, T129 (also referred as TANGO 129). The T129 polypeptide



CC can be expressed by standard recombinant methodology. The T219  
CC polypeptides are useful as modulating agents in regulating a variety of  
CC cellular processes. Agents or modulators which have a stimulatory or  
CC inhibitory effect on T129 activity (e.g. T129 gene expression) as  
CC identified by a screening assay can be administered to individuals to  
CC treat (prophylactically or therapeutically) disorders, e.g. an  
CC immunological disorder associated with aberrant T129 activity, disorders  
CC associated with abnormal lymphoid and/or thymic development, T-cell  
CC mediated immune response, T-cell dependent disorders of the skeletal muscle.  
CC humoral B cell activity, and possibly disorders of the skeletal muscle.  
CC The products can also be used for detection, diagnosis, drug screening  
CC and production of transgenic animals. The present sequence represents a  
CC TNFR/NGFR cysteine-rich domain of T129 polypeptide  
XX  
SQ Sequence 40 AA;

Query Match 73.9%; Score 17; DB 2; Length 40;  
Best Local Similarity 40.0%; Pred. No. 1e+04;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXW 5  
Db 6 FSAW 10

RESULT 36

AAG51555  
ID AAG51555 standard; protein; 40 AA.

XX AC AAG51555;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 65445.

XX KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.

PR 06-APR-1999; 99US-0128234P.

PR 08-APR-1999; 99US-0128714P.

PR 16-APR-1999; 99US-0129845P.

PR 19-APR-1999; 99US-0130077P.

PR 21-APR-1999; 99US-0130449P.

PR 23-APR-1999; 99US-0130510P.

PR 28-APR-1999; 99US-0131449P.

PR 30-APR-1999; 99US-0132048P.

PR 04-MAY-1999; 99US-0132484P.

PR 05-MAY-1999; 99US-0132485P.

PR 06-MAY-1999; 99US-0132486P.

PR 06-MAY-1999; 99US-0132487P.

PR 07-MAY-1999; 99US-0132863P.

PR 11-MAY-1999; 99US-0134256P.

PR 14-MAY-1999; 99US-0134218P.

PR 14-MAY-1999; 99US-0134219P.

PR 14-MAY-1999; 99US-0134221P.

PR 14-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-0134768P.  
PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
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PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
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PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
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PR 22-JUN-1999; 99US-0139899P.  
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PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
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PR 16-JUL-1999; 99US-0144085P.  
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PR 19-JUL-1999; 99US-0144325P.  
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PR 26-JUL-1999; 99US-0145276P.  
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PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
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PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.  
PR 09-AUG-1999; 99US-0147493P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
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PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.

PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.  
  
Query Match 73.9%; Score 17; DB 3; Length 40;  
Best Local Similarity 40.0%; Pred. No. 1e+04;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 FXXXW 5  
|  
Db 33 FSSAW 37  
  
RESULT 37  
AAM37764  
ID AAM37764 standard; protein; 40 AA.  
XX  
AC AAM37764;  
XX  
DT 17-OCT-2001 (first entry)  
XX  
DE Peptide #11801 encoded by probe for measuring placental gene expression.  
XX  
KW Probe; microarray; human; placenta; antenatal diagnosis;  
KW genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200157272-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US0000663.  
XX  
PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
DR WPI; 2001-488897/53.  
XX  
PT Human genome-derived single exon nucleic acid probes useful for analyzing  
PT gene expression in human placenta.  
XX  
PS Claim 27; SEQ ID NO 38033; 654pp; English.  
XX  
CC The present invention relates to single exon nucleic acid probes (SENP;  
CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one  
CC such probe. The probes are useful for producing a microarray for  
CC predicting, measuring and displaying gene expression in samples derived  
CC from human placenta. The probes are useful for antenatal diagnosis of  
CC human genetic disorders  
XX  
SQ Sequence 40 AA;  
  
Query Match 73.9%; Score 17; DB 4; Length 40;  
Best Local Similarity 40.0%; Pred. No. 1e+04;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 FXXXW 5  
|

Db	23	FTSSW 27	8	FAATW 12	Db
RESULT 38					RESULT 39
AAB64755					AAO06835
ID AAB64755 standard; protein; 40 AA.					ID AAO06835 standard; protein; 40 AA.
XX					XX
AC AAB64755;					AC AAO06835;
XX					XX
DT 23-MAR-2001 (first entry)					DT 06-NOV-2001 (first entry)
XX					XX
DE Human secreted protein sequence encoded by gene 36 SEQ ID NO:149.					DE Human polypeptide SEQ ID NO 20727.
XX					XX
KW Human; secreted protein; diagnosis; cytostatic; cardiant; antiinflammatory; anti-rheumatic;					KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW antiarthritic; dermatological; cardiant; antiinflammatory; anti-ulcer;					KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW gastrointestinal; solid tumour; rheumatoid arthritis; psoriasis;					KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW diabetic retinopathy; myocardial angiogenesis; Crohn's disease; ulcer.					KW nervous system disorders; arthritis; inflammation.
XX					XX
OS Homo sapiens.					OS Homo sapiens.
XX					XX
PN WO200077237-A1.					PN WO200164835-A2.
XX					XX
PD 21-DEC-2000.					PD 07-SEP-2001.
XX					XX
PF 01-JUN-2000; 2000WO-US014928.					PF 26-FEB-2001; 2001WO-US004927.
XX					XX
PR 11-JUN-1999; 99US-0138633P.					PR 28-FEB-2000; 2000US-00515126.
XX					PR 18-MAY-2000; 2000US-00577409.
PA (HUMA-) HUMAN GENOME SCI INC.					XX
PA (ROSE/) ROSEN C A.					PA (HYSE-) HYSEQ INC.
XX					XX
PI Rosen CA, Ruben SM, Komatsoulis GA;					PI Tang YT, Liu C, Drmanac RT;
XX					XX
DR WPI; 2001-071280/08.					DR WPI; 2001-514838/56.
XX					DR N-PSDB; AAI86766.
PT Nucleic acids encoding 49 human secreted polypeptides, useful for					XX
PT preventing, diagnosing and/or treating diseases such as tumors,					PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT rheumatoid arthritis, psoriasis and diabetic retinopathy.					PT and treating e.g. leukemia, inflammation and immune disorders.
XX					XX
PS Disclosure; Page 510; 520pp; English.					PS Claim 20; SEQ ID NO 20727; 1399pp + Sequence Listing; English.
XX					XX
CC The polynucleotide sequences given in AAF33037 to AAF33085 encode the					CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC human secreted proteins given in AAB64666 to AAB64714. AAB64715 to					CC the encoded proteins (AAO0010-AAO13910) that exhibit activity elating to
CC AAB64771 represent human secreted polypeptide sequences and proteins					CC cytokine, cell proliferation or cell differentiation or which may induce
CC homologous to them, which are given in the exemplification of the present					CC production of other cytokines in other cell populations. The
CC invention. Human secreted proteins have activities based on the tissues					CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC and cells the genes are expressed in. Examples of activities include:					CC peptide therapy. The polypeptides have various cytokine-like activities,
CC cytostatic; anti-rheumatic; antiarthritic; dermatological; cardiant;					CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC antiinflammatory; gastrointestinal; and anti-ulcer. The polynucleotides					CC activity, tissue growth factor activity, immunomodulatory activity and
CC and polypeptides can be used in the prevention, treatment and diagnosis					CC activin/inhibin activity and may be useful in the diagnosis and/or
CC of diseases associated with inappropriate polypeptide expression.					CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC Disorders that may be treated or prevented include solid tumours,					CC inflammation. Note: The sequence data for this patent did not form part
CC rheumatoid arthritis, psoriasis, diabetic retinopathy, myocardial					CC of the printed specification, but was obtained in electronic format
CC angiogenesis, Crohn's disease and ulcers. The polynucleotides and their					CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
CC complementary sequences may also be used as DNA probes in diagnostic					XX
CC assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate					SQ Sequence 40 AA;
CC the presence of similar nucleic acid sequences in samples, and therefore					
CC which patients may be in need of restorative therapy. The polypeptides					Query Match 73.9%; Score 17; DB 4; Length 40;
CC may also be used as antigens in the production of antibodies against the					Best Local Similarity 40.0%; Pred. No. 1e+04;
CC polypeptide and in assays to identify modulators (agonists and					Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
CC antagonists) of polypeptide expression and activity. The anti-polypeptide					
CC antibodies and antagonists may also be used to down regulate expression					QY 1 FXXXW 5
CC and activity. AAF33028 to AAF33036 and AAB64665 represent sequences used					Db 20 FATTW 24
CC in the exemplification of the present invention					
XX					RESULT 40
SQ Sequence 40 AA;					AAM64830
					ID AAM64830 standard; protein; 40 AA.
					XX
					AC AAM64830;
					XX
					DT 05-NOV-2001 (first entry)

XX DE Human brain expressed single exon probe encoded protein SEQ ID NO: 36935.  
XX DE Human; brain expressed exon; gene expression analysis; probe; microarray;  
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.  
XX OS Homo sapiens.  
XX PN WO200157275-A2.  
XX PD 09-AUG-2001.  
XX PF 30-JAN-2001; 2001WO-US000667.  
XX PR 04-FEB-2000; 2000US-0180312P.  
PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
PA Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-483446/52.  
XX Single exon nucleic acid probes for analyzing gene expression in human  
PT brains.  
XX Example 4; SEQ ID NO 36935; 650pp + Sequence Listing; English.  
XX The present invention provides a number of single exon nucleic acid  
CC probes which are derived from genomic sequences expressed in the human  
CC brain. They can be used to measure gene expression in brain cell samples,  
CC which may enable the diagnosis and improved treatment of nervous system  
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
CC epilepsy and cancers. The present sequence is a protein encoded by one of  
CC the probes of the invention  
XX SQ Sequence 40 AA;

Query Match 73.9%; Score 17; DB 4; Length 40;  
Best Local Similarity 40.0%; Pred. No. 1e+04;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FXXXW 5  
Db 23 FTSSW 27

Search completed: October 18, 2005, 15:26:10  
Job time : 116.529 secs

us-09-214-371-10.ram

GenCore version 5.1.6

OM protein - protein search, using sw model

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Run on:      October 18, 2005, 15:22:12 ; Search time 351.059 Seconds
              (without alignments)
              ;      26.617 Million cell updates/sec
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Title: US-09-214-371-10  
Perfect score: 23  
Sequence: 1 FXXXXXXX 8

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing:	Minimum Match	0%
	Maximum Match	100%
	Listing first	100

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4: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US082_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US083_COMB.pep:*
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37: /cgn2_6/ptodata/1/paa/US60_COMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES



**us-09-214-371-10.max.ram**

OM protein - protein search, using sw model

Run on: October 18, 2005, 15:50:44 ; Search time 314.353 Seconds  
(without alignments) 29.725 Million cell updates/sec

**Title:** US-09-214-371-10  
**Perfect score:** 23  
**Sequence:** 1 FXXXWXXX 8

Scoring table: BLOSUM62

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters:	1237731
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Minimum DB seq length: 0
Maximum DB seq length: 20
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000

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Database : Pending_Patents_AA_Main:*
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4: /cgn2_6/ptodata/1/paa/us08_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/us081_COMB.pep:*
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11: /cgn2_6/ptodata/1/paa/us087_COMB.pep:*
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37: /cgn2_6/ptodata/1/paa/us60_COMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:55:09 ; Search time 49.8824 Seconds  
(without alignments)  
29.915 Million cell updates/sec

Title: US-09-214-371-10  
Perfect score: 23  
Sequence: 1 FXXXXXXX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 850841 seqs, 186528192 residues

Total number of hits satisfying chosen parameters: 171822

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Pending Patents AA New:\*  
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8: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Length	DB	ID
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 19, 2005, 15:41:40 ; Search time 312.471 Seconds  
(without alignments)  
29.904 Million cell updates/sec

Title: US-09-214-371-10  
Perfect score: 23  
Sequence: 1 FXXWXXX 8

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 1237731

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Pending Patents AA Main.\*  
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33: /cgn2\_6/ptodata/1/paa/US107\_COMB.pep.\*  
34: /cgn2\_6/ptodata/1/paa/US108\_COMB.pep.\*  
35: /cgn2\_6/ptodata/1/paa/US109\_COMB.pep.\*  
36: /cgn2\_6/ptodata/1/paa/US110\_COMB.pep.\*  
37: /cgn2\_6/ptodata/1/paa/US60\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run On: October 19, 2005, 15:33:09 ; Search time 50.8235 Seconds  
(without alignments)  
31.758 Million cell updates/sec

Title: US-09-214-371-10  
Perfect score: 23  
Sequence: 1 FXXXWXXX 8

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 897115 seqs, 201758920 residues

Total number of hits satisfying chosen parameters: 172224

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Pending Patents AA New:\*

1:	/cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
2:	/cgn2_6/ptodata/1/paa/US05_NEW_COMB.pep:*
3:	/cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4:	/cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5:	/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6:	/cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7:	/cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep:*
8:	/cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result	Query		
No.	Score	Match Length DB ID	Description
-----			





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 19, 2005, 15:41:40 ; Search time 351.529 Seconds  
(without alignments)  
29.904 Million cell updates/sec

Title: US-09-214-371-11  
Perfect score: 24  
Sequence: 1 XPXXXWXXX 9

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues  
Total number of hits satisfying chosen parameters: 1237731

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Pending Patents\_AA Main:  
1: /cgn2\_6/ptodata/1/paa/PCTUS\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/paa/US06\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/paa/US07\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/paa/US080\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/paa/US081\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/paa/US082\_COMB.pep:\*  
7: /cgn2\_6/ptodata/1/paa/US083\_COMB.pep:\*  
8: /cgn2\_6/ptodata/1/paa/US084\_COMB.pep:\*  
9: /cgn2\_6/ptodata/1/paa/US085\_COMB.pep:\*  
10: /cgn2\_6/ptodata/1/paa/US086\_COMB.pep:\*  
11: /cgn2\_6/ptodata/1/paa/US087\_COMB.pep:\*  
12: /cgn2\_6/ptodata/1/paa/US088\_COMB.pep:\*  
13: /cgn2\_6/ptodata/1/paa/US089\_COMB.pep:\*  
14: /cgn2\_6/ptodata/1/paa/US090\_COMB.pep:\*  
15: /cgn2\_6/ptodata/1/paa/US091\_COMB.pep:\*  
16: /cgn2\_6/ptodata/1/paa/US092\_COMB.pep:\*  
17: /cgn2\_6/ptodata/1/paa/US093\_COMB.pep:\*  
18: /cgn2\_6/ptodata/1/paa/US094\_COMB.pep:\*  
19: /cgn2\_6/ptodata/1/paa/US095\_COMB.pep:\*  
20: /cgn2\_6/ptodata/1/paa/US096\_COMB.pep:\*  
21: /cgn2\_6/ptodata/1/paa/US097A\_COMB.pep:\*  
22: /cgn2\_6/ptodata/1/paa/US097B\_COMB.pep:\*  
23: /cgn2\_6/ptodata/1/paa/US098\_COMB.pep:\*  
24: /cgn2\_6/ptodata/1/paa/US099A\_COMB.pep:\*  
25: /cgn2\_6/ptodata/1/paa/US099B\_COMB.pep:\*  
26: /cgn2\_6/ptodata/1/paa/US100\_COMB.pep:\*  
27: /cgn2\_6/ptodata/1/paa/US101\_COMB.pep:\*  
28: /cgn2\_6/ptodata/1/paa/US102\_COMB.pep:\*  
29: /cgn2\_6/ptodata/1/paa/US103\_COMB.pep:\*  
30: /cgn2\_6/ptodata/1/paa/US104\_COMB.pep:\*  
31: /cgn2\_6/ptodata/1/paa/US105\_COMB.pep:\*  
32: /cgn2\_6/ptodata/1/paa/US106\_COMB.pep:\*  
33: /cgn2\_6/ptodata/1/paa/US107\_COMB.pep:\*  
34: /cgn2\_6/ptodata/1/paa/US108\_COMB.pep:\*  
35: /cgn2\_6/ptodata/1/paa/US109\_COMB.pep:\*  
36: /cgn2\_6/ptodata/1/paa/US110\_COMB.pep:\*  
37: /cgn2\_6/ptodata/1/paa/US60\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 19, 2005, 15:33:09 ; Search time 57.1765 Seconds  
(without alignments)  
31.758 Million cell updates/sec

Title: US-09-214-371-11  
Perfect score: 24  
Sequence: 1 XFXXXWXXX 9

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 897115 seqs, 201758920 residues

Total number of hits satisfying chosen parameters: 172224

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Pending Patents AA New: \*  
1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep:\*  
7: /cgn2\_6/ptodata/1/paa/US11\_NEW\_COMB.pep:\*  
8: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES			
Result	Score	Query	Description
No.	Match	Length	ID
-----			



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:22:12 ; Search time 394.941 Seconds  
(without alignments)  
26.617 Million cell updates/sec

Title: US-09-214-371-11  
Perfect score: 24  
Sequence: 1 XFXXXWXXX 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 116806243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Pending Patents AA Main.\*  
1: /cgn2\_6/ptodata/1/paa/PCTUS\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/paa/US06\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/paa/US07\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/paa/US08\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/paa/US081\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/paa/US082\_COMB.pep.\*  
7: /cgn2\_6/ptodata/1/paa/US083\_COMB.pep.\*  
8: /cgn2\_6/ptodata/1/paa/US084\_COMB.pep.\*  
9: /cgn2\_6/ptodata/1/paa/US085\_COMB.pep.\*  
10: /cgn2\_6/ptodata/1/paa/US086\_COMB.pep.\*  
11: /cgn2\_6/ptodata/1/paa/US087\_COMB.pep.\*  
12: /cgn2\_6/ptodata/1/paa/US088\_COMB.pep.\*  
13: /cgn2\_6/ptodata/1/paa/US089\_COMB.pep.\*  
14: /cgn2\_6/ptodata/1/paa/US090\_COMB.pep.\*  
15: /cgn2\_6/ptodata/1/paa/US091\_COMB.pep.\*  
16: /cgn2\_6/ptodata/1/paa/US092\_COMB.pep.\*  
17: /cgn2\_6/ptodata/1/paa/US093\_COMB.pep.\*  
18: /cgn2\_6/ptodata/1/paa/US094\_COMB.pep.\*  
19: /cgn2\_6/ptodata/1/paa/US095\_COMB.pep.\*  
20: /cgn2\_6/ptodata/1/paa/US096\_COMB.pep.\*  
21: /cgn2\_6/ptodata/1/paa/US097A\_COMB.pep.\*  
22: /cgn2\_6/ptodata/1/paa/US097B\_COMB.pep.\*  
23: /cgn2\_6/ptodata/1/paa/US098\_COMB.pep.\*  
24: /cgn2\_6/ptodata/1/paa/US099A\_COMB.pep.\*  
25: /cgn2\_6/ptodata/1/paa/US099B\_COMB.pep.\*  
26: /cgn2\_6/ptodata/1/paa/US100\_COMB.pep.\*  
27: /cgn2\_6/ptodata/1/paa/US101\_COMB.pep.\*  
28: /cgn2\_6/ptodata/1/paa/US102\_COMB.pep.\*  
29: /cgn2\_6/ptodata/1/paa/US103\_COMB.pep.\*  
30: /cgn2\_6/ptodata/1/paa/US104\_COMB.pep.\*  
31: /cgn2\_6/ptodata/1/paa/US105\_COMB.pep.\*  
32: /cgn2\_6/ptodata/1/paa/US106\_COMB.pep.\*  
33: /cgn2\_6/ptodata/1/paa/US107\_COMB.pep.\*  
34: /cgn2\_6/ptodata/1/paa/US108\_COMB.pep.\*  
35: /cgn2\_6/ptodata/1/paa/US109\_COMB.pep.\*  
36: /cgn2\_6/ptodata/1/paa/US110\_COMB.pep.\*  
37: /cgn2\_6/ptodata/1/paa/US60\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:26:23 ; Search time 58.2353 Seconds  
(without alignments)  
28.827 Million cell updates/sec

Title: US-09-214-371-11  
Perfect score: 24  
Sequence: 1 XFXXXWXXX 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 850841 seqs, 186528192 residues

Total number of hits satisfying chosen parameters: 850841

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Pending Patents AA New.\*  
1: /cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB.pep.\*  
7: /cgn2\_6/ptodata/2/paa/US11\_NEW\_COMB.pep.\*  
8: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on:           October 18, 2005, 15:50:44 ; Search time 353.647 Seconds  
                  (without alignments)  
                  29.725 Million cell updates/sec

Title:           US-09-214-371-11  
Perfect score:   24  
Sequence:       1 XFXXWXXX 9

Scoring table:   BLOSUM62  
                  Gapop 10.0 , Gapext 0.5

Searched:       6959266 seqs, 116806243 residues

Total number of hits satisfying chosen parameters:       1237731

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
                  Maximum Match 100%  
                  Listing first 1000 summaries

Database :       Pending Patents\_AA\_Main:\*  
                  1: /cgn2\_6/ptodata/1/paa/PCTUS\_COMB.pep:\*  
                  2: /cgn2\_6/ptodata/1/paa/US06\_COMB.pep:\*  
                  3: /cgn2\_6/ptodata/1/paa/US07\_COMB.pep:\*  
                  4: /cgn2\_6/ptodata/1/paa/US080\_COMB.pep:\*  
                  5: /cgn2\_6/ptodata/1/paa/US081\_COMB.pep:\*  
                  6: /cgn2\_6/ptodata/1/paa/US082\_COMB.pep:\*  
                  7: /cgn2\_6/ptodata/1/paa/US083\_COMB.pep:\*  
                  8: /cgn2\_6/ptodata/1/paa/US084\_COMB.pep:\*  
                  9: /cgn2\_6/ptodata/1/paa/US085\_COMB.pep:\*  
                  10: /cgn2\_6/ptodata/1/paa/US086\_COMB.pep:\*  
                  11: /cgn2\_6/ptodata/1/paa/US087\_COMB.pep:\*  
                  12: /cgn2\_6/ptodata/1/paa/US088\_COMB.pep:\*  
                  13: /cgn2\_6/ptodata/1/paa/US089\_COMB.pep:\*  
                  14: /cgn2\_6/ptodata/1/paa/US090\_COMB.pep:\*  
                  15: /cgn2\_6/ptodata/1/paa/US091\_COMB.pep:\*  
                  16: /cgn2\_6/ptodata/1/paa/US092\_COMB.pep:\*  
                  17: /cgn2\_6/ptodata/1/paa/US093\_COMB.pep:\*  
                  18: /cgn2\_6/ptodata/1/paa/US094\_COMB.pep:\*  
                  19: /cgn2\_6/ptodata/1/paa/US095\_COMB.pep:\*  
                  20: /cgn2\_6/ptodata/1/paa/US096\_COMB.pep:\*  
                  21: /cgn2\_6/ptodata/1/paa/US097A\_COMB.pep:\*  
                  22: /cgn2\_6/ptodata/1/paa/US097B\_COMB.pep:\*  
                  23: /cgn2\_6/ptodata/1/paa/US098\_COMB.pep:\*  
                  24: /cgn2\_6/ptodata/1/paa/US099A\_COMB.pep:\*  
                  25: /cgn2\_6/ptodata/1/paa/US099B\_COMB.pep:\*  
                  26: /cgn2\_6/ptodata/1/paa/US100\_COMB.pep:\*  
                  27: /cgn2\_6/ptodata/1/paa/US101\_COMB.pep:\*  
                  28: /cgn2\_6/ptodata/1/paa/US102\_COMB.pep:\*  
                  29: /cgn2\_6/ptodata/1/paa/US103\_COMB.pep:\*  
                  30: /cgn2\_6/ptodata/1/paa/US104\_COMB.pep:\*  
                  31: /cgn2\_6/ptodata/1/paa/US105\_COMB.pep:\*  
                  32: /cgn2\_6/ptodata/1/paa/US106\_COMB.pep:\*  
                  33: /cgn2\_6/ptodata/1/paa/US107\_COMB.pep:\*  
                  34: /cgn2\_6/ptodata/1/paa/US108\_COMB.pep:\*  
                  35: /cgn2\_6/ptodata/1/paa/US109\_COMB.pep:\*  
                  36: /cgn2\_6/ptodata/1/paa/US110\_COMB.pep:\*  
                  37: /cgn2\_6/ptodata/1/paa/US60\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 18, 2005, 15:55:09 ; Search time 56.1176 Seconds  
(without alignments)  
29.915 Million cell updates/sec

Title: US-09-214-371-11  
Perfect score: 24  
Sequence: 1 XFXXXWXXX 9

Scoring table: BLOSUM62  
Gapop 10.0 ; Gapext 0.5

Searched: 850841 seqs, 186528192 residues

Total number of hits satisfying chosen parameters: 171822

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Pending Patents\_AA New:\*  
1: /cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB.pep.\*  
7: /cgn2\_6/ptodata/2/paa/US11\_NEW\_COMB.pep.\*  
8: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	70.8	9	7	US-11-222-021-6720 Sequence 6720, Ap
2	17	70.8	9	7	US-11-222-045-6023 Sequence 6023, Ap
3	17	70.8	14	5	US-09-749-280D-9233 Sequence 9233, Ap
4	16	66.7	6	6	US-10-945-751-97 Sequence 97, Appl
5	16	66.7	7	7	US-11-129-741-699 Sequence 699, App
6	16	66.7	8	6	US-10-945-751-71 Sequence 71, Appl
7	16	66.7	8	6	US-10-776-521B-215 Sequence 215, App
8	16	66.7	8	6	US-10-820-067A-239 Sequence 239, App
9	16	66.7	8	6	US-10-820-067A-243 Sequence 243, App
10	16	66.7	8	6	US-10-820-067A-725 Sequence 725, App
11	16	66.7	9	1	PCT-US04-27792A-35 Sequence 35, Appl
12	16	66.7	9	1	PCT-US04-33241-18 Sequence 18, Appl
13	16	66.7	9	6	US-10-817-970-2854 Sequence 2854, Ap
14	16	66.7	9	6	US-10-817-970-3154 Sequence 3154, Ap
15	16	66.7	9	6	US-10-817-970-14185 Sequence 14185, A
16	16	66.7	9	6	US-10-817-970-14186 Sequence 14186, A
17	16	66.7	9	6	US-10-817-970-14188 Sequence 14188, A
18	16	66.7	9	6	US-10-817-970-14189 Sequence 14189, A
19	16	66.7	9	6	US-10-817-970-14419 Sequence 14419, A
20	16	66.7	9	6	US-10-010-748A-797 Sequence 797, App
21	16	66.7	9	6	US-10-010-748A-817 Sequence 817, App
22	16	66.7	9	7	US-11-010-748A-797 Sequence 797, App
23	16	66.7	9	7	US-11-010-748A-817 Sequence 817, App
24	16	66.7	9	7	US-11-027-670-768 Sequence 768, App
25	16	66.7	9	7	US-11-027-670-815 Sequence 815, App



us-09-214-371-10.rapn

OM protein - protein search, using sw model

Title: US-09-214-371-10  
 Perfect score: 23  
 Sequence: 1 FXXXWXXX 8

Searched: 850841 seqs, 186528192 residues

```
Minimum DB seq length: 0
Maximum DB seq length: 20
```

Database : Pending Patents AA New: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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